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**BIOSEMIÓTICA RELACIONAL**

**UNA PROPUESTA DE INTEGRACIÓN DE LA BIOLOGÍA  
RELACIONAL DE ROSEN Y LA SEMIOSIS DE PEIRCE**

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**PROGRAMA DE DOCTORADO EN FILOSOFÍA**

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A Montse.

Como tantas otras cosas, no habría podido hacer esta tesis sin su complicidad incondicional.

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Los conceptos de la biología de códigos y mis discrepancias con este marco teórico sobre la imposibilidad de construir una biosemiótica científica del organismo que se apoye en la semiosis de Peirce fueron elementos clave para concretar el objeto de mi investigación. Le agradezco también al Dr. Barbieri su interés por mi trabajo y su trato amable y cercano.

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## INTRODUCCIÓN

Esta tesis es una contribución a la construcción de un marco unificado para la definición y el estudio de la vida que integra las aportaciones de la biología relacional de Robert Rosen y la semiótica de Charles Sanders Peirce.

La teoría de los signos de Peirce es fundamental para el trabajo de este autor sobre la lógica y para sus estudios científicos y constituye una alternativa filosófica al dualismo cartesiano. Según Peirce, para desarrollar una teoría de la lógica y para estudiar la naturaleza se deben considerar un tipo de acciones que no pueden caracterizarse como acciones físicas ordinarias: las acciones semióticas. La semiosis de Peirce es un estudio lógico y científico de las acciones dinámicas de los signos en la naturaleza; acciones en las que un signo, un objeto y un *interpretant* se unen en una relación triádica que no puede reducirse a relaciones diádicas.

Así, la biosemiótica, disciplina desarrollada a partir de la aplicación de la semiótica a la biología, parte de la idea de que los signos y significados son componentes fundamentales de la vida, y su propósito es mostrar cómo la semiosis nos permite explicar los seres vivos y diferenciarlos del mundo inanimado. Las principales líneas de investigación en biosemiótica se agrupan en la biosemiótica peirceana, disciplina creada por Thomas Sebeok a partir de la semiosis de Peirce y los estudios de Jacob von Uexküll sobre la comunicación animal, y posteriormente combinada con diversas influencias de la teoría general de sistemas. Otras propuestas también sostienen la importancia de los signos en la explicación de la vida, pero niegan la posibilidad de aplicar la semiosis de Peirce al nivel del organismo. Entre estas propuestas, cabe destacar la biología de códigos de Marcello Barbieri y la protosemiosis de Alexei Sharov y Tommi Vehkavaara.

Por su parte, la biología relacional analiza los organismos como sistemas formados por componentes, definiendo un componente como una parte del sistema al que se le puede asignar una función, y propone poner el foco en las relaciones entre los componentes de un organismo antes que en los componentes mismos. Robert Rosen aborda las causas que explican los fenómenos biológicos siguiendo la clasificación aristotélica, reintroduciendo la causa final en la ciencia, como ya habían hecho en otros contextos Charles Darwin y el mismo Peirce, y definiendo un ser vivo como un sistema natural cerrado bajo causación eficiente. De acuerdo con la biología relacional de Rosen, el cierre establece entre las partes de un sistema natural unas relaciones que adquieren realidad diferenciada con características propias, más allá de las de las partes que participan en ellas, convirtiendo dichas partes en los componentes de un organismo que realizan funciones biológicas que surgen al realizarse el cierre.

Este trabajo de investigación se ha estructurado en tres partes, cuyos resultados han dado lugar a tres artículos. En el primero, "A Critique of Barbieri's Code Biology Through Rosen's Relational Biology: Reconciling Barbieri's Biosemiotics with Peircean

Biosemiotics”, publicado en *Biological Theory* en julio de 2018, se analiza la biología de códigos con las herramientas aportadas por la biología relacional. Se argumenta que el rechazo de Barbieri a la biosemiótica peirceana por considerarla no científica se basa en una concepción limitada de la ciencia y en una comprensión incorrecta de la biosemiótica peirceana. Se concluye que, aunque la biología de códigos constituye una biosemiótica que proporciona las herramientas teóricas adecuadas para el desarrollo de la investigación biológica, es posible también desarrollar biosemióticas científicas peirceanas. Además, se muestra que la biología de Rosen también admite una lectura biosemiótica.

El segundo artículo, “An Integrated Account of Rosen’s Relational Biology and Peirce’s Semiosis. Part I: Components and Signs, Final Cause and Interpretation”, publicado en *Biosemiotics* en septiembre de 2021, es una propuesta teórica para una integración de la biología relacional y la semiosis de Peirce. En él se sientan las bases de una biosemiótica basada en la biología relacional (una biosemiótica relacional) en la que se naturalizan los conceptos de relación semiótica, signo, significado, acción semiótica e interpretación. Se define también un método para la identificación y el análisis de signos en un organismo, así como para su clasificación de acuerdo con las categorías definidas por Peirce, basado en la relación existente entre un signo y su objeto, en iconos, índices y símbolos. Por otra parte, se complementa la teoría de Rosen con una lectura biosemiótica.

En el tercer artículo, “An Integrated Account of Rosen’s Relational Biology and Peirce’s Semiosis. Part II: Analysis of Protein Synthesis”, publicado en *Biosemiotics* en julio de 2021, se aplican los conceptos y el método propuestos en el artículo anterior al análisis de la síntesis de proteínas. Esta aplicación concreta demuestra la consistencia teórica y la utilidad práctica de integrar las teorías de Rosen y Peirce. Se identifican signos al nivel celular, distinguiendo un conjunto de símbolos en el proceso de traducción y otro de índices en la regulación de la transcripción. Finalmente, se hace un análisis crítico de la biología de códigos y la protosemiosis, y se reafirma la posibilidad de explicar los signos en un organismo con la semiosis de Peirce.

De este modo, esta investigación ofrece resultados contrastados y publicados que muestran que, en contra de lo defendido por muchos teóricos, es posible integrar en un mismo marco teórico los proyectos de la semiótica peirceana y de la biología relacional, dando lugar a una biosemiótica capaz de dar cuenta de casos biológicos complejos concretos, como muestra el análisis de la síntesis de proteínas que se presenta.



## HIPÓTESIS Y OBJETIVOS

La biología relacional y la biosemiótica comparten la afirmación de que la vida no puede explicarse solo con las leyes que se aplican al mundo inanimado. Ambas teorías sostienen que es necesario extender las leyes heredadas de la física para abordar un estudio científico de la biología.

Sin embargo, estos dos programas de investigación son, a primera vista, muy diferentes. La biología relacional, en lugar de intentar explicar los fenómenos biológicos en sí, aporta un enfoque matemático que se centra en la búsqueda de un principio que gobierne la organización del sistema natural que corresponde a un organismo. Por su parte, la biosemiótica parte de la integración de biología y semiótica, y sostiene que lo que diferencia a los seres vivos del mundo inanimado es la utilización de signos: vida y semiosis son coextensivas.

Desde la biología “estándar” se critican ambos proyectos por la dificultad de encontrarles aplicación en la práctica científica. Para algunos, la biosemiótica debe incluso considerarse una disciplina no científica, pues sería una extensión no justificada del ámbito de aplicación de la semiótica, disciplina apropiada en todo caso para disciplinas como la lingüística o las ciencias sociales.

Las hipótesis de partida de esta tesis son las siguientes: (i) tanto la biología relacional como la biosemiótica son propuestas válidas para fundamentar una nueva ciencia de la biología que no se oponga a los principios y métodos comúnmente aceptados, sino que los complemente; (ii) el carácter científico de la biosemiótica puede sustentarse en la biología relacional; y (iii) ambas teorías pueden integrarse para crear un marco teórico para el estudio de la biología.

Este trabajo tiene como objetivo desarrollar un marco teórico para el estudio científico de la biología integrando la semiosis de Peirce y la biología relacional de Rosen. Este objetivo general se descompone en otros más concretos: la reintroducción de la causa final en la ciencia; la naturalización de los conceptos de relación semiótica, signo, significado, acción semiótica e interpretación; y la definición de un método de identificación y análisis de signos en un organismo.

## MARCO TEÓRICO

El trabajo que se presenta se inscribe en el marco de la fundamentación de la biología y, por tanto, concierne tanto a la biología teórica como la filosofía de la biología.

Se sustenta principalmente en la biología relacional de Robert Rosen y en la teoría de los signos de Charles S. Peirce, aunque las aportaciones de muchos otros autores han sido también imprescindibles, como se indica en las referencias de los tres artículos y se resume al final.

D. Favareau proporciona una revisión general de la biosemiótica, recopilando y comentando artículos escogidos de los principales autores de este campo. Se destacan a continuación las propuestas que han sido más relevantes para el trabajo que se presenta y que han servido de punto de partida para una ampliación de la investigación con la lectura de otros artículos. Comienza con los precursores de Thomas A. Sebeok, creador de la disciplina, destacando el propio Peirce y J. von Uexküll. Recoge después trabajos de dicho autor y otros encuadrables en el mismo proyecto de biosemiótica, como la fitosemiosis de M. Krampen, la endosemiosis de T. von Uexküll, W. Geigges y J. Herrmann, y la semiosis del sistema inmunitario de G. Prodi. En un tercer bloque, se agrupan aproximaciones independientes a la biosemiótica, entre los que debe citarse, al menos a K. Kull, G. Bateson, H. H. Pattee y F. Deacon. De parte final, dedicada a “la interdisciplina contemporánea de la biosemiótica”, cabe destacar los trabajos de S. Brier, J. Hoffmeyer y M. Barbieri.

Tanto Hoffmeyer como Barbieri han sido pilares imprescindibles para este trabajo. El primero como representante especialmente relevante de la biosemiótica de los últimos años y el segundo como principal crítico de la posibilidad de una biosemiótica peirceana científica. El trabajo de Barbieri debe destacarse por la importancia de sus propuestas, que, aunque se critican en el primer y tercer artículo, aportan un método para introducir los signos en el trabajo científico.

La exposición de Thomas L. Short de la teoría de los signos de Peirce ha sido de especial utilidad, especialmente para la explicación del papel de la causa final en la semiosis y en la ciencia en general, y en la introducción de una definición del concepto de interpretación que en esta tesis se ha extendido al nivel del organismo.

## **PUBLICACIONES INCLUIDAS EN LA TESIS**

Las publicaciones que constituyen la tesis doctoral son las que se indican a continuación y se incluyen en este documento.

**A Critique of Barbieri's Code Biology Through Rosen's Relational Biology: Reconciling Barbieri's Biosemiotics with Peircean Biosemiotics**

Biological Theory 2018

<https://doi.org/10.1007/s13752-018-0302-1>

**An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part I: Components and Signs, Final Cause and Interpretation**

Biosemiotics 2021

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**An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part II: Analysis of Protein Synthesis**

Biosemiotics 2021

<https://doi.org/10.1007/s12304-021-09438-8>



# A Critique of Barbieri's Code Biology Through Rosen's Relational Biology: Reconciling Barbieri's Biosemiotics with Peircean Biosemiotics

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## Abstract

Biosemiotics argues that “sign” and “meaning” are two essential concepts for the explanation of life. Peircean biosemiotics, founded by Tomas Sebeok from Peirce's semiotics and Jacob von Uexküll's studies on animal communication, today makes up the mainstream of this discipline. Marcello Barbieri has developed an alternative account of meaning in biology based on the concept of code. Barbieri rejects Peircean biosemiotics on the grounds that this discipline opens the door to non-scientific approaches to biology through its use of the concept of “interpretation.” In this article, it is noted that Barbieri does not adequately distinguish among Peirce's semiotics, Peircean biosemiotics, and “interpretation-based” biosemiotics. Two key arguments of Barbieri are criticized: his limited view of science and his rejection of “interpretation-based” biosemiotics. My argument is based on tools taken from a different approach: Robert Rosen's relational biology. Instead of “signs” and “meanings,” the study begins in this case from the “components” and “functions” of the organism. Rosen pursues a new definition of a law of nature, introduces the anticipatory nature of organisms, and defines the living being as a system closed to efficient cause. It is shown that Code Biosemiotics and Peircean biosemiotics can share a common field of study. Additionally, some proposals are suggested to carry out a reading of Rosen's biology as a biosemiotic theory.

**Keywords** Anticipatory system · Biosemiotics · Code · Interpretation · (M, R)-system · Semiosis

## Introduction

Semiotics studies the systems of signs, their production and functioning. Charles Sanders Peirce (1931–1936) argued that semiosis<sup>1</sup> requires a triadic relationship among a sign, its object, and its interpretant.<sup>2</sup>

Biosemiotics is the union of biology and semiotics. It starts with the idea that signs and meanings are fundamental components of life, and its purpose is to show how semiosis allows us to explain living beings and to differentiate them from the inanimate world. As some contemporary authors claim:

Signs, not molecules, are the basic units in the study of life. (Hoffmeyer 1997, p. 940)<sup>3</sup>

Sign science and life science are coextensive.... semiotics is biology and biology is semiotics. (Kull 2001, p. 3)

The main lines of research in biosemiotics are grouped in Peircean biosemiotics, a discipline created by Thomas Sebeok from Peirce's semiotics and Jacob von Uexküll's studies on animal communication, and later combined with diverse influences from general systems theory.

Marcelo Barbieri, throughout his long career, has developed a theoretical framework that also focuses on the role of signs and meanings in the explanation of biology. However, Barbieri's biosemiotics has developed outside the mainstream, leaning on the concept of code. After a stage

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<sup>1</sup> The term “semiosis” describes the process of producing and responding to signs. Semiotics is the study of semiosis.

<sup>2</sup> Peirce writes: “I define a sign as anything which is so determined by something else, called its Object, and so determines an effect upon a person, which effect I call its interpretant, that the later is thereby mediately determined by the former” (1998, p. 478).

<sup>3</sup> This is the first of the eight theses proposed by Hoffmeyer (1997). A commentary on Hoffmeyer's theses can be found in Emmeche et al. (2002).

of collaboration with other schools, Barbieri departed from the biosemiotics field, considering that Peircean biosemiotics opens the door to nonscientific approaches through the concept of interpretation.

This article shows that Barbieri's rejection of Peircean biosemiotics is based on: (1) a limited conception of science; and (2) an incorrect understanding of Peircean biosemiotics, which misunderstands the scope of application of Peirce's semiotics and does not take into account the rest of the theories on which Peircean biosemiotics is based. Our goal is to show how Peircean biosemiotics and Barbieri's Code Biology can be part of a common field.

Barbieri's work is studied with tools taken from Robert Rosen's relational biology. This author has been chosen for three reasons, in addition to the solidity and beauty<sup>4</sup> of his work. First, it provides a concept of science that allows Barbieri's identification of science with mechanism to be overcome. Second, Rosen's biology can be seen as a basis for Peircean biosemiotics and, therefore, allows for a better understanding of the concepts of that discipline. And finally, by relying on an author who is alien to the discussions of biosemiotic schools, the problem can be analyzed with a novel perspective.

To understand Barbieri's arguments, it is first necessary to briefly state the basic concepts of Peirce's semiotics and Peircean biosemiotics. This is the first section.

In the second section, Barbieri's framework for the study of biology is laid out. His proposals of Code Biosemiotics and his criticism of interpretation-based biosemiotics (which Barbieri identifies with Peircean biosemiotics) are discussed.

The third section discusses the development of Rosen's relational biology that leads him to the concept of anticipatory systems, and the (M, R)-system as a model of organismic organizations. Rosen characterizes living entities as systems that instantiate closure to efficient cause.

These first three sections put together for the reader the necessary elements of the theories to be analyzed. They explain that there are different approaches and objectives, but also shared concepts (that are accepted or rejected, with the same or different meaning), and imply by themselves a first comparison.

In the fourth section, two key proposals of Code Biology are criticized with arguments taken from Rosen's relational biology. The relationship between science and mechanism is discussed, and Barbieri's critique of the concept of interpretation (and with it his rejection of Peircean biosemiotics) is analyzed.

In section five, as an additional result of the research carried out, some lines of a study of Rosen's biology as a

biosemiotic theory compatible with Code Biology and Peircean biology are sketched.

It is concluded that: (1) Code Biology provides the adequate theoretical tools for the development of biological research; (2) it is possible to develop other scientific biosemiotics within the framework of Peircean biosemiotics; (3) Code Biosemiotics and Peircean biosemiotics, despite their different approaches, can be seen as a common framework for biology; and (4) Rosen's biology can also be characterized as a type of biosemiotics.

## Peirce's Semiotics and Peircean Biosemiotics

### Peirce's Semiotics

Peirce's theory of signs is central to his work on logic and his scientific studies, and constitutes a philosophical alternative to Cartesian dualism.

In Peirce's words:

It is important to understand what I mean by semiosis. All dynamical action, or action of brute force, physical or psychical, either takes place between two subjects (whether they react equally upon each other, or one is agent and the other patient, entirely or partially) or at any rate is a resultant of such actions between pairs. But by "semiosis" I mean, on the contrary, an action, or influence, which is, or involves, a cooperation of three subjects, such as a sign, its object, and its interpretant, this tri-relative influence not being in any way resolvable into actions between pairs... and my definition confers on anything that so acts the title of a "sign." (Peirce 1931–1936, vol. 5, p. 484)

Important ideas can be highlighted from the previous quotation. First, to develop a theory of logic and to study nature, a type of actions that cannot be characterized as ordinary physical actions must also have been considered: *semiotic actions*. Peirce's semiotics is a logical and scientific study of dynamic sign action in nature. Second, a semiotic action requires a three-factor relation, a triad. Third, Peirce introduces the *interpretant*, the most distinctive feature of his account.

As Atkin<sup>5</sup> points out, an interpretant should be understood as an interpretive process in a receptive system, an effect upon someone, the understanding an agent reaches of some sign/object relation, the translation or development of the original sign. The meaning of a sign is manifest in the

<sup>4</sup> Robert Rosen was also a physicist and mathematician, and in these disciplines the beauty of the theories is a criterion that counts.

<sup>5</sup> Atkin (2013) provides an interesting overview of Peirce's theory of signs.

interpretation that the interpretant generates in sign users. The three components of the triad are closely related:

For Peirce, then, any instance of signification contains a sign-vehicle,<sup>6</sup> an object and interpretant. Moreover, the object determines the sign by placing constraints which any sign must meet if it is to signify the object. Consequently, the sign signifies its object only in virtue of some of its features. Additionally, the sign determines an interpretant by focusing our understanding on certain features of the signifying relation between sign and object. (Atkin 2013, Sect. 1.3)

### From Zoosemiotics to Biosemiotics

Thomas Sebeok (1963, 1972) extended the communication based on signs, characteristic of human beings, to the animal world, giving rise to *zoosemiotics*. His work had a key antecedent in the evidence of semiosis in the animal world that Jacob von Uexküll (1928) had presented much earlier. Von Uexküll's main proposal, the *unwelt*, is fundamentally a semiotic or biosemiotic concept. The *unwelt* is the representation of the environment inside an animal. The organism interacts with its environment in terms of how it perceives it. From this communication, the environment induces changes in the organism, and the organism modifies the environment.

Combining von Uexküll's *unwelt* and Peirce's semiotics, Sebeok founded biosemiotics as a new paradigm for all biology:

Because there can be no semiosis without interpretability—surely life's cardinal propensity—semiosis presupposes the axiomatic identity of the semiosphere with the biosphere. (Sebeok 2001, p. 68)

### Peircean Biosemiotics

As Søren Brier<sup>7</sup> explains:

Peircean biosemiotics is based on Peirce's theory of mind as a basic part of reality, (in Firstness) existing in the material aspect of reality, (in Secondness) as the "inner aspect of matter" (hylozoism) manifesting itself as awareness and experience in animals, and finally as consciousness in humans. Combining this with a general systems theory of emergence, self-organization and closure/autopoiesis, it forms an explicit theory of how the inner world of an organism is constituted and,

therefore, how first-person views are possible and just as real as matter. (Brier 2008, p. 40)

Following the path initiated by Sebeok, various scholars have developed their proposals within the framework of Peircean biosemiotics, especially in the Copenhagen and Tartu schools of biosemiotics, particularly Jesper Hoffmeyer, Claus Emmeche, Frederik Stjernfelt, Søren Brier, and Kalevi Kull. All of them share a common paradigm for the study of biology, although they differ in the weight that the different theories that have shaped Peircean biosemiotics have in their proposals, as shown in the following examples. First:

The theories of Heinz von Foerster and Humberto Maturana & Francisco Varela have had significant influence on the development of the Copenhagen school of biosemiotics. This school focuses mainly on a new interpretation of biology and life as having an important communicative aspect to their organization. They look at the basically biological aspect of biosemiotics especially as endosemiotics, and its significance for understanding ecological and hereditary relations in a non-reductionistic evolutionary view; it opposes views like Richard Dawkins' theory of selfish genes. (Brier 2008, pp. 47–48)

Second, even belonging to the same school, Hoffmeyer and Brier differ when analyzing different classes of biosemiotics:

Thus Hoffmeyer sees unity on the ontological level including the consequences of an evolutionary view, as Peirce does, but qualitative differences on the epistemological level because the semiotic freedom<sup>8</sup> changes radically when we move into the level of symbol use in language.... Agreeing with Hoffmeyer on these points I (Brier) still think that that there are also important epistemological continuities between the zoosemiotic and the anthroposemiotics levels in the form of the understanding of knowledge coming from Peirce's philosophy of the three categories, his theory of abduction and its connection to deduction and induction. (Brier 2008, pp. 47–48)

As a final example, relevant to our work, we highlight the importance of interpretation and learning in Hoffmeyer's biosemiotics. For Hoffmeyer (2009), genes do not specify the phenotype. Gene expression can be explained as a process of interpretation, in which the *instructions of the environment* condition the *genetic instructions* to be executed. Semiotic interactions do not depend on a causal connection between sign and meaning but on the interpretation of

<sup>6</sup> Peirce used different terms for the signifying element including "sign," "representamen," "representation," and "ground." John Deely (1990) introduced the notion of "sign vehicle" to interpret and develop Peirce's semiotics.

<sup>7</sup> See Brier (2008) for a detailed study of Peircean biosemiotics.

<sup>8</sup> Hoffmeyer defines *semiotic freedom* as "the 'depth of meaning' that an individual or a species is capable of communicating" (1996, p. 62).

an agent, which is based on communication and learning. Hoffmeyer argues that life is essentially historical, in the sense that its continuation depends on the ability to learn, to remember the strategies that have been effective, to interpret them, and to apply them when interacting with the environment. Furthermore, learning requires some type of coded representation. In other words, learning is a semiotic process.

## Code Biology: A Framework for the Study of Biology

### Code Biosemiotics

The starting point for Code Biosemiotics<sup>9</sup> is the assertion that what defines semiosis is coding, in which “a code is always a set of rules that establish a correspondence (or a mapping) between two independent worlds” (Barbieri 2003).

Barbieri’s biosemiotics is based on two key ideas: (1) cells contains an internal codemaker (Barbieri 1981, 1985), and (2) coding cannot be reduced to copying, so natural selection (based on copying) and natural conventions (based on coding) are two different mechanisms of evolution (Barbieri 1985, 2003).

### The Cell and Organic Codes

Barbieri’s analysis of organic codes begins with the study of the cell model that emerges with the genetic code.<sup>10</sup> Barbieri considers that a cell should not be seen as a duality of genotype and phenotype but as a triad of genotype, phenotype, and ribotype: the genetic code requires the existence of internal codemakers.

<sup>9</sup> Over four decades, Barbieri has been developing a theoretical framework for the study of biology. What this author began by calling *Semantic Biology* or *Biosemantics* (Barbieri 1985) was then changed to *Code Biosemiotics* and finally to *Code Biology*. These name changes correspond to three stages, which do not respond to changes in his proposals, but in his relations with other lines of research: a first stage of work independent of other schools that also consider semiosis to be the key to the study of biology; a second stage in which an attempt was undertaken to unify all schools under the common framework of Biosemiotics; and a third in which Barbieri and his collaborators took an independent path again, rejecting the prevailing line in Biosemiotics, considering it based on interpretation and often far from scientific work. In a letter to the editor of *Biological Theory*, published in 2014, Barbieri explained the reasons that led him to join the Biosemiotic movement in 2001 and to abandon it in 2012 to establish Code Biology as an independent research field.

<sup>10</sup> After the discovery of the genetic code, the first researcher to propose that the cell is controlled by signs was Howard H. Pattee (1968, 1972). Pattee has developed his work quite independently of the biosemioticians, but he has had an important influence on them.

In general, a semiotic system is

a system made of two independent worlds that are connected by the conventional rules of a code. A semiotic system, in conclusion, is necessarily made of at least three distinct entities: signs, meanings and code. (Barbieri 2008, p. 578)

This proposal gives priority to the codemaker. The codemaker is the agent of semiosis, while signs and meanings are its instruments. It is the codemaker that creates signs and meanings, which do not exist (as such) outside a codemaking process. In Barbieri’s words “a semiotic system is a set of signs, meanings and code that are all produced by the same agent, i.e., by the same codemaker” (Barbieri 2015, p. 30).

Barbieri focuses on organic codes, in which the worlds to connect are two sets of different molecules. In this case, a third type of molecular structures, which act as adapters and independently bind to molecules of both sets, is required. The adapters establish an indirect correspondence that does not respond to the physical properties of the molecules of the connected sets but to conventional rules. Only an authentic code guarantees biological specificity.<sup>11</sup> Adapters are organic codemakers, i.e., molecules that reveal the existence of organic codes.

These considerations can be applied not only to the genetic code<sup>12</sup> but also to the other codes and codemakers that can be identified in living beings. Barbieri’s works (2015, Sect. 3) analyze various organic codes at the cellular and supracellular levels and include a large number of references to works on the identification of this type of code (2015, Introduction). Examples of organic codes are splicing codes, signal transduction codes, cytoskeleton codes, and compartment codes. In the fourth section there is a subsection entitled “Barbieri’s Concept of Mechanism,” in which Barbieri’s account of signal transduction codes is summarized.

### Information, Sign, and Meaning

Barbieri (2008) considers the classification of signs into natural signs and conventional signs. In conventional signs, there is no physical relationship between signs and meanings; each relationship is defined by an arbitrary rule

<sup>11</sup> The application of (conventionally established) rules determines which pairs of molecules are related. This relationship gives each molecule of the first set a *meaning* in the second set, and the expression of that meaning defines biological specificity.

<sup>12</sup> In the case of the genetic code, the correspondence between codons and amino acids can only be the result of conventional rules. The genetic code had to appear at the same time as the translation apparatus. The result is a codemaker, a machine to produce proteins from a template and a code.

(convention). Barbieri analyzes nucleotides as signs and concludes that they behave as natural signs in the copying process, but they are also conventional signs in the coding process. In the first case, organic information comes into play, while the second gives rise to organic meaning. Organic information and organic meaning are not, therefore, intrinsic properties of the molecules that carry them but the results of natural processes. Faced with the cohabitation of two different paradigms of biology, the “chemical paradigm” (the idea that life is chemistry) and the “information paradigm” (the idea that life is chemistry + information), Barbieri poses that: “(T)he copying of the genes and the coding of proteins are equally fundamental processes, and this leads to a third theoretical framework that is referred to as the ‘code paradigm’ (the idea that life is chemistry + information + codes)” (Barbieri 2015, p. XV).

Barbieri generalizes these considerations for all organic codes and provides the following definitions. The sequence used (or produced) by a copymaker during a copying process is *organic information*. The sequence used by a codemaker during a coding process is an *organic sign*. The sequence produced by a codemaker during a coding process is an *organic meaning*. An *organic code* is a set of rules of correspondence between signs and meanings.

For Barbieri (2015), recognizing the existence of a code, whether mental (or neural) or organic, entails affirming the existence of a meaning. A code establishes a correspondence between two entities and, with it, converts one into a sign and another into its meaning. If the code is neural, the meaning is a mental entity; if the code links two types of molecules, the sign and meaning are organic entities. It is possible, therefore, to affirm the existence of organic signs and meanings if the existence of organic codes is demonstrated. Barbieri proposes as a biological research goal the identification of organic codes at all levels as an integral part of life.

## Unification and Rupture

Barbieri (2009) reports that in 2004, several schools of biosemiotics agreed to place what united all of them (the introduction of meaning in biology) ahead of their differences and to consider Sebeok's (2001) claim that *life and semiosis are coextensive* as a foundational principle of biosemiotics. This principle and the assertion that signs, meanings, and codes are natural entities were agreed upon as necessary and sufficient conditions for the establishment of biosemiotics as a natural science and as the basis of minimal unity among different schools.

However, at the end of 2012, Barbieri left the common field of biosemiotics and, together with 11 colleagues, founded the *International Society of Code Biology* (ISCB). Barbieri and his colleagues said they were rebelling against

what they considered the application of Peirce's semiotics to all living beings and the growing presence of humanities studies in biosemiotics. These researchers considered it necessary to preserve the scientific approach, and abandoned the biosemiotic community to constitute a different theoretical framework for biology: Code Biology. In the constitution of the ISCB, Code Biology is defined as “the study of all codes of life with the standard methods of science” (Barbieri 2014, p. 247).

## Codes Versus Interpretation

Barbieri (2009) compares the following definitions of code-based and interpretation-based semiotics:

The necessary and sufficient condition for something to be a semiosis is that A provides a conventional association between B and C, where A is a set of adaptors and B and C are the objects of two independent worlds. (Barbieri 2008, p. 236)

The necessary and sufficient condition for something to be a semiosis is that A interprets B as representing C, where A is the interpretant, B is an object and C is the meaning that A assigns to B. (Posner et al. 1997, p. 4)

Peircean semiotics argues that all living beings, from a cellular level, maintain a behavior that depends on their context and that they can do so because they are able to interpret the world. Conversely, Barbieri argues that a cell can respond to the changing environment without performing any interpretation. A combination of several organic codes is sufficient to show context-dependent behavior. At the cellular level, he advocates for a unique semiosis based on organic codes, which can play three different and complementary roles: (1) *manufacturing* (production of new objects, such as proteins); (2) *signaling* (association of objects from independent worlds, as in signal transduction); and (3) *regulation* (as in the control of transcription of genes). Biosemiotics based on interpretation leads, according to Barbieri, to the abandonment of scientific objectivity and the conversion of biology into a division of the humanities.

## Theoretical Frameworks for the Study of Biology

Barbieri (2015) analyzes the Modern Synthesis and systems biology as main theoretical frameworks for the study of biology. The Modern Synthesis focuses on the population aspects of the problem of life, and its main mechanism (its only mechanism of evolution) is natural selection. Systems biology prioritizes the study of the individual organism as a system that is self-manufactured, and its central process is autopoiesis (self-production).



As a critique of the Modern Synthesis, Barbieri believes that evolution requires a second mechanism of evolution, natural conventions, based on codes. Further, faced with systems theory, he asserts that the organism is not explained by autopoiesis but by codepoiesis, which is the ability to acquire codes and maintain them. For Barbieri, “the cell is a codepoietic system, i.e., a system that is capable of creating and conserving its own codes” (2015, p. 176). There are two distinct versions of Code Biology. In the restricted version, only organic codes are studied. In the general version, Code Biology examines all codes of life: organic, neural, and language.<sup>13</sup> Accordingly, Barbieri proposes Code Biology as a third and very ambitious framework for biology.

The stated intention of the International Society of Code Biology is the study of all codes of life using the standard methods of science. Barbieri argues that this intention is already applied rigorously in the study of organic codes, but he admits that the study of neural and language codes remains a more speculative field that requires both scientists from various disciplines and linguists and philosophers (Barbieri 2015).

### Science and Mechanisms

According to Barbieri, to understand something is equivalent to explaining it with a model that is a mechanism, which has the logic of a machine. Further, scientific knowledge is obtained by constructing mechanistic models of what we observe in nature.

Barbieri considers the study of organic codes to be a strictly scientific discipline since it proposes a model from which to perform experiments: a mapping between two sets of independent molecules interconnected by a third set of molecules that act as adapters. The discovery of adapters reveals the presence of organic codes. The semiosis of Barbieri is explained by the mechanisms by which adapters associate signs and meanings. In addition, coding “is a generative mechanism, a mechanism of evolution” (Barbieri 2015, p. 180).

<sup>13</sup> Barbieri classifies life into three worlds. The first world is based only on organic semiosis. Its mechanism is coding, and its codes are organic codes. The second world incorporates animal semiosis, which is characterized by two mechanisms (coding and interpretation) and two types of codes (organic and neural). The third world adds human semiosis. It is based on three mechanisms (coding, interpretation, and language) and three types of codes (organic, neural, and language).

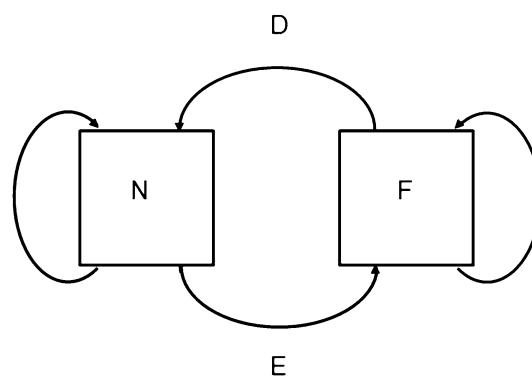


Fig. 1 Natural law and model. Modified from Rosen (1991, p. 60, Fig. 3H.2)

### Relational Biology of Robert Rosen

Relational biology began with Nicolas Rashevsky (1954) and his attempt to develop a “mathematical” biology. Initially, Rashevsky tried to model each of the organismic functions and formalize the whole organism from its components. However, he soon became convinced that this strategy was not viable and, therefore, proposed that it is necessary to focus on the search for a principle that governs the organization, rather than on the phenomena themselves.

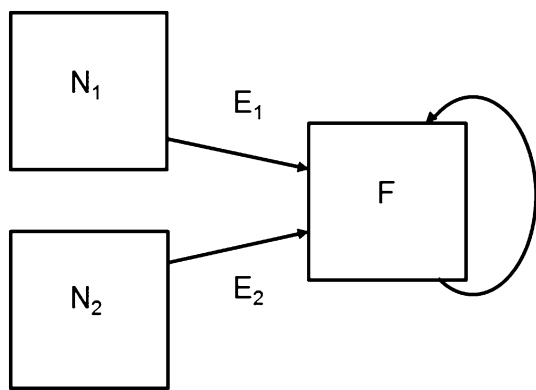
Continuing the line of work initiated by his professor, Rosen considered that the study of life must be based on the notion of function and on the relationships among the components of the organism. He proposed a theoretical framework for the study of biology that escapes the conception of science that has remained valid since Newton. Rosen argued that anticipatory behavior, which depends on the existence of predictive models, is the general rule of biological systems. He defined a type of system, the (M, R)-system, which incorporates the fundamental functions of living beings.

### Laws, Models and Mechanisms

#### Laws of Nature and Models

Rosen (1991) explains that the concept of law of nature is based on the assertion that there exists, and can be established, a relation between two different modes of implication: the causality of natural systems and the inferential implication of formal systems. This relation is established through a model.

Consequently, a natural law would be the congruence between two systems of implications: one corresponding to a natural system and the other to a formal system that is a model of the natural system. (See Fig. 1 for Rosen’s representation of it.)



**Fig. 2** Two natural systems encoded into the same formal system. Modified from Rosen (2012, p. 75, Fig. 2.2)

As Rosen described it, formal system **F** is a model of a natural system **N** as long as we obtain the same result in the following two cases:

1. Moving from one phenomenon to another in **N**; and
2. Encoding (**E**), applying **F**, and decoding (**D**).

In this case, **F** is a model of **N**, and **N** is a realization of **F**.

The model defines an encoding of the qualities of **N** into the formal objects of **F**. The objects of **F** are vehicles of signs that represent the qualities of **N** with which they are associated. The formal relations among the objects of **F** (the inferences that occur among them) correspond, once **F** is decoded into **N**, to causal relations among the qualities of the system **N**. Inferences in **F** allow us to make predictions about **N**.

A natural system **N** can have two or more formal models. One might wonder what types of models are possible, what the class of all formal models of **N** is, and whether there is a model that is the largest.

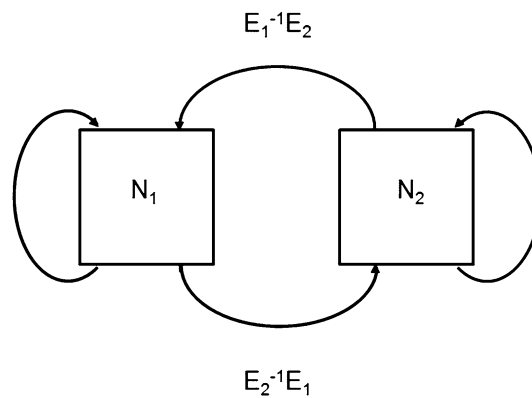
**Models and Analogy**

Consider two systems, **N**<sub>1</sub> and **N**<sub>2</sub>, which can be encoded into the same formal system **F**, as shown in Fig. 2.

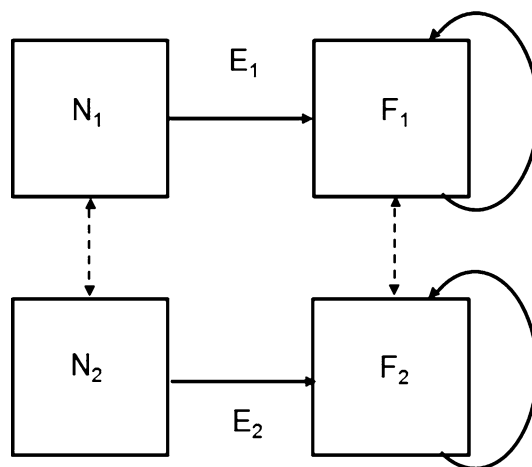
**N**<sub>1</sub> and **N**<sub>2</sub> share a common model and can be considered alternative realizations of formal system **F**. **N**<sub>1</sub> and **N**<sub>2</sub> are analogous systems. As Rosen (2012) suggests,  $E_2^{-1}E_1$  can be seen as the encoding of **N**<sub>1</sub> into **N**<sub>2</sub>, and  $E_1^{-1}E_2$  as the encoding of **N**<sub>2</sub> into **N**<sub>1</sub>. Thus, a relation of analogy establishes a modeling relation between two natural systems. **N**<sub>1</sub> contains a model of **N**<sub>2</sub>, and **N**<sub>2</sub> contains a model of **N**<sub>1</sub>.

These outcomes are shown in Fig. 3.

Once an analogy has been established between two natural systems, we can learn about one of them by studying the other. As is explained in the “Anticipatory Systems” section



**Fig. 3** Analogy between two natural systems

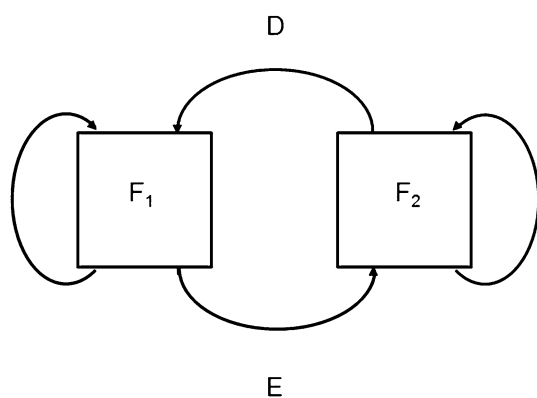


**Fig. 4** Two natural systems that encode into two different formal systems. Modified from Rosen (2012, p. 76, Fig. 2.3)

below, the concept of analogy is the basis of the definition of an anticipatory system.

**Models and Metaphors**

Figure 4 shows two natural systems that encode into two different formal systems. Consider the case in which formal systems **F**<sub>1</sub> and **F**<sub>2</sub> satisfy some mathematical relation, although there is no objective function between sets of encoded propositions that preserve the structure. In this case, an analogy between **N**<sub>1</sub> and **N**<sub>2</sub> cannot be established (a system is not a model of the other), but the existence of a certain relationship between the two natural systems can be affirmed. We say that **N**<sub>1</sub> is a *metaphor* of **N**<sub>2</sub> (and **N**<sub>2</sub> is a metaphor of **N**<sub>1</sub>), indicating that their models share some property. This notion of metaphor also allows for learning about a natural system from the study of the other. Rosen acts metaphorically in his analysis of the concepts of fitness,



**Fig. 5** Modeling between two formalisms. Modified from Rosen (1991, p. 53, Fig. F.2)

adaptation, natural selection, and evolution, as well as in the concept of learning (see the “[Anticipatory Systems](#)” section).

### Model and Simulation

The concept of simulation provides a method for comparing formalisms that is different from modeling.

Consider Fig. 5. Let  $F_1$  and  $F_2$  be two formalisms such that  $F_2$  is a model of  $F_1$ . An inference in  $F_1$  equates to an encoding of  $F_1$  into  $F_2$  plus an inference in  $F_2$  plus a decoding of  $F_2$  into  $F_1$ . Note that the inferential structure of  $F_1$  is not implicated by  $F_2$ .

Let’s now analyze a simulation. Consider that, in Fig. 5,  $F_1$  is a map to be simulated, and  $F_2$  is the simulator. To perform the simulation, the map  $F_1$  is incorporated into  $F_2$ . The left part of the graph ( $F_1$ ,  $E$ , and  $D$ ) disappears inside the right part:  $F_1$  becomes the effect of  $F_2$ . In this case,  $F_1$  is simulated by  $F_2$ , congruence between two inferential structures is not established, and we cannot learn anything about the simulated map from its simulation.

According to Rosen, a mapping is simulable (or computable) if it is definable by an algorithm, i.e., if it is evaluable by a mathematical (Turing) machine.

### Mechanisms

Rosen (1991) argues that an organism is different from a mechanism. He claims that a natural system  $N$  is a mechanism if and only if all its models are simulable, and his analysis concludes that, if a natural system  $N$  is a mechanism, then:

1.  $N$  has a maximal model that is the largest of all its models and includes everything that can be known about  $N$ , according to the laws of nature;
2. There is a finite set of minimal models of  $N$ ;

3. The maximal model is equal to the direct sum of the minimal models, allowing us to define states for the maximal model in terms of the minimal models;
4. In the category of all models of  $N$ , analytic and synthetic modeling coincide (the direct product is equal to the direct sum<sup>14</sup>); and
5. Every property of  $N$  is fractionable.<sup>15</sup>

Rosen’s exposition concludes that, unlike a mechanism, an organism cannot be decomposed as a direct sum, i.e., it is not fractionable into components.

Rosen (1991) studies mechanisms from a relational perspective (see the “(M, R)-Systems” section for Rosen’s definitions of *relational model* and *efficient cause*) and analyzes the implications among their different parts. For each component  $f$ , the answer to the question “why  $f$ ?” (that is, the efficient cause of  $f$ ) must be found in another component of the system or in the environment. Rosen’s analysis concludes that there can be no closed path of efficient causation in a mechanism. Conversely, an organism is a system in which all its components are implied by other components of the system. Organisms manifest maximal implication.

According to these arguments, mechanisms are systems in which syntactics and semantics coincide. Conversely, an organism, like a natural language, possesses semantic modes of implication that do not appear in any formal piece that we can extract and study syntactically. The concept of mechanism is a (restrictive) means of expressing a law of nature. Mechanisms are specializations. A mechanism is a purely syntactic construct; it is a simple (not complex) system. Unlike mechanisms, an organism is a complex system, in which complexity should not be seen as a property of a particular coding but as the capacity to define different codings of a natural system.<sup>16</sup>

That a system is not a mechanism does not mean that it cannot have mechanistic models. However, in an organism, the limit of its mechanistic models is not a mechanism;

<sup>14</sup> According to Rosen (1991), a natural system  $N$  can have analytical and synthetic models. Analytical models are tied to the idea of the Cartesian (or direct) product of quotient spaces, while synthetic models are linked to the idea of the direct sum of subspaces.

<sup>15</sup> Consider a property of system  $N$ , embodied in a model  $M$ , which is smaller than the maximum model, and the maximum model can be decomposed as the direct sum of two summands, with  $M$  being one of them. If this process can be performed for all of the properties of  $N$ , then we say that  $N$  can be fractionated, and its properties are fractionables.

<sup>16</sup> “I call a system which is not simple ‘complex’. Complex systems cannot be exhausted by any finite number of simple (mechanical) models; they cannot be described as software to a ‘machine’” (Rosen 2006, p. 21).

an organism is a system congruent with an impredicative model.<sup>17</sup> A living system must have non-computable models.

According to Rosen, physics is the science of mechanisms and a special science, while biology is a more general science that studies complex systems that should consider more types of models, some of which are non-simulable.

## Anticipatory Systems

### Definition of Anticipatory Systems

Tentatively, Rosen defines an *anticipatory system* as

...a system containing a predictive model of itself and/or of its environment, which allows it to change state at an instant in accord with the model's predictions pertaining to a later instant. (Rosen 2012, p. 313)

Later, Rosen (2012, Sect. 6.1) specifies the concept by requiring five conditions that a system must fulfill to be an anticipatory system, leading to the following formal definition:

An anticipatory system  $S_2$  is one which contains a model of a system  $S_1$  with which it interacts. This model is a predictive model; its present states provide information about future states of  $S_1$ . Further, the present state of the model causes a change of state in other subsystems of  $S_2$ ; these subsystems are (a) involved in the interaction of  $S_2$  with  $S_1$ , and (b) they do not affect (i.e., are unlinked to) the model of  $S_1$ . In general, we can regard the change of state in  $S_2$  arising from the model as an adaptation, or pre-adaptation, of  $S_2$  relative to its interaction with  $S_1$ . (2012, pp. 317–318)

Since  $S_1$  and  $S_2$  are two natural systems, we can see that the basis of the concept of an anticipatory system is the property of an analogy between two natural systems.

### Adaptive Behavior and Anticipatory Systems

Rosen (2012, Sect. 6.5) explains metaphorically the concepts of fitness, adaptation, natural selection, and evolution. He begins by studying a simple organism that can move on a two-dimensional surface and develops its metaphor, idealizing the type of behavior found. From this metaphor, he extracts the essential aspects that characterize any system in which the concepts of fitness, adaptation, and selection can be defined. Following this line, Rosen states that adaptive

behavior implies anticipation and that “a behaviour or phenotype which is adaptive necessarily is of an anticipatory character” (Rosen 2012, p. 345). Moreover, “(t)he retrospective or reactive mode through selection generates adaptation, becomes converted in the adapted organism to a prediction about how present behaviour will affect future behaviour” (2012, p. 346).

Finally, Rosen shows that the organism analyzed meets the conditions required in the rigorous definition of an anticipatory system.

In conclusion, selection and adaptation in fact generate specific predictive models, in such a way that the behavior of an organism at an instant of time bears a definite relation to an internal prediction about a later instant. Additionally, although without developing his statement, Rosen claims that “a general theory of macroevolution can readily be built on the framework we have introduced, incorporating all of the traditional biological features of the Darwinian picture” (2012, p. 350).<sup>18</sup>

### Learning and Anticipatory Systems

Rosen (2012, Sect. 6.6) analyzes the relation between evolution and learning. Both concepts turn out to be inseparable, and show how learning is the basis of anticipatory ability.

The apparently disparate phenomena of evolution and of learning are in fact linked to each other, in the sense that a metaphor for the one is, at the same time, a metaphor for the other. In fact, we can translate an evolutionary metaphor into a learning metaphor by means of a specific mapping process in which observables of the former are simply re-interpreted, or translated, into observables of the latter. From this it will immediately follow, from the arguments of the preceding chapter, that learning processes generate predictive models. (Rosen 2012, p. 352)

[Learning] can be regarded either as a part of adaptation, or as a metaphor for it. (Rosen 2012, p. 357)

## (M, R)-Systems

### The Relational Model

The formal systems proposed by Rosen to model natural systems are relational systems. Consider a separable part of a system. The difference in the behavior of the complete system, versus the case in which a part has been separated, defines the function of the separate part. A component is

<sup>17</sup> A definition is said to be impredicative if it invokes the set being defined. It is a property that important mathematicians and logicians, especially Russell, wanted to leave out of their disciplines, but it has long been proved that elimination leads to having to abandon much of mathematics.

<sup>18</sup> Unlike Barbieri, Rosen argues that only one mechanism of evolution is necessary: natural selection.

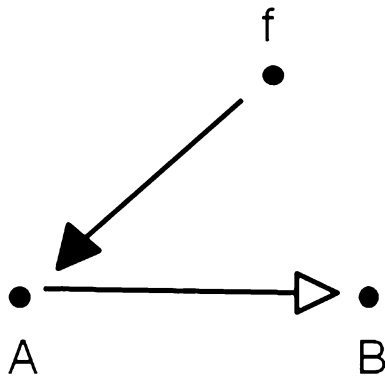


Fig. 6 A component  $f$

a part of the system that can be assigned a function and is the basic unit of the organization of the system. It can be represented as a mapping between two sets,  $f: \mathbf{A} \rightarrow \mathbf{B}$ , where

- $\mathbf{A} \rightarrow \mathbf{B}$  represents the flow from  $\mathbf{A}$  to  $\mathbf{B}$ ; and
- $f$  corresponds to the *efficient cause*<sup>19</sup> exerted on that flow, which is the efficient cause of  $\mathbf{B}$  (of each element of  $\mathbf{B}$ ).

See Fig. 6. We can say that the mapping

- encodes component  $f$ ; and
- is an implication that can be expanded as  $f \longrightarrow (a \longrightarrow \mathbf{f}(a))$ , for every  $a \in \mathbf{A}$ , being  $\mathbf{f}(a) = \mathbf{b} \in \mathbf{B}$ . (Hollow-headed arrows represent the flow, and solid-headed arrows symbolize the effect of the component.)

The models of natural systems are *abstract block diagrams* (ABDs). A combination of mappings constitutes an ABD of the relational system to which it corresponds and the organization it describes. However, mappings can also be elements of sets; for example,  $f$  belongs to the set of all mappings that can be set between  $\mathbf{A}$  and  $\mathbf{B}$ . Therefore, *augmented abstract block diagrams* (AABDs) can be defined, which could include mappings that are the results of other mappings, increasing the organizational level of the system described. At the limit, all elements of the diagram could be implied by others.

### Closure to Efficient Cause

As Mossio (2013) notes, the concept of closure, in general terms, designates a feature of biological systems by virtue of which their constitutive components and operations depend

<sup>19</sup> Taking Aristotelian causes as a reference, we can consider that  $\mathbf{A}$  is the *material cause* of  $\mathbf{B}$  (each element of  $\mathbf{A}$  is the material cause of an element of  $\mathbf{B}$ ), whereas  $f$  is the efficient cause of the occurrence of the flow, i.e., the *efficient cause* of  $\mathbf{B}$  (of each element of  $\mathbf{B}$ ).

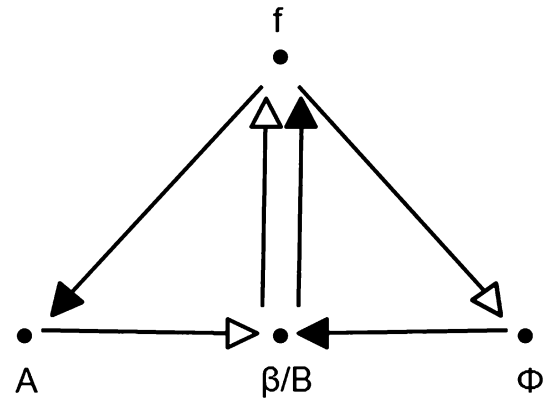


Fig. 7 An  $(M, R)$ -system. Modified from Rosen (1991, p. 251, Fig. 10C.6)

on each other for their production and maintenance and collectively contribute to determining the conditions under which the system itself can exist.

Among the closure proposals, mention should be made of operational closure (Varela 1979), the closure of catalytic functions (Kauffman 2000), and the closure of constraints (Moreno and Mossio 2015). These three closure models respond to the problems of metabolism and self-maintenance of an organizationally closed but thermodynamically open system.

In Rosen's account, a material system is an organism if and only if it is closed to efficient cause (Rosen 1991).

### $(M, R)$ -Systems

Rosen proposed the  $(M, R)$ -system first as a cell metaphor (2012)<sup>20</sup> and then as a general model for an organism (1991).

To change from a self-organized system to a living being, closure to efficient cause must resolve not only the problem of metabolism but also the self-repair and organizational invariance of the system.

According to Rosen, an organism is a closure among the following three classes of functions.

- Metabolism  $f: \mathbf{A} \rightarrow \mathbf{B}$
- Repair  $\Phi: \mathbf{B} \rightarrow f$
- Replication  $\beta: f \rightarrow \Phi$

<sup>20</sup> The first edition of *Anticipatory Systems* dates from 1985.

The relationship among the three classes of functions, as shown in Fig. 7, gives rise to what Rosen called the metabolism-repair system or (M, R)-system.<sup>21</sup>

### Anticipation in (M, R)-Systems

As Pattee (2007) points out, *Life Itself* (hereafter LI; Rosen 1991) represents a qualitative change compared to Rosen's previous work, specifically versus *Anticipatory Systems* (hereafter AS; Rosen 2012). In both works, the modeling relation is the same, but its application is different:

In LI Rosen no longer characterized life by its internal predictive models that allow adaptive evolution. Instead he develops a timeless relational concept of organisms based on natural and inferential "entailments" derived from Aristotle's causal categories .... (T)he central issue in LI is no longer the evolving predictive model in the organism, but the limitations of formal models in our brain. (Pattee 2007, p. 2274)

However, in both AS and LI, the concept of anticipation is key to the definition of an organism. (M, R)-systems—which in AS are a metaphor for the cell, while in LI they are a model—respond to this requirement. According to Rosen:

Anticipatory behaviour is in fact damned as "acausal", because causality is construed precisely as allowing only the past to affect the present. I initially softened this by interposing a "predictive model" as a transducer between now and later. But nevertheless, the presumed telic or finalistic aspects of anticipation seemed to violate the one-way causal flow on which "objective science" itself is presumed to rest. And I noticed that my own (M, R)-systems have an inherent anticipatory aspect, built into their very organisation. (Rosen 2006, p. 11)

Rosen argues as follows. In mathematics, the analogue to anticipation is impredicativity. An (M, R)-system is a mathematical construction that inherently manifests an impredicative loop.<sup>22</sup> In conclusion, an (M, R)-system is a system that includes anticipatory behavior.

With (M, R)-systems, Rosen reaffirms the anticipatory character as an intrinsic property of organisms. Without needing to return to the technical definition of anticipatory systems, the concept of anticipation can be applied to (M, R)-systems: the model of an (M, R)-system allows the

system to change its state in an instant, according to its predictions about a later instant.

## Relational Biology Versus Code Biology

Having analyzed the theoretical frameworks proposed by Barbieri and Rosen, I will now discuss some key proposals of the former in light of the latter.

### Science and Mechanisms

#### The Meanings of "Mechanism"

Mechanisms have received renewed attention in the philosophy of biology during the last 25 years. Among the *new mechanists* William Bechtel, Carl Craver, Lindley Darden, Stuart Glennan, and Peter Machamer stand out. It is beyond the scope of this work to analyze the points in common and the differences between the proposals of these scholars.

To compare the role that Rosen and Barbieri give to the mechanisms in science and, more specifically, in biology, it is convenient to clarify what meaning each author gives to the concept of *mechanism*. My argument will lean on the analysis of Nicholson (2012). According to this author, in biology the term "mechanism" is used with different meanings,<sup>23</sup> which can be defined as follows:

- (a) *Mechanicism* the philosophical thesis that conceives living organisms as machines that can be completely explained in terms of the structure and interactions of their component parts.
- (b) *Machine mechanism* the internal workings of a machine-like structure.
- (c) *Causal mechanism* a step-by-step explanation of the mode of operation of a causal process that gives rise to a phenomenon of interest. (Nicholson 2012, p. 153)

The *causal mechanism* sense of "mechanism" has become predominant today in biology. Causal mechanisms enable the identification of causal relations. To inquire about the causal mechanism of a phenomenon is to inquire about the causes that explain how it is brought about.

<sup>21</sup> " $\beta/B$ " has been used instead, where "B" appears in Rosen's original diagram, to avoid the usual error of identifying  $\beta$  with  $B$ , or with an element  $b$  of set  $B$ . According to Rosen (1991),  $\beta$  is the inverse of an operator constructed from  $b \in B$ .

<sup>22</sup> See Rosen's quotation in the next section.

<sup>23</sup> Nicholson shows the problems generated by not separating the three meanings, even among the new mechanists, quoting an example (Craver and Darden 2005, p. 234) in which "(T)he concept is used in different senses, sometimes even in the same passage (Nicholson 2012, p. 154)."

Traditionally, *mechanicism* and *machine mechanisms* share an ontological status.<sup>24</sup> Conversely, Nicholson argues that causal mechanisms “are actually better understood as heuristic models which target specific causal relations and thereby facilitate the explanation of the particular phenomena scientists investigate” (2012, p. 154). And,

This view of causal mechanisms significantly departs from the ontic conception of them as autonomous systems akin to machine mechanisms (defended by Glennan, Bechtel, and at times by Craver...), given that the parts of a causal mechanism do not even need to be structurally demarcated. All that matters is that they are causally relevant to the production of the explanandum phenomenon. (Nicholson 2012, p. 160)

Contemporary philosophers of science refer to *mechanistic explanations*, even when they appeal to causal mechanism. However, “Mechanistic explanations are ones in which wholes are accounted for in terms of the structure and interactions of their parts” (Nicholson 2012, p. 154). Nicholson refers to *mechanismic explanations* for the explanations given in terms of causal mechanisms.

### Barbieri’s Concept of Mechanisms

Barbieri (2015) provides a definition that partially conforms to the *machine mechanism* concept. He talks about *machine-like models* and gives descriptions of *fully functional working systems*. To propose his mechanisms based on codes, he starts from the examples of mechanistic models of mechanism and machine mechanism: the clock-machine, steam-engine-machine, and the computer-machine.

However, Barbieri’s mechanisms should better be understood as causal mechanisms. In his analysis of the functioning of codes (Barbieri 2008, 2015, Chap. 5), he explains step-by step the causal processes that give rise to the phenomena studied.

Consider, for example, Barbieri’s explanation of the signal transduction codes. The transfer of information from environment to genes takes place in two distinct steps: one in which the external signals (first messengers) are transformed into internal signals (second messengers), and a second path from second messengers to genes, which is known as signal integration. Rosen, quoting Alberts et al. (2007), highlights that there are hundreds of first messengers (hormones, growth factors, neurotransmitters, etc.), whereas the known second messengers are only of four types (cyclic AMP or GMP, calcium ions, inositol trisphosphate, and

diacylglycerol). First and second messengers belong to two very different worlds, and there is no necessary connection between first and second messengers because it has been proved that the same first messengers can activate different types of second messengers, and that different first messengers can act on the same type of second messengers. The explanation proposed by Barbieri is that signal transduction is based on organic codes, which must be identified finding the molecules that play the role of adaptors. In Barbieri’s words:

The transduction system consists of at least three types of molecules: a receptor for the first messengers, an amplifier for the second messengers, and a mediator in between (Berridge 1985). The system performs two independent recognition processes, one for the first and the other for the second messenger, and the two steps are connected by the bridge of the mediator. The connection, however, could be implemented in countless different ways since any first messenger can be coupled with any second messenger, and this makes it imperative to have a code in order to guarantee biological specificity.

In signal transduction, in short, we find all the three characteristics of the codes: (1) a correspondence between two independent worlds, (2) a system of adaptors that give meanings to molecular structures, and (3) a collective set of rules that guarantee biological specificity. (Barbieri 2008, p. 588)

Barbieri’s explanation of signal transduction codes is comparable to that given by Nicholson (2012) of the causal mechanism for the membrane trafficking of the delta-opioid receptor (DOR) induced by pain stimulation. What Nicholson affirms of that causal mechanism can also be applied to Barbieri’s description of signal transduction codes:

It is a step-by-step explanation of the mode of operation of the signal transduction pathway .... The causal mechanism is abstracted both temporally and spatially... [O]nly the features that are causally relevant ... (i.e., the explanandum phenomenon) are featured... [T]he organismic context (in this case, the cell) is almost completely abstracted away and yet it is heavily presupposed, as it provides the enabling conditions that are ultimately necessary. (Nicholson 2012, pp. 160–161)

Barbieri’s mechanisms should be seen as heuristic models with causal relations that facilitate the explanation of the phenomena. The explanation is not based on the general and autonomous organization of a machine but on the parts of a causal mechanism that are causally relevant to the production of the explanandum phenomenon.

<sup>24</sup> As Nicholson (2012, p. 154) explains, “The new mechanism discourse is not committed to a mechanistic worldview, nor does it prescribe a mechanistic approach in biology.”

Barbieri does not attribute to mechanisms an ontological status, and makes clear his rejection of the typical characteristics of mechanism: "Mechanism is not reductionism... is not determinism... is not physicalism..." (Barbieri 2015, p. 16).

Barbieri argues that the scientific method is based on the definition of models, and identifies mechanisms with models, which leads him to identify mechanism with the scientific method: "Mechanism, in other words, is 'scientific modelling'" (Barbieri 2015, p. 16). Finally, Barbieri admits the limitations that models have in explaining reality.

### Rosen's Concept of Mechanism

We now analyze the concept of mechanism in Rosen's work according to Nicholson's taxonomy. First, Rosen's concept of mechanism (discussed above) is intrinsically linked to the definition of law of nature inherited from Newton and prevailing in contemporary science. Therefore, his definition of mechanism should be considered as a formalization of the machine mechanism concept, although deprived of any ontological status.

Rosen rejects mechanistic biology. As we have seen, he argues that a mechanism is a restrictive way of expressing a law of nature that is not sufficient to account for biology. He does not reject the use of mechanisms as an explanation of some organismic biological processes, but holds that there may be processes in an organism that cannot be explained as mechanisms; and, in any case, a complete description of an organism cannot be a description of a mechanism. An organism is a complex system that *can have mechanistic* (and nonmechanistic) models, but the limit of which is not a mechanism.

On the other hand, Rosen shares with present-day biologists the use of the term "mechanism" in the study of biological processes. For example, Rosen (2012) includes expressions like "sensory mechanism," "effector mechanism," "morphogenetic mechanisms," "mechanism for replication," "anticipatory mechanisms," "selection mechanism," or "integrating mechanisms." However, Rosen bases his explanations of the corresponding processes on the concept of metaphor. Consider, for instance, his accounts of morphogenesis and natural selection.

On morphogenesis, he holds that:

The biologist knows that there are three basic kinds of processes underlying all specific morphogenetic or developmental phenomena. These are: (1) Differentiation...; (2) Morphogenetic movement...; and (3) Differential birth and death... It will be observed that these are exactly the three processes manifested meta-

phorically in the Ising model,<sup>25</sup> arising from the different interpretations of state transitions of individual lattice elements. Thus, the Ising model provides us with *metaphors for all of these basic morphogenetic mechanisms*. (Rosen 2012, p. 180; emphasis and footnote added)

Regarding natural selection, Rosen's mathematical study of the movement of an idealized organism on a two-dimensional surface, such as the one mentioned in the "Anticipatory Systems" section above, leads to a definition of a selection mechanism. If natural selection actually took place in that two-dimensional surface, it could be argued that Rosen describes a machine mechanism. However, the metaphorical approach to the selection mechanism in the real world makes the argument and results comparable to a causal mechanism.

It is important to highlight that Rosen's metaphorical explanations share with the *mechanistic explanations*, based on causal mechanism, that both are idealized representations, abstractions of the processes being studied.

### Some Criticisms of Rosen's Account of Mechanism

Before comparing the conceptions of science of Rosen and Barbieri, it is convenient to discuss a couple of criticisms that are posed to Rosen's arguments.

First, it can be questioned if the new mechanists' account of mechanism invalidates Rosen's arguments. For example, Bechtel (2007) analyzes Rosen's work from his mechanistic perspective and concludes that the rupture with mechanistic science can be avoided by considering self-organization, autonomy, and closure to efficient cause as a help "to fill out the picture of what mechanisms are capable of doing when they are organized appropriately" (p. 273).

According to Bechtel, "[a] mechanism is a structure performing a function in virtue of its components parts, component operations, and their organization... The orchestrated functioning of the mechanism is responsible for one or more phenomena" (Bechtel 2006, p. 26). Moreover, his explanation of biological phenomena of an organism (such as digestion, cell division, and protein synthesis) must take into account not only the organization of the components and operations of the mechanism, but the entire organism, that is, "the particular modes of organization that are required in biological systems" (Bechtel 2007, p. 269).

To save mechanistic science, Bechtel adds system organization, typical of systems biology, to causal mechanism. This addition strengthens mechanistic science (and systems

<sup>25</sup> The Ising model is usually considered *a mathematical model* of ferromagnetism, although Rosen points out: "[T]he Ising model is a *metaphor* for phase transitions, and not a 'model' in our sense" (Rosen 2012, p. 179; italics in original).



biology). However, it does not justify the claim that an organism is a mechanism.

Furthermore, according to Nicholson (2012), system organization is not present in mechanistic explanations (including Bechtel's explanation of biological processes):

[M]echanistic explanations specify only those features of the underlying causal networks that biologists deem most relevant for manipulating and controlling the phenomena whilst at the same time presupposing a great deal of the organismic context that makes them possible. (Nicholson 2012, p. 159)

With his extended definition of mechanism, Bechtel seeks to avoid the problem of laws in biology:

Until the recent rise of mechanist accounts, most philosophical accounts of explanation viewed universal laws as the key element in an explanation.... This has seemed particularly problematic in the context of biology. (Bechtel 2007, footnote 2)

Bechtel, like Barbieri, identifies science with mechanism. In contrast, Rosen argues the need for (new) laws for biology that bring us closer to understanding what life is, notwithstanding accepting other tools (models, analogies, metaphors, simulations, even mechanisms) to understand the biological processes.

Finally, Bechtel's mechanistic science, unlike Rosen's biology, does not adequately distinguish between model and nature. According to Nicholson (2012, p. 158):

The fact that the overwhelming majority of mechanistic philosophers speak of them as "real systems in nature" (Bechtel 2006, p. 33) I attribute to an inadvertent transposition of the ontic status of machine mechanisms... onto the notion of causal mechanism.

Consider now a second criticism of Rosen's proposals. Rosen's claim that biological systems are not mechanisms is directly related to another claim, i.e., that organisms have non-simulable models. To be more precise, what Rosen states can be decomposed into two statements: (R1) an organism must have non-simulable models; and (R2) an (M, R)-system is a general model for an organism. Some authors have tried to refute Rosen's statements, by means of both formal demonstrations and practical examples.

For instance, an analysis in terms of  $\lambda$ -calculus (Mossio et al. 2009) concludes that a system closed to efficient causation can certainly have computable models. However, Cárdenas et al. (2010) offer a detailed reply to Mossio's analysis and claim that:

The conclusion of Mossio et al. (2009) that (M, R)-systems can have computable models is based on an analysis of the fundamental equations of (M, R)-sys-

tems in terms of the theory of computer programming, specifically in terms of  $\lambda$ -calculus. Their analysis omits an essential part of the argument, however, and arrives in consequence at a result that we contest. (Cardenas et al. 2010, p. 85)

Furthermore, the examination of the work of other authors leads Cárdenas et al. (2010, p. 90) to a more general conclusion: "Efforts to mathematically disprove Rosen's contention that an organism cannot have simulable models have not resolved the question."

In addition, Cornish-Bowden and his group have proposed a biochemical model of an (M, R)-system, and they have simulated it in a computer. They account for a simulation of a model of an (M, R)-system (i.e., a *simulation of a model of a model* of an organism) that, as they explain:

In terms of this distinction between models and simulations, the results that we shall discuss in the remainder of this paper are clearly not computer models of organisms, but they can still be models of (M, R)-systems, which themselves incorporate some (but not all) of our understanding of the way an organism is organized. (Cornish-Bowden et al. 2013, p. 387)

And, moreover:

In attempting here to relate the biochemical model to Rosen's mathematical formalism we have oversimplified some points in the hope of remaining intelligible in chemical terms. It is hardly possible at the present state of understanding to resolve all the problems and arrive at a mathematically rigorous analysis, but we can note some points that will need to be clarified in the future. (Cardenas et al. 2010, p. 85)

Consequently, Rosen's statements R1 and R2 cannot be considered formally refuted. On the other hand, Cornish-Bowden's model does not exclude the need for an additional mathematical analysis of Rosen's model.

### Barbieri's and Rosen's Conceptions of Science

Although Barbieri's and Rosen's definitions of mechanism are different, both have points in common that are relevant to our argumentation. For both Barbieri and Rosen, mechanisms are *only* models, and science is constructed from models. Both scholars use mechanistic explanations, and also other explanations based on causal abstractions of the processes they study (*mechanistic* explanations and metaphorical explanations). However, while Barbieri identifies mechanism with scientific modeling, according to Rosen's account, the scientific task should not be restricted to mechanistic models. In Rosen's words:

My (M, R)-systems inherently manifest such an impredicative loop; one which cannot be straightened out without losing everything. They are thus not approachable via “machines” in the usual sense; they are not purely syntactic objects. They are what I call complex; they must have non-computable models. I would argue that, precisely by excluding temporally closed causal loops, and indeed by identifying this exclusion with science itself, we have lost not only life, in my sense, but most of its material basis, its physics, as well. To invoke a parallel mentioned earlier: just as the “closed system” is too impoverished, too special, to be a basis for (say) the physics of morphogenesis, exactly so is the simple system, one which can be described entirely as software to a machine, too impoverished to accommodate the living. In fact, these two situations are closely related, but it would take too long to explain that relation here. (Rosen 2006, p. 12)

Other authors (for example, Kauffman 2000), with arguments different from those of Rosen, also defend the non-simulability of living beings, the basis of our criticism of Barbieri's limited conception of science.<sup>26</sup> Further studies must also consider that the claim that mechanisms are not sufficient to explain an organism is closely related to Gödel's incompleteness theorem.

The science of life can draw not only from Newton's sources but also from Rosen's and others. The study of biological mechanisms and, in particular, of those associated with coding, is indisputable as a scientific method, but is not necessarily the only possible way to carry out a scientific biosemiotics.

## Interpretation

### Interpretation According To Barbieri

It is necessary to first present some considerations about the fact that Barbieri does not distinguish properly among three different (although related) theories and concepts: Peirce's semiotics, Peircean biosemiotics, and interpretation.

As we have seen in the first section, Peircean biosemiotics is more than the application of Peirce's semiotics to biology (other varied influences contribute to this field of study);

<sup>26</sup> It has been argued that Rosen's assertions on non-simulability of (M, R)-systems have not been refuted. In any case, although the non-simulability of the (M, R)-systems was refuted, as long as the non-simulability of the organisms is maintained, the claim that an organism is not a mechanism, and, therefore, the science of biology must be broader than the science of mechanisms remains valid. This would be sufficient to support our criticism of Barbieri's limited vision of science, and to defend the compatibility of Barbieri's biosemiotics with Peircean biosemiotics.

and within Peircean biosemiotics, there are important differences between schools and authors, both in the application of Peirce's semiotics, and in the weight they give to the other theories that make up Peircean biosemiotics. When Barbieri rejects biosemiotics, he really seem to refer to *his reading of Hoffmeyer's work*.

On the other hand, it should be kept in mind that Barbieri's definition of interpretation-based semiosis is taken from Posner and not directly from Peirce. Surely, putting the weight on the interpretant rather than on the interpretation would bring Code Biology closer to Peircean biosemiotics.

In any case, what Barbieri rejects is the application of the concept of interpretation in biology, and this is what we analyze in this section.

Barbieri (2015) discards interpretation-based semiosis because:

- Interpretation is based on abduction, and abductive reasoning is extrapolation, i.e., the jump to a conclusion from limited data;
- What is interpreted is not the world but representations of the world; and
- The result of the interpretation depends on the environment and previous experience (interpretation requires memory).

According to Barbieri, it is not appropriate to define decoding at the cellular level as a type of interpretation. He holds that it is necessary to distinguish between two forms of semiosis: one based only on the processes of encoding and decoding; and another also based on interpretation.

He argues that semiosis based only on codes is the only type present at the cellular level. He specifies it for the process of protein synthesis, although he makes it extendible to the remaining organic codes:

- The existence of the genetic code demonstrates the existence in the cell of organic semiosis based on a code;
- The genetic code does not depend on interpretation, it is always the same; and
- The genetic code has only internal meaning (sense, in Frege's (1892) terminology, not reference).

However, even in prokaryotic cells, the application of the genetic code is not automatic. Gene expression is subject to a regulation that depends on the interaction between the regulatory proteins and the environment of the cell. According to Barbieri, it is the combination of a signal transduction code with the genetic code that allows the cell to regulate the synthesis of proteins according to the signals that arrive at the cell from its surroundings, which in turn causes the cell to acquire behavior dependent on the environment (Barbieri 2015). Moreover, this could be extended to more complex

processes simply by adding more codes. What Barbieri proposes is the construction of a complex mechanism assembling elementary mechanisms that correspond to each code.

Conversely, the animal world, in addition to code-based semiosis, would also require interpretation-based semiosis, which includes two types of meanings: sense and reference.

Barbieri (2015) believes that Peircean biosemiotics implies adopting an ad hoc definition of interpretation, and argues against this approach.

- This approach would only lead to a reformulation, in terms of Peirce's semiotics, of what we already know about biological processes. What would be achieved would be a new description, but not new knowledge.
- Interpretation-based biosemiotics assumes, in fact, the approach of the humanities, betting more on storytelling than on the mechanisms as instruments of study of the processes of life.
- Only a scientific approach to biosemiotics can lead to new scientific knowledge.
- Code Biosemiotics (Code Biology) aims to define a theoretical framework to perform experiments and obtain new scientific knowledge.

### Interpretation In Rosen's Work

Rosen's proposals for the explanation of organisms (from the individual cell)—anticipatory systems and (M, R)-systems—include models that go beyond the mechanisms and imply a semiosis that includes and surpasses code-based semiosis.

On the one hand, an anticipatory system contains a model of itself and/or its environment. Those systems can change their state in an instant according to the predictions of the model about a later time. Consequently, it seems appropriate to state that *the system interprets* what its model indicates about what might occur in the future, from its state and the environment in the present.

On the other hand, as seen above, (M, R)-systems have an inherent anticipatory character constructed in their organization. This capacity of anticipation is an intrinsic property of organisms. The (M, R)-systems are theoretical tools that grasp the ability of the organism to interpret the information that resides in its organization. The behavior of organisms represents neither internal *organization* nor external *information* but interpretations of one through the other.<sup>27</sup>

Moreover, predictive capacity depends on the environment and the previous experience (learning, memory) of

the system,<sup>28</sup> which are qualities that Barbieri attributes to interpretation and the reason for which he rejects the use of this concept. As explained above, Rosen stated that (1) selection and adaptation generate predictive models; (2) learning can be seen as a part of adaptation or as a metaphor for it; and (3) learning processes generate predictive models.

If Barbieri rejects the concept of interpretation as the basis of cellular semiosis, it is because he believes that this concept opens the door to nonscientific formulations of biosemiotics. However, his association between interpretation and the humanities is not a mandatory consequence of the concept of interpretation but an abuse of the concept by some theorists that can be considered a pretext to abandon the rigor of science. Like Barbieri, Rosen also seeks to lay the foundation for a new scientific study of biology.

As an additional consideration, it is worth noting that when we speak of interpretation and meaning in the study of the cell, we refer to interpretation performed "by the cell" and meaning produced and used "by the cell." Both concepts must therefore be linked to the utility of the associated processes (encoding and decoding, or interpretation) by/for the cell itself. This linkage unites the justification of the concepts of meaning and interpretation to the concept of function, which is the starting point of Rosen's approach.

### Rosen's Biology as Biosemiotics

From the comparison of the theoretical frameworks of Barbieri and Rosen, it is possible to obtain an additional conclusion, which I point out in this section but will leave its fuller development to future study: Rosen's biology not only provides support for biosemiotics, it can also be read as a biosemiotic theory.

### Code-Based Biosemiotics

The concept of code (or mapping between sets) is present in Rosen's proposals in various ways. First, the congruence between a natural system  $\mathbf{N}$  and a formal system  $\mathbf{F}$ , which constitutes the definition of a natural law, is based on the encoding of the qualities of  $\mathbf{N}$  into the formal objects of  $\mathbf{F}$ .

Second, the analogy between two natural systems  $\mathbf{N}_1$  and  $\mathbf{N}_2$  that share a common model assumes a modeling relation between both systems, in which the qualities of  $\mathbf{N}_1$  are encoded into the qualities of  $\mathbf{N}_2$ .  $\mathbf{N}_1$  and  $\mathbf{N}_2$  are two independent worlds joined by coding rules (a code), such

<sup>27</sup> Note that this last sentence, which here applies to Rosen, is literally included in Brier's explanation of Hoffmeyer (Brier 2008, p. 49).

<sup>28</sup> Pattee's biosemiotics also requires memory. Biological constraints can only occur in individuals with memory maintained by natural selection. Only individuals with memory-based control can learn from the environment and evolve (Pattee and Kull 2009).

as those proposed by Barbieri, and this concept of coding between natural systems, associated with the concept of analogy, is the basis of the definition of an anticipatory system.

Third, abstract block diagrams that Rosen proposed as models of natural systems are constructed with mappings. The (M, R)-system, proposed by Rosen as a model of organisms, is nothing more than a special type of abstract block diagram, in which the mappings condense three types of functions (three types of encodings): metabolism, repair, and replication. As previously stated, Barbieri speaks of two independent worlds connected by a code (two sets of molecules bound by adapters, which are organic codemakers); and Rosen of two sets related by a mapping, which is the efficient cause that leads from each element of the first set to an element of the second. The formal similarity between both definitions requires, however, a clarification. In an organism, many processes in which elements of two different worlds are connected by a third type of elements (or processes) are carried out. Only some of these connections are arbitrary, and only arbitrary connections correspond to a code. Likewise, not all the mappings of an augmented abstract block diagram necessarily represent processes subject to arbitrary efficient causes. Only those mappings that correspond to arbitrary processes are comparable to Barbieri's codes. Nevertheless, both Barbieri's explanation of biological specificity and Rosen's defense of non-simulability of organisms imply that life requires some arbitrariness. Surely, the parallelism between Barbieri and Rosen can be reinforced through the concept of interpretant. Peirce speaks of sign, object, and interpretant; and Brier (2008, p. 50), explaining the concept of "code" in Peircean biosemiotics, states:

A code is a set of process rules or habits (for instance how the ribosome works) which connect elements in one area (for instance genes) with another area (for instance a sequence of amino acids in proteins) in a specific meaning context (here the procreation, function, and survival of the cell) .... From Peircean biosemiotics one argues that codes are part of triadic sign processes where an interpretant makes the motivated connection between objects and signs (representamens). The functioning of living systems is based on self-constructed codes. (Brier 2008, p. 50)

Finally, it should be noted that Rosen distinguishes two different types of encodings: (1) the establishment of a correspondence between a natural system **N** and a formal system **F**; and (2) the construction of **F** from components (mappings, codes). Barbieri assumes the encoding and decoding between **N** and **F** and does not explicitly distinguish between natural system (the cell) and its

formalization (the cell model): his notion of code refers directly to what happens inside a biological system.

Rosen's biology not only meets the requirements demanded by Barbieri for Code Biosemiotics but also allows the role played by the codes for the cell itself to be distinguished from what they mean to the biologist who studies it.

## Peircean Biosemiotics

In the "Relational Biology versus Code Biology" section, we have seen that Rosen's proposals, both anticipatory systems and (M, R)-systems, conform to interpretation-based biosemiotics. The importance given by Rosen to previous experience, learning, and memory has been highlighted, and it has been seen that Rosen's concepts of memory and interpretation are consistent with Hoffmeyer's, as discussed in the first section.

We will only mention here, without developing them, some ideas that reinforce the argument that Rosen's relational biology fulfills the conditions for inclusion in the field of biosemiotics. First, an analogy can be drawn between Rosen's efficient cause and the interpretant. Rosen's mappings conform to Peirce's definition, quoted above, of semiosis and to the characterization of the interpretant that we have summarized from Atkin. Second, as indicated by Brier, self-organization and closure are two of the concepts on which Peircean biosemiotics is built. Both anticipatory systems and (M, R)-systems interpret models that are implemented in their own organization, and closure to efficient cause is the key concept in Rosen's definition of life.

In conclusion, Rosen's biology can be seen as a basis for Peircean biosemiotics, but can also be read as a Peircean biosemiotic theory.

## Conclusions

### Barbieri and Biosemiotics

The incorporation of a discipline from the humanities (semiotics) to the study of life requires determining what requirements should be demanded in the construction of a scientific framework for biology. Pattee indicates that biosemiotics must decide whether or not to be a science and act accordingly:

if Biosemiotics claims that symbolic control is the distinguishing characteristic of life, and if it also claims to be a science, then it must clearly define symbols and codes in empirical scientific terms that are more familiar to physicists and molecular biologists. (Pattee and Kull 2009, p. 328)

Barbieri's answer to this concern is Code Biology. The pillars of this proposal for the study of biology can be summarized as follows: (1) meaning is an essential component explaining biology; (2) what defines semiosis in the cell is coding (not interpretation); (3) a code is a set of (conventional) rules that establish the correspondence between two independent worlds; (4) in organic codes, codemakers are molecules that are independently attached to molecules of two different types; (5) it is necessary to introduce a second mechanism of evolution (natural conventions) that arises from codification; and (6) the aim is to define a new framework for the scientific study of biology, in which science and mechanism are assimilated.

According to Barbieri, the framework of Code Biology conforms to the requirements of standard science. The concepts of organic information, organic signs, organic meaning, and organic codes are operationally defined. Organic codes are the basis for conducting experiments and obtaining new scientific knowledge. Therefore, we must conclude that Code Biology is a type of biosemiotics and has all of the elements to be considered as a genuine scientific discipline.

### Barbieri from Rosen's Perspective

In this article, some of Barbieri's proposals have been criticized, using arguments taken from Rosen's biology. The emphasis has been placed on two major points. First, Barbieri identifies mechanism with scientific modeling, which leads him to limit the study of biology to the identification and study of mechanisms, specifically, coding mechanisms. In contrast, although Rosen admits the use of mechanisms in scientific research, he does not limit modeling to them. According to this author, physics is the science of mechanisms, while biology also requires nonmechanistic models. Each mapping that is part of a block diagram can be assimilated to a code-signs-meanings triad (and, with it, to a coding mechanism), but the (M, R)-system (the model of an organism) is neither a mechanism nor (only) a set of mechanisms.

Second, Barbieri rejects the possibility of a scientific biosemiotics based on interpretation. However, Rosen's anticipatory systems and (M, R)-systems respectively interpret an internal model of the system and the organization of the system itself. In Rosen's work we can find answers to Barbieri's criticisms of the use of interpretation in biosemiotics: in his relational biology, interpretation has a different meaning from that assumed by humanities disciplines, to the extent that it is not limited to a reformulation of what we already know and can lead to new scientific knowledge. Like Code Biology, Rosen's biology aims to define a theoretical framework to obtain new scientific knowledge.

Barbieri rejects interpretation at the cellular level, branding it as unscientific, and that caused his rupture with

Peircean biosemiotics. However, as has been argued in this article, Rosen's approach offers us the theoretical tools to develop a different approach in which (1) mechanisms are a key tool for scientific research, but science is not synonymous with mechanisms; (2) the scientific study of biology requires defining the laws of nature with a different (broader) approach than that of the science inherited from Newton; and (3) scientific biosemiotics can be developed including the concept of interpretation, although not all uses of this concept in biology conform to what is required of science.

Rosen's biology provides support for Peircean biosemiotics to be considered an appropriate framework for the development of the science of biology; a framework compatible with Code Biology, which should aim to provide new scientific conceptual tools that allow for the generation of new knowledge.

The point is that, as Favareau indicates:

[T]he goal of biosemiotics is to extend and to broaden modern science, while adhering strictly to its foundational epistemological and methodological commitments—it does not seek in any genuine sense of the term to “oppose” much less “supplant” the scientific enterprise, but to continue it, re-tooled for the very challenges that the enterprise itself entails, if not demands. (Favareau 2006, p. 4)

### Biosemiotics in the Work of Rosen

As an additional result of the study carried out here, it has been pointed out that a biosemiotic reading of Rosen's biology can also be conducted.

On the one hand, for Rosen coding is a core notion. It is the basis of concepts such as modeling, natural law, anticipatory systems, or (M, R)-systems. This prominent role of coding in Rosen's definition of life is in accordance with the requirements demanded by Barbieri for Code Biosemiotics.

On the other hand, interpretation is also present in Rosen's biology. Anticipatory systems and (M, R)-systems interpret organismic and environmental information and rely on previous experience (memory) to make predictions about their future. Furthermore, Rosen's biology can be analyzed as a Peircean theory.

Pattee and Kull (2009) agree on the presence of semiosis in Rosen's work. According to Pattee, relational biology depends on semiotic relations, rather than on material ones.<sup>29</sup> As Kull claims, Rosen practiced biosemiotics,

<sup>29</sup> “(H)is emphasis on ‘relational biology’ depended on semiotic rather than material relations. Rosen and I were friends for many years beginning with our studies of hierarchy theory in the 1960s. To us, hierarchies, like measurement, are also dependent on semiotic distinctions because hierarchical levels are recognized by the necessity of different descriptions” (Pattee and Kull 2009, p. 327).

probably without being conscious of it or, at least, without using that term.

The study of Rosen's biology as a biosemiotic theory deserves further work. A promising starting point could be to develop the potential connections between the concepts of interpretant and efficient causation; and between the interpretation that an organism performs and the closure to efficient causation that it realizes.

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# An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part I: Components and Signs, Final Cause and Interpretation

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## Abstract

Robert Rosen's relational biology and biosemiotics share the claim that life cannot be explained by the laws that apply to the inanimate world alone. In this paper, an integrated account of Rosen's relational biology and Peirce's semiosis is proposed. The ultimate goal is to contribute to the construction of a unified framework for the definition and study of life. The relational concepts of component and mapping, and the semiotic concepts of sign and triadic relation are discussed and compared, and a representation of semiotic relations with mappings is proposed. The role of the final cause in two theories that account for what differentiates living beings, natural selection and relational biology, is analyzed. Then the presence of the final cause in Peirce's semiosis is discussed and, with it, the similarities and differences between the theories of Rosen and Peirce are deepened. Then, a definition of a semiotic relation in an organism is proposed, and Short's definition of interpretation is applied. Finally, a method to identify and analyze semiotic actions in an organism is proposed.

**Keywords** Relational biology · Semiosis · Sign · Component · Final cause · Interpretation.

## Introduction

In relational biology, organisms are analyzed as systems made up of components that are related to each other, producing system closure to efficient cause. It is closure that defines the living being, turns the parts of a natural system into components that perform functions and gives the relations between natural entities its own reality.

On the other hand, biosemiotics maintains that it is the use of signs that characterizes the living being. Unlike dynamic actions, semiotic actions correspond to triadic relations

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between the subjects that make up the semiotic relation (sign, object and interpretant) that cannot be reduced to dyadic relations.

Moreover, as has been explained by various authors (e.g. Hoffmeyer<sup>1</sup>), the concept of a sign is a relational concept. Furthermore, it is argued below that semiosis is doubly relational: a semiotic relation is a local triadic relation among three subjects, and the semiotic action participates in the systemic closure that defines the organism.

In this paper, an integrated account of Rosen's relational biology and Peirce's semiosis is proposed.

Section on "[Components, Signs, Mappings and Triadic Relations](#)" begins with the presentation of Rosen's concepts of natural law, model, component and mapping and his analysis of Aristotelian causes. Next, considering Peirce's definition of a sign, the possibility of representing semiotic relations with mappings is discussed and a proposal is made. Finally, it is argued that, although the action of a component and the interpretation of a sign can be reduced to dyadic relations, the semiotic relation, which includes the interpretation of the sign and determination of the interpretant, cannot.

In section "[Final Cause](#)", the similarities and differences between the theories of Rosen and Peirce previously pointed out are deepened. First, natural selection is presented as an instrument to explain the reintroduction of the final cause in science and for the inspirational power it had for Peirce. Second, it is discussed Rosen's proposal for the final cause, based on the concept of closure. Both natural selection and relational biology are applied to living beings and they complement each other: one explains how new organisms appear through the reproduction of existing ones and the other characterizes what differentiates living beings from inanimate matter. Finally, the role of the final cause in Peirce's semiosis is studied. All three theories require the introduction of new explananda (natural selection, closure to efficient cause and Peirce's sign) that are part of three corresponding new explanans.

The similarities and differences established in the previous sections between the theories of Rosen and Peirce, as well as the analysis of the role that the final cause plays in them constitute an adequate tool to discuss the existence of signs that realize and are interpreted inside organisms. Section "[Signs in an Organism](#)" begins with the analysis of Short's definition of interpretation. However, Short argues that only in the animal realm can one speak of sign, interpretation and meaning. To overcome this limitation and extend the use of these concepts to the level of the simplest organism, the conceptualization of "intentionality" in biosemiotics is reviewed. As a result, a semiotic relation in an organism is defined. Finally, the concepts of purpose and interpretation are discussed, and it is analyzed who is the agent that performs the interpretation in an organism.

Finally, the section "[A Method of Analysis](#)", presents the steps to follow to identify the presence of signs in an organism.

## **Components, Signs, Mappings and Triadic Relations**

### **Components, Mappings and Aristotelian Causes**

According to Rosen (2012):

<sup>1</sup> (...) the essence of the sign is its formal relational character of evoking an awareness of something which it is not itself – and thereby implying the full Peircean triad of sign, object and interpretant (Hoffmeyer, 2008, p. 18).



A natural system is essentially a bundle of linked qualities, or observables, coded or named by the specific percepts which they generate, and by the relations which the mind creates to organize them. (...) A formal system, on the other hand, is entirely a creation of the mind, possessing no properties beyond those which enter its definition and their implications. (...) We are going to force the name of a percept to be also the name of a formal entity; we are going to force the name of a linkage between percepts to also be the name of a relation between mathematical entities; and most particularly, we are going to force the various temporal relations characteristic of causality in the natural world to be synonymous with the inferential structure which allows us to draw conclusions from premises in the mathematical world (pp. 71–72).

As explained in Rosen (1991), the concept of natural law is based on the assertion that there exists, and can be established, a relation between two different modes of implication: the causality of natural systems and the inferential implication of formal systems. This relation is established through a model. Consequently, a natural law would be the congruence between the causality of a natural system and the inferential implication of a formal system that is a model of the natural system.

The formal systems proposed by Rosen to model natural systems are relational systems. Consider a separable part of a natural system. The difference in the behavior of the complete system, compared to the case in which a part has been separated, defines the function of the separated part. A component is a part of the system that can be assigned a function and is the basic unit of the organization of the system. A component can be represented as a mapping between two sets,  $f: \mathbf{A} \rightarrow \mathbf{B}$ . This implication can be expanded as  $f \longrightarrow (a \longrightarrow \triangleright f(a))$ , for every  $a \in \mathbf{A}$ , with  $f(a) = b \in \mathbf{B}$ , and represented graphically as indicated in Fig. 1A and B, where hollow-headed arrows represent the flow from  $\mathbf{a}$  to  $\mathbf{b}$ , and solid-headed arrows symbolise the effect of the component. In a component,  $f$  entails that  $\mathbf{a}$  entails  $\mathbf{b}$ .

In Fig. 1B,  $\mathbf{b}$  represents a quality of the natural system. To explain the realization of this quality, to answer the question “why  $\mathbf{b}$ ?” Rosen relies on the four Aristotelian causes: material, efficient, formal and final.

Following Rosen, we find two of them represented in the mapping. First, the qualities represented by  $\mathbf{A}$  are the material causes of the qualities represented by  $\mathbf{B}$ . In short, we will say that  $\mathbf{A}$  is the material cause of  $\mathbf{B}$ , and specifically, each element of  $\mathbf{A}$  is the material cause of an element of  $\mathbf{B}$ . Second,  $f$  corresponds to the efficient cause of  $\mathbf{B}$  (of each element of  $\mathbf{B}$ ).

On the other hand, according to Louie, we can consider that the formal cause is represented by the mapping structure shown in Fig. 2:

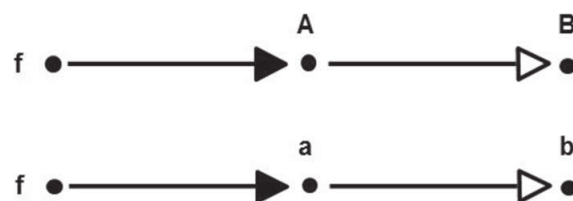


Fig. 1 A representation of a component, B Component action on a specific input



Fig. 2 Representation of the formal cause, according to Louie

The mapping's form, or its statement of essence, is the structure of the mapping itself as a morphism (...) the formal cause of the mapping is thus the ordered pair of arrows (Louie 2009, p. 111).

Finally, Louie also proposes a representation for the final cause (See Fig. 3):

The Greek term  $\tau\acute{\epsilon}\lambda\omicron\varsigma$  (télos, translated into finis in Latin), meaning 'end' or 'purpose', covers two meanings: the end considered as the object entailed (i.e., **b** itself), or the end considered as the entailment of the object (i.e., the production of **b**). In both cases, the final cause may be identified as **b**, whence also the hollow-headed arrow that terminates on the output (Louie 2009, p. 113).

However, when we ask, "why **b**?" the answer cannot be "because **b**".

In section "Final Cause", the final cause in relational biology is analyzed and a proposal is made on its representation.

### Signs and Mappings

It is worth considering now whether it would be possible to represent semiotic relations with mappings, and if this representation could be useful in the analysis of semiotic actions.

To answer this question, it is appropriate to start with Peirce:

A sign, or representamen (...) addresses somebody, that is, creates in the mind of that person an equivalent sign, or perhaps a more developed sign. That sign which it creates I call the interpretant of the first sign. The sign stands for something, its object. It stands for that object, not in all respects, but in reference to a sort of idea, which I have sometimes called the ground of the representamen.

A Sign, or Representamen, is a First which stands in such a genuine triadic relation to a Second, called its Object, as to be capable of determining a Third, called its Interpretant (Peirce as quoted in Favareau (2009, p. 122)).



Fig. 3 Representation of the final cause, according to Louie



Fig. 4 Determination of the interpretant

I define a sign as anything which is so determined by something else, called its Object, and so determines an effect upon a person, which effect I call its interpretant, that the latter is thereby mediately determined by the former” (Peirce 1998, p. 478).

Two comments deserve to be extracted from these quotations. First, an object determines a sign insofar as not just any subject can stand for that object. The object determines a sign among the subjects that present some aspects that can stand for it. The same object can determine several signs that have different characteristics that can stand for it, which would give rise to several semiotic relations.

Second, the aspects of the sign that are suitable to stand for the object determine the idea that is created. Then, the determination of the sign determines the interpretant. In this sense, the object entails that the sign entails the interpretant. Consequently, the determination of the interpretant can be represented as shown in Fig. 4, where I, S and O stand respectively for the interpretant, the sign and the object.

Dashed lines are used in the mapping that represents the determination of the interpretant to indicate that it is a mapping that does not correspond to a component of an organism.

On the other hand, as explained in Short’s definition of interpretation (Short, 2007) discussed in the section named “Signs in an Organism”, the interpretation responds to the purpose of an agent for which the interpretant leads from the representamen to the object. For the agent, the interpretant entails that (excepting failures) the sign entails the object. Accordingly, the interpretation of the sign (the semiotic action) can be represented as shown in Fig. 5.

Continuous lines are used in the mapping that represents the interpretation of the sign since, as argued in the aforementioned section, if it is a sign that belongs to an organism, its interpretation corresponds to the action of one of its components.

Putting the above considerations together, a semiotic relation can be represented with two mappings as shown in Fig. 6, corresponding to its realization and interpretation.

Neither of the two mappings by itself fully represent the semiotic relation. What represents the semiotic relation is the union of both.



Fig. 5 Interpretation of the sign



**Fig. 6** A semiotic relation

## Dyadic and Triadic Relations

A component of a relational system could be associated, in principle, with the triadic relation (**f**, **a**, **b**).<sup>2</sup> However, as discussed above, **f** entails that **a** entails **b**, and thus the component action can be reduced to nested dyadic relations (**f**, (**a**, **b**)). Conversely, in Peirce's semiosis, the concepts of interpretation and meaning are inseparable from the relation that is established between sign, object, and interpretant; a triadic relation that cannot be reduced to dyadic relations.

As argued below, in a natural system, the interpretation of a sign corresponds to the action of a component of an organism. Accordingly, it could be explained as the triadic relation (interpretant, sign, object) that can be reduced to the nested dyadic relations (interpretant, (sign, object)). However, the definition of the sign also requires the presence of the formal relation that corresponds to the determination of the interpretant. The recursive relations established between interpretant, sign and object that are represented with the two mappings in Fig. 6 can be associated to a triadic relation that cannot be reduced to dyadic relations. Although the interpretation of the sign, considered separately, can be reduced to dyadic relations, the semiotic relation, which includes the interpretation and determination of the interpretant, cannot.

Finally, it is important to note that, whenever the interpretant of a sign is associated with the efficient cause of a component, it would be more correct to associate it with the union of the efficient and formal causes. As indicated in footnote 2, in a natural system, efficient and formal causes are not separable. To simplify the discussion, references to the formal cause are omitted.

## Final Cause

The ultimate and distinctive goal of biology is the definition of life, the explanation of what differentiates an organism from an inanimate system. According to Rosen, the explanation of life requires a science broader than that which explains the inanimate world.

In relational biology, an organism is a set of interrelated components. But the organism is more than the sum of all its parts. According to Rosen, life cannot be explained with the laws of physics alone; a complete description of an organism cannot be the description of a mechanism.<sup>3</sup> An organism is a complex system that can have mechanistic (and non-mechanistic) models, but the limit of which is not a mechanism.

<sup>2</sup> In principle, the tetradic relation (**f**, **for**, **a**, **b**), where **f**, **for**, **a** and **b** stand respectively for the efficient and formal causes, the input and the output, should be considered. However, it must be borne in mind that, in a natural system, efficient and formal causes are not separable; they lead together from the input **a** to the output **b**. For simplicity, references to the formal cause are omitted.

<sup>3</sup> Rosen's concept of mechanism is intrinsically linked to the definition of law of nature inherited from Newton. For an analysis of this point, see Vega (2018).

In each component of the system, obtaining the output from the input can be explained by its material, efficient and formal causes; it can, in principle, be explained with the laws of physics alone; it admits, in principle, a mechanistic explanation. However, for the explanation of life, these three Aristotelian causes are not enough, the laws of physics are not sufficient, mechanistic explanations are not enough. Explanation of life requires the introduction of the final cause.

In this section, the role of the final cause in natural selection, relational biology and Peirce's semiosis is discussed.

### **Final Cause in Natural Selection**

As Short (2002) explains, Aristotle conceives final causes as types of outcomes. While an efficient cause always leads to a particular outcome, a final cause is a type of outcome that can be realized in different ways and, furthermore, the actualization of a particular of that outcome type may fail. However, not all types of outcomes are final causes; a type of outcome is a final cause only if it explains why there tend to be instances of that type.

The reintroduction of the classical concept of final cause in modern science is necessary because there are questions that efficient causes cannot answer. Short argues that there are explananda that are not mechanistically explainable:

My point is that a pattern discernible in events is an aspect distinct from the sum of the individual events that compose the pattern. Thus, the pattern requires an explanation – unless, indeed, it is coincidental – distinct from the logical union of the explanations of the individual events (2002, 331).<sup>4</sup>

Furthermore, to explain an explanandum of this type, the final cause must also provide a different form of explanation; a way in which the explanandum figures in the explanans. The tendency for outcomes of a certain type to occur is explained by what that type is. The aforementioned work analyzes what natural selection explains and how it does it, and it is stated that Darwin's use of the concept of final cause coincides with that of Aristotle. The development of adaptations, and the evolution and diversity of species constitutes the distinctive explanandum of natural selection. An explanandum for which the laws of physics<sup>5</sup> are not sufficient, as it cannot be explained just by tracing mechanical processes.

Moreover, the explanandum figures in the explanans: the consequences that explain the existence of adaptive traits are the consequences that these traits have, and the consequences precede the effect they explain. However, the final causation is not a "backwards causation" because the type of outcome is not a particular outcome: there is no particular outcome that has influence on a particular income that precedes it in time.

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<sup>4</sup> See the correspondence between this statement and the tenets of relational biology.

<sup>5</sup> When referring to the laws of physics in this work, this expression must be understood in a broad sense from two perspectives. First, it is about the laws of nature that come from Newton but that include recent contributions to this discipline, even those that incorporate different conceptions from the traditional ones, such as quantum mechanics. Second, it also includes the laws of science that can be derived, in principle, from physics, such as chemistry.

According to natural selection, evolution is shaped by types of outcome, and the outcomes that are realized are explained by the types they exemplify. The types of outcomes are, therefore, final causes, and they are explanatory because outcomes are selected for being of those types.

In natural selection, the selected type is different from the selected genotype. The type selected is part of the explanation for the selection of a particular genotype. This genotype is selected for exemplifying that type more efficiently than the other genotypes available at the time the selection is made.

### Final Cause in Relational Biology

Rosen (1991) posits that relying on natural selection to explain final causes is a false solution to the problem. He recalls that the way in which the parts of a system interact between themselves and contribute to the overall functioning of the system constitutes its physiology, whereas the way the system was formed from different parts constitutes its origin. The modes of implication involved in evolutionary processes and those involved in physiological processes are different.

Both natural selection and relational biology are applied to living beings; the first to explain how new organisms appear through the reproduction of existing ones, the second to characterize what differentiates living beings from inanimate matter. In Darwin's account, the mechanisms of inheritance introduce in natural science a new explanatory principle, natural selection, which account for the selection of characteristics for types of effects that lead to reproductive success. According to Rosen, the definition of life also requires the introduction of a new explanatory principle: closure to efficient cause, explained below. In relational biology, the explanation of the final cause and the definition of an organism is based on the concept of closure to efficient cause, and this closure explains what the system is like at the present time, without referring to its origin.

The analysis of Rosen's concept of final cause should start from highlighting something that differentiates it from other Aristotelian causes: clearly, the material, efficient and formal causes of the effect produced by a component in the system to which it belongs imply said effect; conversely, the final cause must be defined in terms of something implied by the effect.

According to Rosen, in a certain sense, the effect entails the component:

(...) it is perfectly respectable to talk about a category of final causation and to identify a component as the effect of its final cause, its function in the diagram (...) a component is entailed by its function (...) we gain (...) another independent mode of entailment, it is a mode that entails a mapping (...) I shall call it functional entailment<sup>6</sup>, distinct from the inner and outer entailments (...) (Rosen 1991, p. 134).

As Hoffmeyer points out:

<sup>6</sup> Louie (2009) calls this type of entailment "immanent entailment", and uses "functional entailment" for the case in which the output of a mapping is another mapping.

Rosen defended a return to Aristotle's broader understanding of causality, but subjected the term "functional entailment" in place of "final cause", using functional in its biological sense (Hoffmeyer, 2013, footnote 29, p. 166).

Then, an answer to the question "why **b**?" can be "because **b** performs a function that entails the component of which **b** is an output".

The explanatory principle proposed by Rosen is the closure to efficient cause. The concept of closure<sup>7</sup> in general terms designates a feature of biological systems by virtue of which their constitutive components and operations depend on each other for their production and maintenance and also collectively contribute to determine the conditions under which the system itself can exist.

Varela (1979) proposed the "Closure Thesis", according to which every autonomous system is an operationally closed system. For Varela, closure is understood as closure of processes. Starting from any point in a component production network, the chained processes convert inputs into outputs and back to the starting component. An autopoietic system (Maturana and Varela 1973, Varela 1979) is an operationally closed system and therefore a system capable of self-maintaining, reproducing and generating diversity. An autopoietic system is, for them, a living being. Following Maturana and Varela, the question "why **b**?" in Fig. 1B can be answered "because **b** contributes to the operational closure of the system". Thus, in an organism, the final cause of a process is its contribution to the operational closure of the system and thus its contribution to self-maintenance and reproduction of the system, and to the generation of diversity.

In Rosen's (1991) account, a material system is an organism if and only if it is closed to efficient cause. A system is closed to efficient cause if its components have efficient causes generated within the system, and effects that contribute to the production of other efficient causes. Furthermore, the functions of the components contribute to the production of other functions, and to the organization and maintenance of the system. In a system subjected to a closure to efficient cause, a component that contributes to that closure exerts a function, and performing a function is equivalent to contributing to closure. Closure to efficient cause generates a set of functions: functionality is an emergent property of closure. The question "why **b**?" can be answered "because **b** contributes to closure to efficient cause of the system to which the component is part", or, equivalently, "because **b** performs a function in the system". Therefore, the final cause of a component of an organism is the biological function that the component performs in that organism, or, equivalently, the contribution of the biological function to the closure of the system.

When explaining the (M, R)-systems, Rosen (1991) points out that it is closure to efficient cause that solves the problems of metabolism, repair and replication of the system. In an organism, the final cause of a component is its contribution to the self-maintenance of the (metabolism, self-repair and organizational invariance of the) system.

Uniting Rosen's concepts of functional entailment (final cause) and closure, the question "why **b**?" can be answered "because **b** performs a function that, through closure to efficient cause, entails the component of which **b** is an output".

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<sup>7</sup> The notion of organizational closure was introduced in 1967 by Piaget (1967).

Consequently, it is proposed to represent the final cause as shown in Fig. 7. In a relational model, the representation of the final cause of a component is not found within the mapping that represents the component, but in the relation of said mapping with those that represent other components with which it contributes to the closure of the system<sup>8</sup>.

Besides, it is worth asking not only for the final cause of a component, but also for the final cause of an organism as such. (“Why is there a system closed to efficient cause?”). Closure to efficient cause is a type of organization that explains why there tend to be systems that exemplify that type. The realization of a closure to efficient cause is explained by the relations established between the functions performed by the components of an organism, but also each function is explained by its contribution to the closure to efficient cause. As in the case of natural selection, also in relational biology the explanandum to which the theory wants to respond is part of the explanans.

To finish this section, it is relevant to note the similarity between the concept of closure, which defines the organism in relational biology, and that of the organism’s form in Aristotle’s teleology, which explains the existence of an internal agency that maintains the purposes of the organism:

The end is “internal” to the organism because it is the organism’s form. And that form is a cause since, “Except for the organism’s form (...) none of the parts that contribute to the organism’s life would come to be or exist”. Those parts come to be, or are retained, because they support that form, and the form is therefore a cause qua end (Lenox as quoted in Short (2002, 325–326)).

### **Piece’s Signs and Final Cause**

According to Short (2002, 2007), Peirce takes Aristotle’s explanation of the final cause as opposed to the efficient cause, and argues the need to introduce the former into modern science:

(...) we must understand by final causation that mode of bringing facts about according to which a general description of result is made to come about, quite irrespective of any compulsion for it to come about in this or that particular way (...) The general result may be brought about at one time in one way, and at another time in another way (...) Efficient causation, on the other hand, is a compulsion determined by a particular condition of things, and is a compulsion acting to make that situation begin to change in a perfectly determinate way; and what the general character of the result may be in no way concerns efficient causation (Peirce, as quoted in Short (2007, 136)).

<sup>8</sup> The union of a solid and a hollow arrowhead represents the fact that the outputs of the components can be efficient and material causes of other components in the organism.



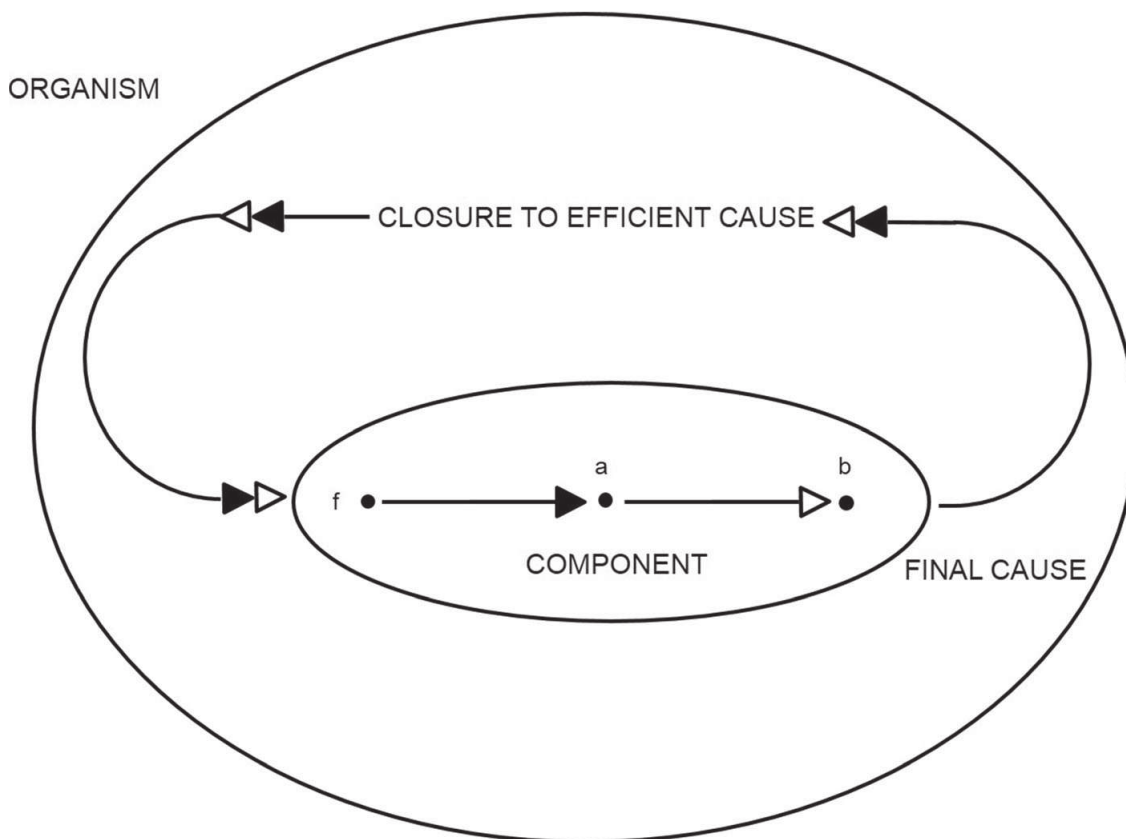


Fig. 7 Representation of the final cause

Peirce was inspired by statistical mechanics and natural selection, which, in contrast to Newton's mechanics, could not be explained by the natural science concept of cause. In these disciplines, mechanistic explanations were no longer sufficient; a teleological explanation was also needed. Peirce realized that Darwin had introduced a new explanatory principle, natural selection, according to which characteristics are selected for the types of effects that lead to reproductive success. These characteristics are selected for a purpose, even if they are sometimes unable to fulfill that purpose. Natural selection had reintroduced purposes, Aristotle's final cause, into modern science.

Peirce's semiosis is a logical and scientific study of signs action in nature and, to develop a theory of logic and to study nature, a type of actions that cannot be characterized as ordinary physical actions must also be considered, semiotic actions:

It is important to understand what I mean by semiosis. All dynamical action, or action of brute force, physical or psychological, either takes place between two subjects (whether they react equally upon each other, or one is agent and the other patient, entirely or partially) or at any rate is a resultant of such actions between pairs. But by "semiosis" I mean, on the contrary, an action, or influence, which is, or involves, a cooperation of three subjects, such as a sign, its object, and its interpretant, this tri-relative influence not being in any way resolvable into actions between pairs (...) and my definition confers on anything that so acts the title of a "sign." (Peirce 1931–1936, vol. 5, p. 484).

Semiotic actions constitute the explanandum posed by Peirce's theory of signs. As in the cases of natural selection and relational biology, it is an explanandum that cannot be explained with the laws of physics alone; an explanandum that requires a new explanans. And in this case too, the explanandum is part of the explanans.

The concepts of sign, object and interpretant are inseparable from the triadic relation established between them. These three "subjects" are not a sign, an object and an interpretant by themselves, but by the role that each one of them plays in the semiotic relation. The semiotic action is explained by the realization of the interpretant, the sign and the object as subjects of the semiotic relation, but on the other hand, it is the semiotic action that defines the interpretant and the sign and the object as such, and the triadic relation. Peirce's sign is an explanandum that figures in the explanans and his semiosis rests on the concept of final cause.

Returning to the comparative analysis of the theories of Peirce and Rosen, it is appropriate to analyze the final cause in Peirce's semiosis relying on the representation of a semiotic relation with two mappings and following a method similar to that used when studying the final cause of a component of a relational model. The representation of the semiotic relation that has been proposed shows that the analysis of the final cause of a semiotic action can be broken down into two questions that correspond to the realization of the interpretant and the interpretation of the sign. Why the interpretant? Because it leads the agent from the sign to the object. Why the object? Because it determines that the sign determines the interpretant. Unlike the final cause of a component of an organism in relational biology, whose answer only requires the closure to efficient cause of the system, the explanation of the final cause of a semiotic relation also requires a local closure between the two constituents of the semiotic relation: the definition of the sign and its interpretation.

## Signs in an Organism

The formal similarities and differences established in the previous sections between the theories of Rosen and Peirce, as well as the analysis of the role that the final cause plays in them constitute an adequate tool to discuss the existence of signs that realize and are interpreted inside organisms, including the simplest. It is convenient to start with the concept of interpretation.

### Short's Account of Interpretation

Short's (2007) definition of interpretation builds on the naturalized account of purpose, where a purpose is a general type of outcome or effect which explains the existence of something because it is selected for having effects of that general type. A purpose is a type of outcome that explains why there are outcomes of that type and it is explanatory because it is selected-for as a means.

Applying the concept of purpose to the sign defined by Peirce, Short's definition of interpretation is as follows:

An interpretant interprets a representamen as a sign of an object if and only if (a) the interpretant is or is a feature of a response to the representamen for a purpose, (b) the interpretant is based on a relation, actual or past or apparent or supposed, of the representamen to the object or of things of the type of the representamen to things of the type of the object, and (c) obtaining the object has some positive bearing on the appropriateness of the interpretant to the purpose. (Short 2007, 158)<sup>9</sup>.

Two comments on the role played by the representamen, the object and the interpretant according to this definition. First, saying that a representamen is interpreted as a sign of an object does not imply that the presence of the representamen leads in all cases to obtaining the object. The object might not be obtained due to the fact that the interpretant is based on a relation of things of the type of the representamen to things of the type of the object that is either an actual but fallible relation, or a past or apparent or supposed relation.

Second, when “the interpretant interprets” is said, it should not be understood that the interpretant is the agent that performs the interpretation. The interpretant is just one of the three subjects that are part of the triadic relation that defines a semiotic relation, in which the object determines that the representamen determines the interpretant (“an effect upon a person”).

And, Short points out:

A purpose has to be some agent's, that selects for that type of outcome; or it has to be some mean's, that is, something that is selected for its having results of that type. A purpose, in other words, must be possessed by something either as agent or means (2007, 135).

Neither the sign, nor the object, nor the interpretant act according to a purpose, and neither does the semiotic relation as a whole. The one who acts purposefully is the interpreter of the sign. Interpreters produce interpretants as a means to an end:

The sign's ‘action’ therefore depends on its relevance to the purposes of an agent; only so does it have an effect. The sign makes or can make a difference: in that sense it ‘acts’, when it acts at all. But it acts only through influencing an agent that, independently of that sign, is pursuing some purpose. Talk of a sign's action is only another way of talking about how a sign determines its interpretant. Nothing is a sign except for its objective relevance to the purposes of possible agents (Short, 2007, 172).

In Peirce's semiosis, the purpose is not of the sign, nor of the object, nor of the interpretant; the purpose is of the interpreter.

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<sup>9</sup> In Short's original, interpretant, representamen, object, and purpose are represented by the letters R, X, O, and P. To facilitate explanation, in this quotation the letters have been replaced by the concepts they stand for.

## Intentionality

On the other hand, Short (2007) argues that, as the concepts of sign, interpretation and meaning are intentional concepts, in which the objects that are assigned to the signs do not need to exist to be assigned, and the intentional action is limited to animals, then only in the animal realm can one speak of sign, interpretation and meaning.

Conversely, the application of the concept of semiotic action to the analysis of the simplest organism is advocated below, based on what has been stated about relational biology, Peirce's semiosis and Short's definition of interpretation. The concept of sign is naturalized, analyzing the requirements that must be fulfilled to affirm the existence of signs in an organism. Previously, it is convenient to make a brief comment on the concept of intentionality, as it is understood in biosemiotics.

Favareau and Gare (2017) conducted a survey among experts in biosemiotics from different fields of study, in which respondents were presented with nine selected quotations and asked to report how suitable or unsuitable to the biosemiotic analysis they found the conceptualizations of "intentionality" reflected in each quotation.

The quotations that got the most approval from respondents were Hoffmeyer and Stjernfelt. It is interesting to copy the later:

It is the cyclical organization of metabolism which makes it meaningful to speak of 'intention' (whether conscious or not), because the directedness of intention, be it inside the organism or directed outwards into the niche is governed by the cyclical attractor of metabolism. ...Thus the biosemiotics vocabulary centered, like Kant predicted and Cassirer further argued, around the concept of intentionality, of telos, formally interpreted as cyclic pattern or order, gives meaning in relation to the notion of the cyclical flow of metabolism. (Stjernfelt as quoted in Favareau and Gare (2017, pp. 227–228)).

In accordance with what is stated in this paper, to properly grasp the concept of intentionality, "the cyclical organization of metabolism" should be replaced by "the closure to efficient cause of the system", which explains the self-maintenance, the self-repair and the replication of the system.

## Components and Signs

According to relational biology, an organism is a material system closed to efficient cause and it can be analyzed as a set of components and the relations established between them. It is closure that gives the relations their own reality<sup>10</sup>, different from the properties of the components, and which differentiates living beings from inanimate material systems.

On the other hand, affirming the existence of a semiotic action in a cell is equivalent to affirming that both the definition of a semiotic relation (the determination of the interpretant) and its interpretation are realized within it. Furthermore, the three subjects

<sup>10</sup> According to Bateson (1972), the reality of ontological relations is exactly what distinguishes life from non-life.

that constitute the triadic relation (the sign, the object and the interpretant), should be natural entities<sup>11</sup>. Consequently, a sign in an organism should necessarily be built on the components and relations that define it.

Suppose there are semiotic actions that are performed in an organism, such that signs are created and interpreted within it. In view of the above, the formal similarity that exists between the production of an output from an input in a component of an organism and the interpretation of a sign should be noted; such a similarity is specified in the correspondences between the interpretant and the efficient cause<sup>12</sup>, the representamen and the input, and the object and the output; a similarity by which the statement “the efficient cause produces the output from the input” would be equivalent to “the interpretant interprets the representamen as a sign of the object”.

Thus, a relationship can be established between the concepts of component and semiotic relation in an organism and, with this, a definition of a semiotic relation can be proposed:

In an organism, a semiotic relation is the union of a component of the system and a relation between the entities that are part of that component, by which the output determines that the input determines the efficient cause. In this case, the efficient cause, the material cause and the output of the component correspond respectively to the interpretant, the sign and the object of the semiotic relation, and the action of the component corresponds to the interpretation of the sign.

Accordingly, the two constituents of a semiotic action, the formation of the semiotic relation and the interpretation of the sign are inseparable.

Moreover, it is convenient to distinguish between the two mappings with which a semiotic relation has been represented. First, as has been explained, the mapping in Fig. 5 corresponds to a component that, according to relational biology, contributes to the closure of the system to efficient cause, and has its efficient cause (the interpretant) generated inside the organism by the closure of the system. Furthermore, Fig. 5 represents the interpretation of the sign.

On the other hand, the mapping in Fig. 4 does not represent a component; it does not correspond to the production of the interpretant from the object and the sign. The interpretant is not the result of a component represented by this mapping (in fact this mapping does not represent any component). Rather, it is the result of some other component of the system that, with the production of the entity that will act as the interpretant, also contributes to the closure to the efficient cause of the organism. What the mapping in Fig. 4 represents is the determination of the interpretant, which is not the production of an entity that acts as such but its selection from among those produced by the closure of the system.

In conclusion, the realization of a semiotic action in an organism, the formation and interpretation of a sign, requires two types of closures; first, the closure to efficient cause that turns the material system into an organism, and to which the component that forms part of the semiotic relation contributes, and second, the closure established between the interpretation and the determination of the interpretant, which defines the semiotic relation.

<sup>11</sup> The term “entities” refers to objects, processes, or a mixture of both.

<sup>12</sup> As explained above, the correspondence must actually be established between the interpretant and the union of the efficient and formal causes.

Consequently, an organism that included a sign could be represented as shown in Fig. 8.

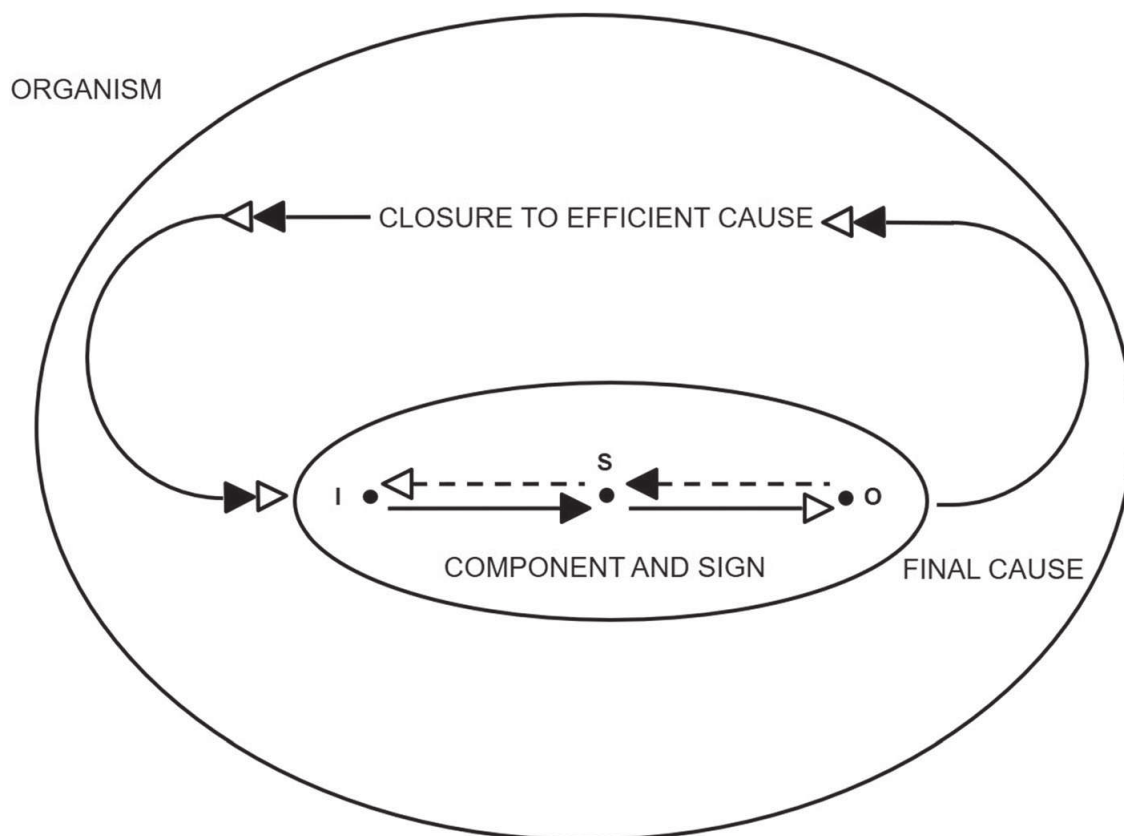
### Purposes, Agents and Interpretation

As previously argued, what makes a sign be a sign is its relevance to the purposes of an agent. The interpretant is a response to the sign for the purpose of an agent, where a purpose is a type of outcome that explains why there are outcomes of that type and it is explanatory because it is selected-for as a means. The one who acts purposefully is the interpreter of the sign.

Consequently, to account for the existence of signs in an organism, the question must now be posed as to which agent creates and interprets these signs.

As stated above, according to relational biology, (1) the final cause of the output of each component of an organism is its contribution to the closure to efficient cause and, with it, to the self-maintenance of the metabolism, self-repair and replication of the system; and (2) the realization of the closure to efficient cause is explained by the relations established between the functions performed by the components of an organism, but also each function is explained by its contribution to the closure to efficient cause.

Furthermore, it must be stated that if an organism includes a sign whose interpretation corresponds to the action of a component of the organism, then the purpose of the sign is the self-maintenance of the system, and the agent performing the



**Fig. 8** An organism that includes a sign

interpretation is the organism itself. Consequently, it can be stated that interpretation is a systemic process.

On the other hand, according to Hoffmeyer (2010, p.371), "The act of interpretation (...) seems to be a key to the production of meaning when this word is used in a situated local sense".

Two considerations are necessary to clarify this apparent contradiction. First, in an organism, the action of a component is locally performed but responds to the global self-maintenance of the system, i.e. to its closure to efficient cause.

Second, as stated, the existence of a sign in an organism implies the realization of two closures, a local one that defines the semiotic relation, and a global one, that defines the organism. Both closures constitute the necessary and sufficient condition for the realization of a sign in an organism. The action of a component corresponds to the interpretation of a sign only if the efficient cause is determined by the output of the component.

Accordingly, in an organism, the interpretation of a sign is locally realized but only because the systemic closure is realized. Thus, the interpretation of a sign in an organism is both a local and a systemic process.

Thus, the question of which agent performs each interpretation in an organism admits two complementary answers. A local one, which would correspond to the local production of meaning indicated by Hoffmeyer: the interpretation is realized by a part of the organism. But also, a global one: the interpretation is realized by the complete system defined by the closure: the organism. The interpretation of a sign, the production of a meaning, corresponds to the realization of a local biological function that contributes to the self-maintenance of the whole organism.

Furthermore, in an organism, it is necessary to distinguish different levels in which a hierarchy of closures and also a hierarchy of interpretations are articulated.

Consider, for example, the simplest multicellular organism. From the point of view of relational biology, in addition to the closure that defines each cell, the higher-level organism requires at least the realization of a closure to efficient cause in which its components are the cells that are part of it. It is the cells and the relations between them that define the multicellular organism.

On the other hand, there may be signs in the multicellular organism whose interpretation corresponds to the action of the cells, in which it should be true that a cell interprets an input it receives from outside as the sign of an output it produces, and the output that is produced determines (the state of) said cell.

## **A Method of Analysis**

As a conclusion of the preceding sections, a method of analysis for the identification of signs in an organism is now defined. The goal pursued is to identify, if they exist, those biological processes that correspond to semiotic actions. The steps to pursue are the following.

First, to identify those processes that biology explains using concepts such as signals, codes or information, although it does not attribute any semiotic character to them. This is the case, for example, of the translation of messenger RNA chains into proteins or of the communication between distant cells.

Second, to carry out a relational analysis, identifying the candidate process for semiotic action with the action of a component of the organism. To do this, the level of detail of the relational model to be used must be adequate for the biological process under study. The identification of the component implies the identification of its efficient cause, its input and its output, and also, due to the closure to efficient cause that defines the organism, its final cause, its function.

Third, to establish a correspondence of the entities identified as efficient cause, input and output with the concepts of interpretant, sign and object, and analyze if the object determines that the sign determines the interpretant. But, saying that the output entails that the input entails the efficient cause means not only that a specific input leads to a specific output (which occurs in all components), but that the efficient cause is also specific. If this is the case, the definition of a semiotic relation in an organism proposed above would be fulfilled and the presence of a sign could be affirmed whose formation responds to the determination of the interpretant (the efficient cause) and whose interpretation coincides with the action of the component and, therefore, with the realization of the analyzed process.

It should be noted that a sign identified by following these steps is a sign present in the organism (it is a sign for the organism), in which the entities identified as interpretant, sign and object form a triadic relation, and its interpretation conforms to Short's definition. In this case, it would be confirmed that the chosen process is really a semiotic action in which the concepts of sign, object, interpretant and interpretation (in its double aspect, local and systemic) have a precise definition, applicable to an organism.

Additionally, once a sign has been identified in an organism, it is worth asking what type of sign it is, according to Peirce's classification into icons, indices and symbols, a classification that is based on the type of relationship that exists between the sign and the object. The sign will be an icon if there are complementarities or correspondences between the sign and the object. It will be an index if it is not an icon, but the sign is actually affected by the object. Finally, it will be a symbol if it does not belong to either of the two previous types and its representative character consists precisely in its being a rule that determines the interpretant. An analysis of this relationship will certainly contribute to better understand the biological process being studied.

The proposed method combines the standard description of biological processes with an integrated account of Rosen's relational biology and Peirce's semiosis. In Vega (2021-II) it is applied to protein synthesis.

## Conclusions

Life cannot be explained by the laws that apply to the inanimate world alone. Relational biology and biosemiotics propose theoretical frameworks to cover this gap. In this paper an integrated account of Rosen's Biology and Peirce's semiosis has been presented, highlighting the common points that can be found in these theories, but also the differences between them.

According to the analysis carried out, relational biology has been extended taking into account the relational character of the sign and the role of semiotic actions in the closure to efficient cause.



Furthermore, the semiotic explanation of the organism has been based on the naturalization of the concepts of sign and interpretation, which have been built upon Rosen's biology. Short's definition of interpretation has also been an important tool for this task.

Three specific conclusions can be summarized as follows. First, in an organism, a semiotic relation is the union of a component of the system and a relation between the entities that are part of it, by which the output determines that the input determines the efficient cause. In this case, the efficient cause, the material cause and the output of the component correspond respectively to the interpretant, the sign and the object of the semiotic relation, and the action of the component corresponds to the interpretation of the sign.

Second, the existence of a sign in an organism requires the realization of two closures, a local one that defines the semiotic relation, and a systemic one, that defines the organism. The action of a component corresponds to the interpretation of a sign only if the efficient cause is determined by the output of the component. The interpretation of a sign in an organism (defined above) is both a local and a systemic process: it takes place locally but only because the system closure to efficient cause occurs.

And third, the application of the concepts expounded, allows the definition of a method of identification of signs in an organism and its classification in icons, indices and symbols. In Vega (2021-II), the proposed concepts and the method of identifying signs in an organism are applied to the analysis of protein synthesis, integrating the descriptions of standard biology, relational biology and semiotics.

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# An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part II: Analysis of Protein Synthesis

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## Abstract

In a previous paper (Vega, [n.d.](#)), an integrated account of Rosen's relational biology and Peirce's semiosis has been proposed. Both theories have been compared and basic concepts have been posited for the definition of a unified framework for the study of biology, as well as a method for the identification and analysis of the presence of signs in an organism. The analysis of the existence of semiotic actions in an organism must, without a doubt, begin by considering each of the rules that constitute the genetic code as a candidate for a semiotic relation. Transcription and translation, which constitute protein synthesis, are the basis of the specificity that the organism needs to maintain itself in its environment and reproduce, and the precondition of the existence of any other possible semiosis. Applying the concepts and method of the aforementioned work, this paper analyzes which of the biological processes involved in protein synthesis correspond to semiotic actions and the type of the signs identified, according to Peirce's classification of icons, indices and symbols. The results of this work demonstrate the theoretical consistency and the practical utility of integrating the theories of Rosen and Peirce, offer a way to identify other signs in an organism, and support a critical analysis of code biology and protosemiosis, two accounts that deny the possibility of explaining the signs in an organism with Peirce's semiosis.

**Keywords** Relational biology · Semiosis · Sign · Component · Final cause · Interpretation · Translation · Transcription · Code biology · Protosemiosis

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## Introduction

In Vega (n.d.), Peirce semiotic relations are formally compared to the components of a system in Rosen's relational biology.<sup>1</sup> The role of final cause is then analyzed and, with it, the similarities and differences between both theories are deepened. As results, definitions of semiotic relation and interpretation applicable at the cellular level are proposed. Finally, a method of analysis to identify the presence of signs in an organism is presented.

The conclusions of the aforementioned paper that apply here are the following, starting with the definition of a semiotic relation:

In an organism, a semiotic relation is the union of a component of the system and a relation between the entities that are part of it, by which the output determines that the input determines the efficient cause. In this case, the efficient cause, the material cause and the output of the component correspond respectively to the interpretant, the sign and the object of the semiotic relation, and the action of the component corresponds to the interpretation of the sign (Vega, n.d., p. NN).

A semiotic relation can be represented with two mappings as shown in Fig. 1 corresponding to the determination of an interpretant and the interpretation of a sign.<sup>2</sup>

A semiotic relation is defined jointly by the determination of the interpretant and the interpretation of the sign (which corresponds to the action of a component). For a semiotic relation in an organism, the letters I, S, and O (which stand for interpretant, sign, and object) must be understood to also stand respectively for efficient cause, input, and output of the component<sup>3</sup>.

The existence of a sign in an organism implies the realization of two closures, a local one that defines the semiotic relation, and a global one, that defines the organism. Accordingly, semiosis is doubly relational: a semiotic relation is a local triadic relation between three subjects (sign, object and interpretant) and the corresponding semiotic action participates in the systemic closure that defines the organism.

Furthermore, according to Short:

An interpretant interprets a representamen as a sign of an object if and only if (a) the interpretant is, or is a feature of, a response to the representamen for a purpose, (b) the interpretant is based on a relation, actual or past or apparent or supposed, of the representamen to the object or of things of the type of the representamen to things of the type of the object, and (c) obtaining the object has

<sup>1</sup> In this paper, a knowledge of the basic concepts of Rosen's relational biology and Peirce's semiosis is assumed. For a better understanding of what is expounded here, it is convenient to read first Vega (n.d.). More information on relational biology and its relationship with biosemiotics can be found in Vega (2018).

<sup>2</sup> The mapping of continuous lines corresponds to the representation of a component in relational biology. Dashed lines are used in the mapping representing the determination of the interpretant.

<sup>3</sup> Whenever the interpretant of a sign is associated with the efficient cause of a component, it would be more correct to associate it with the union of efficient and formal causes. However, in a natural system, efficient and formal causes of a component lead together from the input to the output. For simplicity, references to the formal cause are omitted.



**Fig. 1** A semiotic relation

some positive bearing on the appropriateness of the interpretant to the purpose.  
(Short, 2007, 158)<sup>4</sup>.

When “the interpretant interprets” is said, it should not be understood that the interpretant is the agent that performs the interpretation. The interpretation in an organism is both a local and a systemic process and therefore requires two complementary explanations. A local one—the interpretation is realized by a part of the organism—but also a global one—the interpretation is realized by the complete organism defined by the closure. The interpretation of a sign corresponds to the realization of a local biological function that contributes to the self-maintenance of the whole organism.

Finally, Vega (n.d.) proposes a method to identify and analyze signs in an organism, which is followed below and consists of the following steps.<sup>5</sup> First, to identify a process that is a candidate to be a semiotic action. Second, to carry out the relational analysis and identify the efficient cause, the input and the output of the component that would correspond to the interpretant, the sign and the object of a semiotic relation. And third, to analyze whether the output entails that the input entails the efficient cause. If so, the three entities that make up the component correspond to the three subjects of a semiotic relation. Finally, once a sign has been identified, it should be identified either as an icon, an index or a symbol, studying the type of relationship that exists between the sign and the object.

In this paper, the proposed concepts and method are used to analyze the two processes into which protein synthesis is divided. The choice of these processes lies in the key role played by the genetic code in the discussion about the real existence of signs in an organism. To streamline the argument, translation is studied first and then transcription, paying special attention to its regulation.

Below, it is argued that transcription is not a semiotic action, while translation and regulation of transcription are. Furthermore, it is posited that, while translation is a symbolic action, regulation of transcription is an indexical action.

The results of this work show the theoretical consistency and the practical utility of integrating the theories of Rosen and Peirce, and open a way to identify other signs in an organism.

Finally, the proposals defended are the appropriate theoretical framework and method of analysis to critically analyze two outstanding alternative explanations of the existence of signs in an organism, code biology and protosemiosis, two accounts that deny the possibility of explaining the presence of signs in an organism with Peirce's semiosis.

<sup>4</sup> In Short's original, interpretant, representamen, object, and purpose are represented by the letters R, X, o, and P. To facilitate explanation, in this quotation the letters have been replaced by the concepts they stand for.

<sup>5</sup> For a more detailed description, see the quoted paper.

## Translation

The process of translation, the second of the steps in the synthesis of proteins from DNA, is the process in which a ribosome (R) and a set of aminoacyl tRNA synthetases (aaRS) produce a chain of amino acids (aa) from a chain of messenger RNA codons (CmRNA).

To study the translation process, its account has been broken down into three parts<sup>6</sup>: the binding of a CmRNA and an aminoacyl tRNA (aatRNA), the translation of two consecutive codons and the binding of the resulting pair of amino acids, and the role of the aminoacyl tRNA synthetases. Next, it is argued that translation is a symbolic semiotic action.

### Binding of an mRNA Codon and an Aminoacyl tRNA

The first step in the translation process, the binding of a CmRNA and an aatRNA inside a ribosome, is represented in Fig. 2A.<sup>7</sup>

The process can be summarily explained as follows<sup>8</sup>. During the process of translation, a ribosome moves along a chain of mRNA codons. For each codon in the mRNA chain, two sub-processes occur. First, the ribosome causes the codon to be placed inside it in the proper position to receive an aminoacyl tRNA. Second, the ribosome, with the CmRNA in the correct position, receives the adequate aatRNA, which binds to the codon (the anticodon bases of the aatRNA pair with those of the mRNA codon).

The placing of the CmRNA in the adequate position can be explained by studying the movement of the ribosome and the correspondence of the codon and the site it occupies. The CmRNA-aatRNA binding is explained by the correspondence of the aatRNA and the site it occupies, and the complementarity between the bases of the mRNA codon and the anticodon of the aatRNA.

From the point of view of relational biology, Fig. 2A represents a component in which the ribosome is the efficient cause, the pair (CmRNA, aatRNA) is the input (the material cause), the CmRNA-aatRNA junction is the output and the mapping structure (the union of the two continuous arrows)<sup>9</sup> is the formal cause. According to Vega (n.d.), the final cause is the contribution of the output of the component to the closure to efficient cause of the organism of which it is a part.<sup>10</sup>

Accordingly, the union of a CmRNA and an aatRNA establishes a relation between both molecules that is represented in Fig. 2B, in which it is highlighted that the CmRNA-aatRNA junction implies that an aminoacyl tRNA is associated with each mRNA codon.

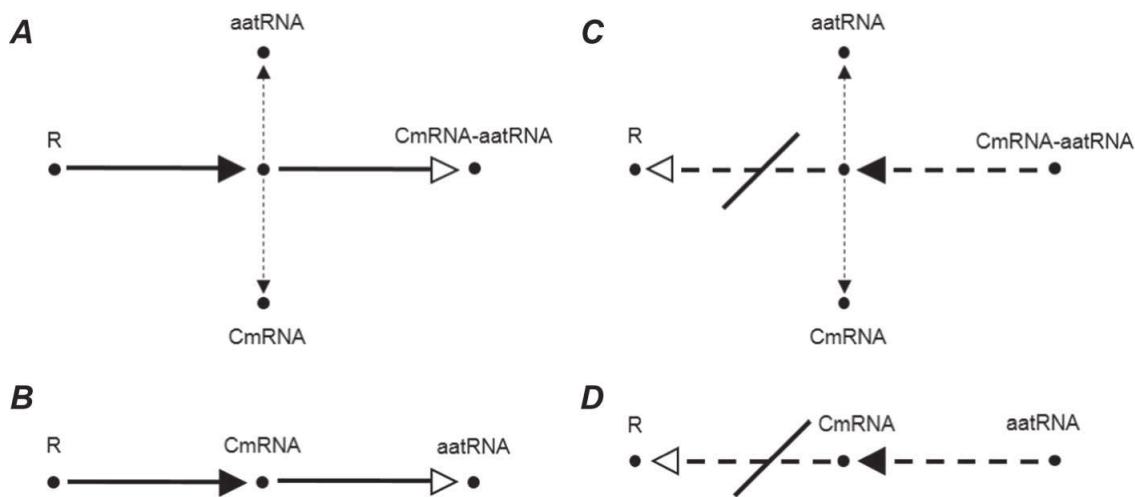
<sup>6</sup> A complete description of the phases into which the translation process breaks down is not presented here, and only the elements necessary for the argument are considered.

<sup>7</sup> The figures in this paper represent the concurrence of one or more elements to form the efficient cause, the input or the output of a component, with dotted lines. In this case, the input is formed by an mRNA codon and an aminoacyl tRNA.

<sup>8</sup> Descriptions of standard biology, relational biology and semiotics are integrated in the analysis presented. The last two perspectives are rolled out in this paper and in Vega (n.d.). A more detailed description of all the biological processes studied in this paper according to standard biology can be found in Freeman et al. (2019).

<sup>9</sup> Louie, 2009, p. 113.

<sup>10</sup> The synthesis of proteins considered globally, and each of the steps into which it can be broken down, contribute to the closure to efficient cause of the organism.



**Fig. 2** **A** Binding of an mRNA codon and an aminoacyl tRNA. **B** Association of a CmRNA with an aatRNA. **C** The binding of an mRNA codon and an aminoacyl tRNA does not determine the ribosome. **D** The association of a CmRNA with an aatRNA does not determine the ribosome

It is worth wondering if the first step of translation, summarized in Fig. 2A and B, must be explained as a semiotic action; if the process carried out by the component corresponds to the interpretation of a sign; and if the ribosome interprets a CmRNA as a sign of an aatRNA.

To answer this question, it is necessary to analyze whether the object of the supposed sign determines the sign that determines the interpretant.

It is clear that a union CmRNA-aatRNA determines a pair (CmRNA, aatRNA) because only the binding of a specific pair of CmRNA and aatRNA produces a specific CmRNA-aatRNA. Similarly, it can also be stated that an aatRNA determines a CmRNA because of the complementarity between the bases of the mRNA codon and those of the anticodon of the aatRNA.

To affirm that the analyzed process corresponds to the interpretation of a sign, it should also be true that the aspects of the sign that are suitable to stand for the object determine the interpretant. However, this is not true in this case. It cannot be stated that the aspects of a pair (CmRNA, aatRNA) that are suitable to stand for a CmRNA-aatRNA determine the ribosome. Similarly, neither is it true that the aspects of a CmRNA that are suitable to stand for an aatRNA determine the ribosome.

The result of this analysis is shown in Fig. 2C and D.

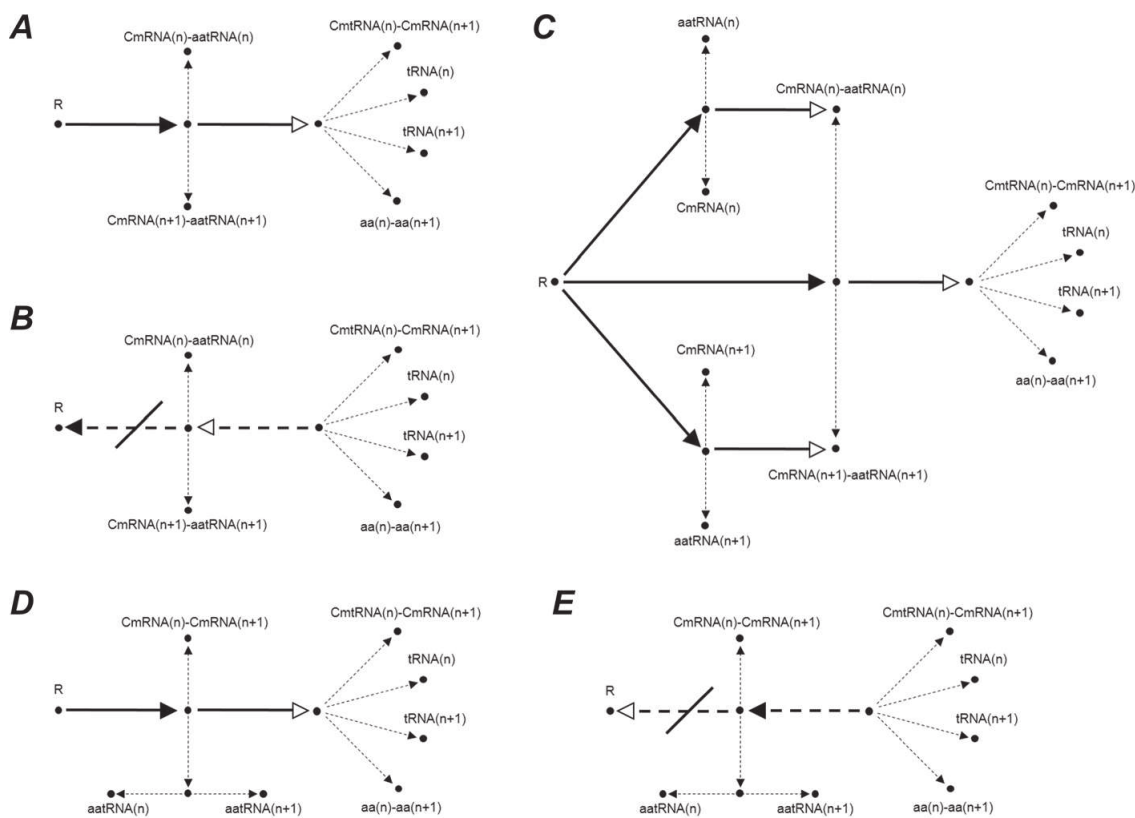
Consequently, it must be concluded that the binding of an mRNA codon and an aminoacyl tRNA does not correspond to a semiotic action.

### Translation of Two Codons and Binding of the Resulting Amino Acids

Now consider the binding of two amino acids, which is represented in Fig. 3A and described below.

Once the process previously described has been carried out for the codon that occupies position  $n$  in the mRNA chain, the following steps occur.

First, the ribosome moves the mRNA chain, and consequently the CmRNA( $n$ )-aatRNA( $n$ ), so that the position previously occupied by the CmRNA( $n$ ) becomes



**Fig. 3** **A** Binding of two amino acids. **B** The binding of two amino acids does not determine the ribosome. **C** Translation of two mRNA codons and binding of the two resulting amino acids. **D** Translation of two mRNA codons and binding of the two resulting amino acids. **E** The translation of two mRNA codons and the binding of the two resulting amino acids does not determine the ribosome

occupied by the CmRNA(n + 1). Then, a new aatRNA enters the ribosome and binds to the codon resulting in the union CmRNA(n + 1)-aatRNA(n + 1).

Second, the binding of the CmRNA(n) and the CmRNA(n + 1), and the ribosome structure put the CmRNA(n)-aatRNA(n) and the CmRNA(n + 1)-aatRNA(n + 1) together, which facilitates the approach of the aa(n + 1) to the aa(n) and the formation of a peptide bond between them.

And third, the next movement inside the ribosome causes the separation and exit of the mRNA codons (which are still part of the chain that is being translated), the amino acids (which are linked into the chain that is the result of translation) and the transfer RNAs.

Figure 3A represents a component of the relational model of a cell. The ribosome is the efficient cause that, from two consecutive CmRNA-aatRNA compounds, produces the binding of the two amino acids that result from translation.

Consider now whether the process depicted in Fig. 3A corresponds to a semiotic action; if the process carried out by the component corresponds to the interpretation of a sign; if the ribosome interprets two consecutive CmRNA-aatRNA compounds as a sign of an object composed of the products of the process.

An analysis similar to that carried out previously also leads to similar conclusions in this case. The elements that make up the output of the component determine the elements that make up the input since, as explained above, the elements that are part of the input have the specific characteristics to produce the elements of the output.

However, it cannot be stated that the aspects of two consecutive CmRNA-aatRNA compounds that are suitable to stand for the output in Fig. 3A determine the ribosome.



The result of this analysis, which is shown in Fig. 3B, is that the binding of amino acids is not a semiotic action.

Integrating Figs. 2A and 3A, the translation of two consecutive mRNA codons and the binding of the two resulting amino acids is depicted in Fig. 3C.

Then, summarizing the translation process in a single mapping, Fig. 3D is obtained.

Thus, from the analysis carried out, it must be concluded that the translation of two mRNA codons and the binding of the two resulting amino acids does not determine the ribosome, so this process does not correspond to a semiotic action.

### The Formation of an Aminoacyl tRNA

In Fig. 3D, which summarizes the translation of two mRNA codons and the binding of the two resulting amino acids, it is shown that the input of the mapping is made up of both mRNA codons that are part of a chain and aminoacyl tRNA molecules.

The mRNA chain that is translated is the result of the transcription of a DNA chain, which is discussed in a later section. The formation of each aaRNA is now analyzed.

Research has shown that enzymes called aminoacyl tRNA synthetases are responsible for the synthesis of aaRNAs from amino acids and tRNAs, as shown in Fig. 4A.

According to the experiments, the action carried out by the aminoacyl tRNA synthetase can be broken down into three consecutive steps. First, the aaRS binds a specific amino acid to it (there are 20 aaRS, one per amino acid). Second, it binds an appropriate tRNA (one or more tRNAs are associated with each aaRS). And third, the aaRS facilitates the aaRNA binding and separation.

This explanation, which responds to the order in which the steps that make up the process occur, should not be misleading. The fact that one process occurs in time after another does not necessarily imply that there is dependency or continuity between them. Furthermore, a relational model does not reflect the order in which the different components of an organism act, but rather the relations between them.

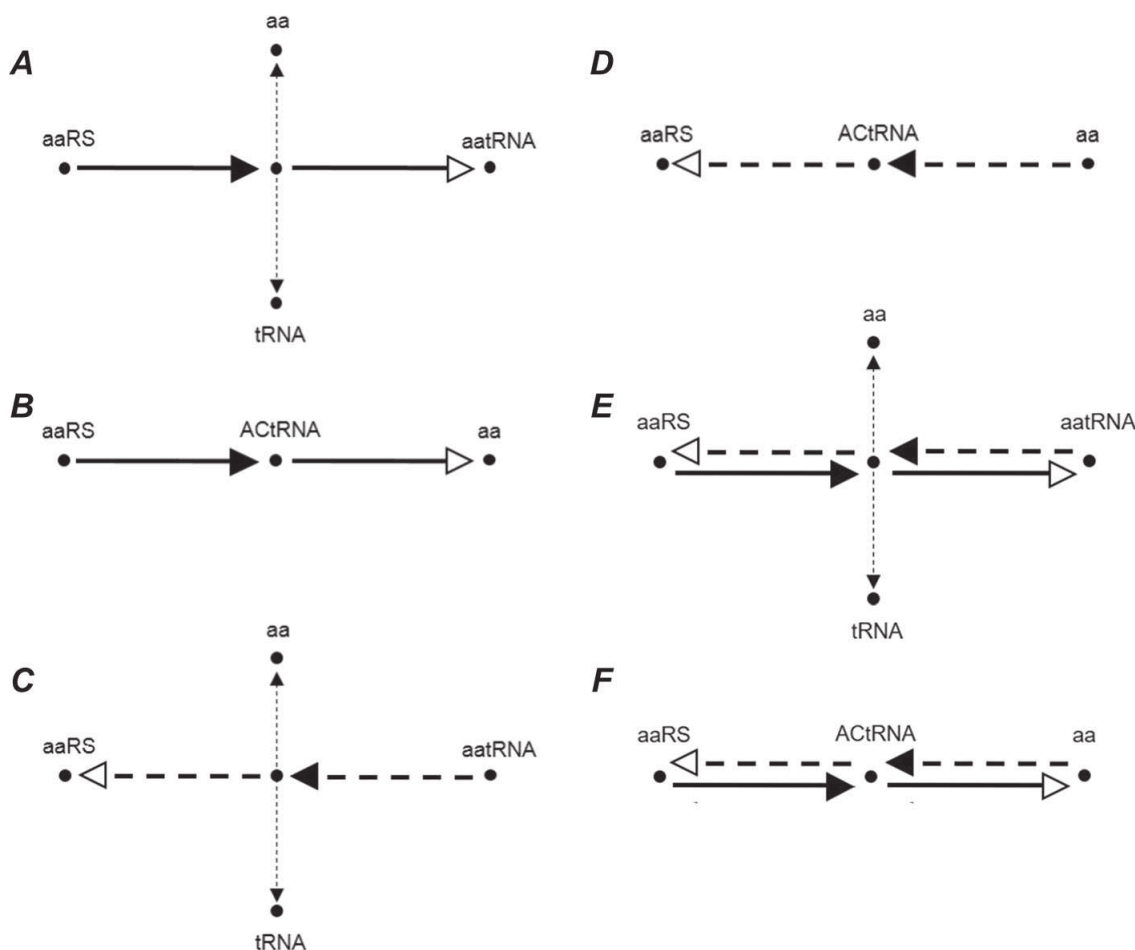
It is necessary to emphasize that the recognition of an amino acid by the aaRS is independent of the recognition of an anticodon of tRNA. In fact, the anticodon does not play any role in the entry of tRNA into the aaRS, nor in its binding to the aa.

According to relational biology, Fig. 4A represents a component in which the aaRS is the efficient cause, the pair (tRNA, aa) is the input (the material cause) and the aaRNA is the output. The final cause is the contribution of the aaRNA to the closure to efficient cause of the organism of which it is part.

The union of a specific tRNA and an amino acid establishes a relation between the anticodon of the tRNA (ACtRNA) and the amino acid that is represented in Fig. 4B.

Once again, the question is whether the process we are analyzing corresponds to the interpretation of a sign; if the aaRS interprets the anticodon of a tRNA as a sign of an amino acid; if an aaRS, the anticodon of a tRNA and an amino acid form a triadic relation that corresponds to a semiotic relation.

This analysis is carried out by following Fig. 4A and B. First, an aaRNA determines the corresponding pair (aa, tRNA) since those specific aa and tRNA are the only molecules that can form that specific aaRNA. Similarly, it can also be stated that an amino acid determines an RNA anticodon because of the complementarity between the bases of both.



**Fig. 4** **A** Formation of an aminoacyl tRNA. **B** Association of a tRNA anticodon with an amino acid. **C** The aminoacyl tRNA determines the pair (tRNA, aa) that determines the aminoacyl tRNA synthetase. **D** The amino acid determines the ACtRNA that determines the aaRS. **E** The semiotic relation: interpretant = aaRS, sign = (aa, tRNA), object = aaatRNA. **F** The semiotic relation: interpretant = aaRS, sign = ACtRNA, object = aa

Additionally, it can be stated that a specific pair (aa, tRNA) determines an aaRS as long as the aspects of the pair of molecules that are suitable to represent their union determine the aaRS. Only a specific aaRS can lead to the production of a specific aaatRNA from a pair (tRNA, aa). The aspects of the amino acid and the tRNA that are suitable to stand for the aaatRNA determine the aaRS. Equivalently, it can be stated that an ACtRNA determines an aaRS insofar as only that aaRS can associate the anticodon with the corresponding amino acid. Furthermore, it should be noted that the explanations above of the formation of an aaatRNA are not sufficient to account for why a specific amino acid is assigned to each anticodon. If only the explanatory elements used are taken into account, any other set of amino acid-anticodon pairs could have been established.

The determination of an aaRS is shown in Fig. 4C and D.

Consequently, as detailed below, it must be stated that the formation of an aminoacyl tRNA is a semiotic action that corresponds to the semiotic relation that is represented in Fig. 4E and F.

## The aatRNA: a Semiotic Action

As explained in Vega (n.d.), the action of a component can be explained by its material, efficient and formal causes; it can, in principle, be explained with the laws of physics alone; it admits, in principle, a mechanistic explanation. Furthermore, in a natural system, the interpretation of a sign corresponds to the action of a component and, therefore, admits the same explanation as it.

However, explanation of life requires the introduction of the final cause and a new explanatory principle. Closure to efficient cause is a new explanandum that requires a new explanans of which it is also a part. Similarly, the determination of the interpretant cannot be explained with the laws of physics alone and a new explanatory principle is required. In this case, Peirce's sign is also an explanandum that figures in the explanans of which it is also a part, and his semiosis also rests on the concept of final cause.

To argue that an aatRNA corresponds to a semiotic action, it is convenient to begin by delving into the similarities and differences between the biological processes represented in the mappings in Figs. 2A and 4A (or, what is equivalent, those in Figs. 2B and 4B) according to relational biology and Peirce's semiosis.

From the point of view of relational biology, these are two formally similar processes. In both cases, the mappings represent formally similar components that identify the efficient cause, the input and the output of a biological process.

In both cases, the action of the component can, in principle, be explained with the laws of physics and the relation that unites efficient cause, input and output can be expressed as the pair of nested dyadic relations (efficient cause, (input, output))<sup>11</sup>. Lastly, in both cases the final cause is the contribution of the output of the component to the closure to efficient cause of the system and, therefore, to the self-maintenance of the metabolism, self-repair and organizational invariance of the organism.

By contrast, from the point of view of Peirce's semiosis, the second process exhibits a characteristic that is not present in the first. As previously stated, the union of an mRNA codon and an aminoacyl tRNA does not correspond to a semiotic action, but the formation of an aminoacyl tRNA does. This difference has been made manifest above and is represented in the mappings in Fig. 4C to F.

The component in Fig. 4B corresponds to the interpretation of a sign that conforms to Short's (2007) definition of interpretation:

An aaRS interprets a tRNA anticodon as a sign of an amino acid if and only if (a) the aaRS is or is a feature of a response to the tRNA anticodon for a purpose, (b) the aaRS is based on a relation, actual or past or apparent or supposed, of the tRNA anticodon to the amino acid or of things of the type of the tRNA anticodon to things of the type of the amino acid, and (c) obtaining the amino acid has some positive bearing on the appropriateness of the aaRS to the purpose.

As explained, an aatRNA determines a pair (aa, tRNA) that determines an aaRS (or, what is equivalent, an amino acid determines a tRNA anticodon that determines an aaRS). Furthermore, there is a relation among three specific elements—an aa, a tRNA anticodon, and an aaRS—that cannot be explained by the laws of physics alone. As stated above, there is nothing in these laws to prevent any other set of amino acid-anticodon pairs from being established.

<sup>11</sup> The efficient cause entails that the input entails the output.

Finally, in the formation of an aminoacyl tRNA, the systemic closure that defines the organism in relational biology is joined by the local closure that defines the semiotic relation.

In view of both closures, it is convenient to review the concept of interpretation. Interpretation realizes to fulfill the purpose of an agent. When “the aaRS interprets” is said, it should not be understood that this molecule is the agent that performs the interpretation. The aaRS is just one of the three subjects that are part of the triadic relation that defines the semiotic relation, in which the aa determines the tRNA anticodon that determines the aaRS. Furthermore, the semiotic action of the interpretation of a sign corresponds to the action of a component in relational biology, an action that realizes because its output (the object) contributes to the closure that defines the organism.

Thus, the question of who is the agent that performs each interpretation admits of two complementary answers. A local one, which would correspond to the local production of meaning indicated by Hoffmeyer<sup>12</sup>: the interpretation is realized by a part of the organism; but also, a global one: the interpretation is realized by the complete system defined by the closure: the organism. The interpretation of a tRNA anticodon as a sign of an amino acid corresponds to the realization of a local biological function that contributes to the self-maintenance of the whole cell. The purpose (of the closure) of the organism is its self-maintenance.

### **The aatRNA: a Symbolic Action**

On the other hand, if it is affirmed that Fig. 4E and F represent the semiotic relation that corresponds to the formation of an aatRNA, it is worth wondering what type of sign the aaRS is according to the classification proposed by Peirce. Peirce divides the signs according to three trichotomies, the second of which is of interest for the argument that follows. His presentation can be summarized with a few sentences:

(...) according as the relation of the sign to its object consists in the sign's having some character in itself, or in some existential relation to that object, or in its relation to an interpretant (...) a Sign may be termed an Icon, an Index, or a Symbol.

An Icon is a sign which refers to the Object that it denotes merely by virtue of characters of its own (...) it may represent its object mainly by its complementarity (...) An icon is a sign fit to be used as such because it possesses the quality signified.

An Index is a sign which refers to the Object that it denotes by virtue of being really affected by that Object (...) An index is a sign fit to be used as such because it is in real relation with the object denoted.

A Symbol is a sign which refers to the Object that it denotes by virtue of a law, usually an association of general ideas, which operates to cause the Symbol to be interpreted as referring to that Object (...) A Symbol is a Representamen whose

<sup>12</sup> Hoffmeyer (2010, p.371): “The act of interpretation ... seems to be a key to the production of meaning when this word is used in a situated local sense”.

representative character consists precisely in its being a rule that will determine its Interpretant (Peirce as quoted in Favareau (2009, p. 123–126, 131, 137)).

The application of these definitions leads to the following considerations. First, as explained, the recognition of an amino acid by the aaRS is independent of the recognition of an anticodon of tRNA. The anticodon does not have any quality that relates it to the amino acid. The relation between an amino acid and a tRNA anticodon in an aatRNA is not based on complementarities or correspondences between said elements, so it is not an icon.

Second, each anticodon is not in real relation to its corresponding amino acid. The correspondence established by each aaRS between them does not respond to the physical properties of the molecules of the connected sets. It cannot be said that the anticodon tRNA refers to the amino acid by virtue of being really affected by it, so it is not an index either.

The relation of an amino acid and a tRNA anticodon in an aatRNA, as has been shown, cannot be explained by the laws of physics alone. The aaRS implement in aatRNAs the rules that bind the amino acids and the tRNA anticodons. Each aatRNA implements a symbolic relation,<sup>13</sup> as long as any other set of amino acid-anticodon pairs could have been established. The synthesis of the aatRNAs corresponds to the definition of a system of conventional (arbitrary) semiotic relations.

### **The aatRNA: Origin and Use of the Sign**

It is worth asking now about the origin and use of the sign that has been analyzed.

According to Darwin, the origin of the components of an organism is explained by natural selection. On the other hand, considering Rosen's (1991) account, the presence of the components in an organism is explained by its closure to efficient cause. In neither of the two cases are the laws of physics sufficient, but it is necessary to introduce an additional explanatory principle.

According to the proposed definition of a semiotic relation, these statements are applicable to the process of interpreting a sign, which coincides with the action of a component of the organism. It remains, therefore, to explain the other element that defines semiotic relation, the determination of the interpretant.

It should be noted that the three subjects whose triadic relation defines a semiotic relation are also the entities that are part of the corresponding component. Semiotic relations correspond to components in which these three entities perform a local closure that determines their efficient cause. In an organism, a component does not imply the existence of a semiotic relation, but a semiotic relation does require the existence of a component. The semiotic actions (the interpretations of the signs of an organism) are a subset of the actions corresponding to the components of that organism.

The production of aaRSs can be explained by natural selection or by closure to efficient cause, depending on whether the focus is on the origin of the organism or its physiology. In any case, the production of aatRNAs responds to rules that are

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<sup>13</sup> The incorporation of an amino acid and a tRNA anticodon into an aatRNA should not be considered a real relation between them that defines an index (because it has not originated from the laws of physics alone), but rather the materialization of a symbol.

conventional in the sense that they had a historical origin. They are rules that comply with the laws of physics but are not defined by them alone.

It is necessary to note what these signs contribute to an organism. The presence of the semiotic relations defined in the aaRNAs (the genetic code) adds specificity to the elements on which natural selection acts and to the closure that realizes the organism, and with it, increases the organism's capacity for development, self-maintenance and contribution to open evolution.

### Translation is Symbolic Semiotic Action

The translation process, including the formation of aminoacyl tRNAs, is now described. Joining Figs. 2A and 4A, Fig. 5A is obtained.

Furthermore, the two maps of Fig. 5A can be summarized into one as shown in Fig. 5B.

Finally, also taking into account Fig. 3A, the translation of two consecutive codons and binding of the resulting amino acids can be represented with the mapping in Fig. 5C.

Accordingly, an analysis like the one in the previous sections can be carried out.

The translation apparatus (TA), made up of a ribosome and a set of aaRSs, produces the elements represented as the output of the mapping from the elements represented at its input.

The description of the biological process that is represented in Fig. 5C is the union of the previous descriptions of the biological sub-processes that compose it.

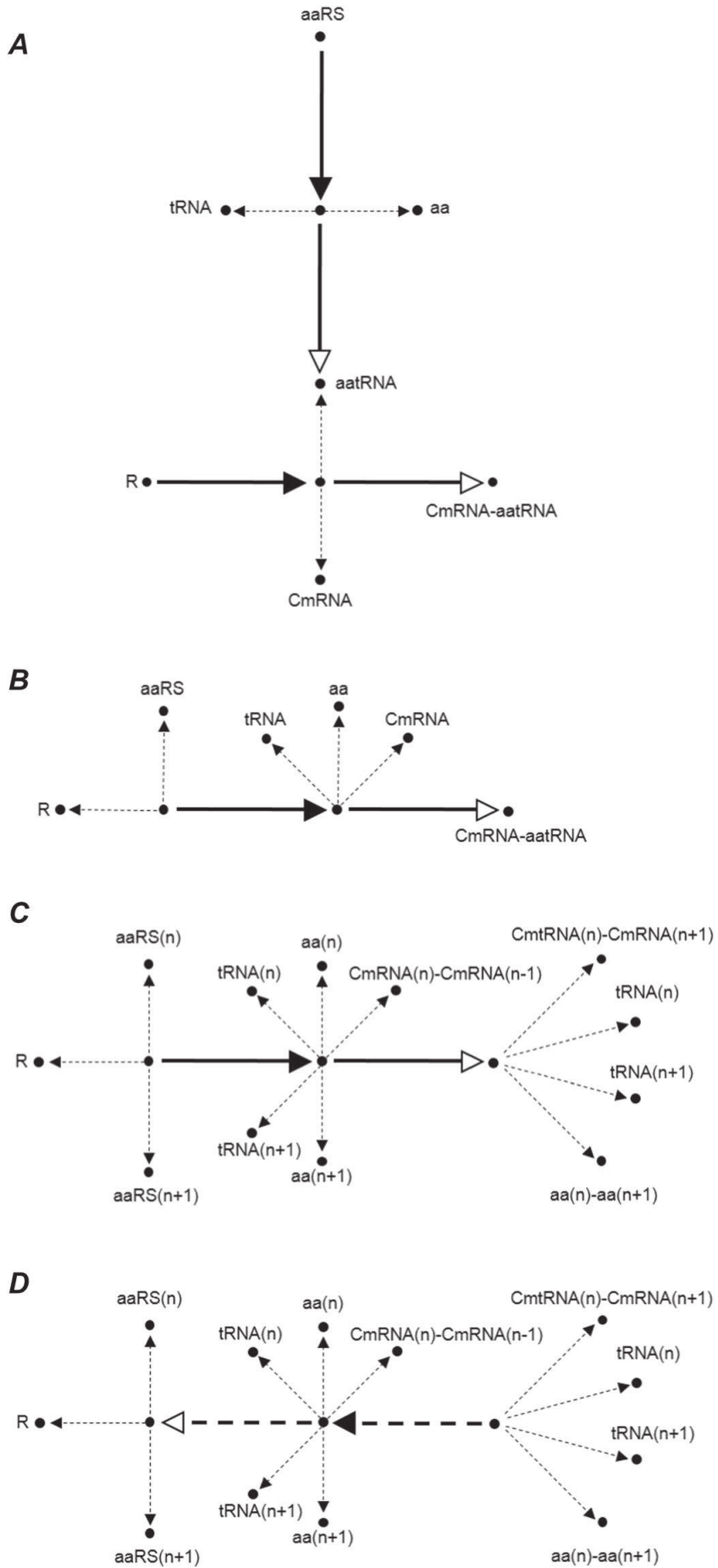
According to relational biology, translation corresponds to the action of a component of the system in which the translation apparatus is the efficient cause and the inputs and outputs are those represented in the mapping. Furthermore, the final cause of translation is the contribution of the component's output to the closure to efficient cause of the system.

A semiotic approach to the translation process is derived from the integration of the results obtained for each of the steps in which its analysis has been decomposed. Previously, it has been concluded that neither the binding of an mRNA codon and an aminoacyl tRNA nor the translation of two mRNA codons and the binding of the two resulting amino acids by themselves constitute semiotics actions. Conversely, it has been stated that the formation of an aminoacyl tRNA corresponds to a semiotic action, to the interpretation of a sign.

Figure 5D represents that the product of the translation process determines that the input of said process determines the translation apparatus.

The semiotic character of this process is a consequence of the semiotic character of the formation of the aaRNAs. The determination of the translation apparatus as the interpretant of a semiotic relation is a consequence of the determination of the aaRSs.

**Fig. 5** **A** Formation of an aminoacyl tRNA and binding of a CmRNA and an aaRNA. **B** Formation of an aminoacyl tRNA and binding of a CmRNA and an aaRNA summarized. **C** Translation of two consecutive mRNA codons. **D** Determination of (R, aaRS(n), aaRS(n + 1)). **E** The semiotic relation: interpretant = (R, aaRS(n), aaRS(n + 1)); sign = (CmRNA(n)-CmRNA(n + 1), tRNA(n), tRNA(n + 1), aa(n), aa(n + 1)); object = (CmRNA(n)-CmRNA(n + 1), rRNA(n), tRNA(n + 1), aa(n)-aa(n + 1)). **F** Translation of a chain of mRNA codons into a chain of amino acids. **G** Determination of the translation apparatus. **H** The semiotic relation: interpretant = translation apparatus; sign = chain of CmRNA; object = chain of amino acids



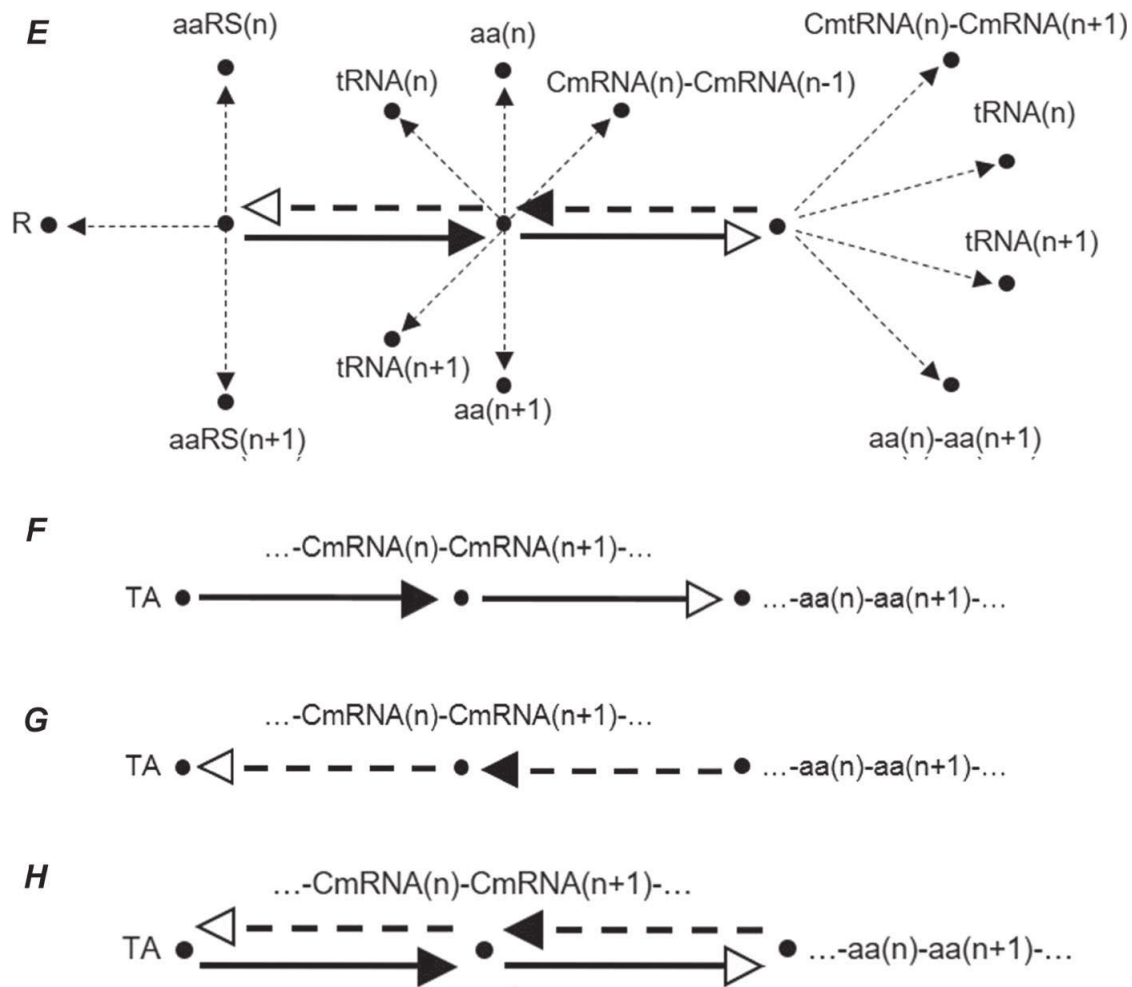


Fig. 5 (continued)

The semiotic relation depicted in Fig. 5E is a consequence of the semiotic relation depicted in Fig. 4E and F.

It is not the ribosome but the aaRSs that make translation a semiotic action.

Furthermore, the translation of an mRNA codon chain into an amino acid chain is represented in Fig. 5F.

The determination of the interpretant is now summarized in Fig. 5G, which should be read as follows. A specific chain of amino acids determines the corresponding chain of mRNA codons that determine the specific translation apparatus. It should be noted that the specificity of the translation apparatus of a specific translation process resides in the aaRSs that produce the aa-tRNAs that establish the relations between the tRNA anticodons and the amino acids involved in said translation.

The semiotic relation corresponding to the process of translation of an mRNA codon chain into an amino acid chain, including the interpretation of the sign and the determination of its interpretant, is represented in Fig. 5H.

Finally, since the formation of each aa-tRNA is a symbolic action, from the analysis carried out, it must be concluded that translation is a symbolic semiotic action.



## Transcription

The transcription of a DNA strand into an RNA strand is now discussed. To this end, the separation of the two strands of the DNA helix, the transcription of a DNA nucleotide and the elongation phase are analyzed separately. Finally, the regulation of transcription is studied.

Once again, only the elements necessary for the argument are considered.

### Separation of the Two Strands of the DNA Helix

The separation of the two strands of the DNA helix is depicted in Fig. 6A.

The enzyme RNA polymerase (RNAP) and one or more general transcription factors (GTFs), attached to a promoter DNA as explained below, separate the double-stranded DNA into a coding strand (cDNA) and a non-coding strand (ncDNA).

According to the relational account, the RNAP and the GTFs are the efficient cause of the component represented in the figure, the double-stranded DNA is the input (the material cause) and the coding and noncoding strands are the output. The final cause is the contribution of the pair of strands obtained (specifically, of the non-coding strand, which serves as the basis for the formation of the mRNA chain) to the synthesis of proteins and, with it, to the closure to efficient cause of the organism of which it is a part.

On the other hand, it is clear that a pair (cDNA, ncDNA) determines a cDNA-ncDNA, but it cannot be stated that the aspects of a cDNA-ncDNA that are suitable to stand for a (cDNA, ncDNA) determine the pair (RNAP, GTFs). Consequently, the separation of the two strands of the DNA helix does not correspond to a semiotic action.

### Transcription of a DNA Nucleotide

The transcription of a DNA nucleotide is represented by the mappings in Fig. 7A and B.

The RNA polymerase moves through the non-coding strand of DNA and synthesizes one mRNA molecule for each DNA molecule, adding a complementary ribonucleotide to the latter.

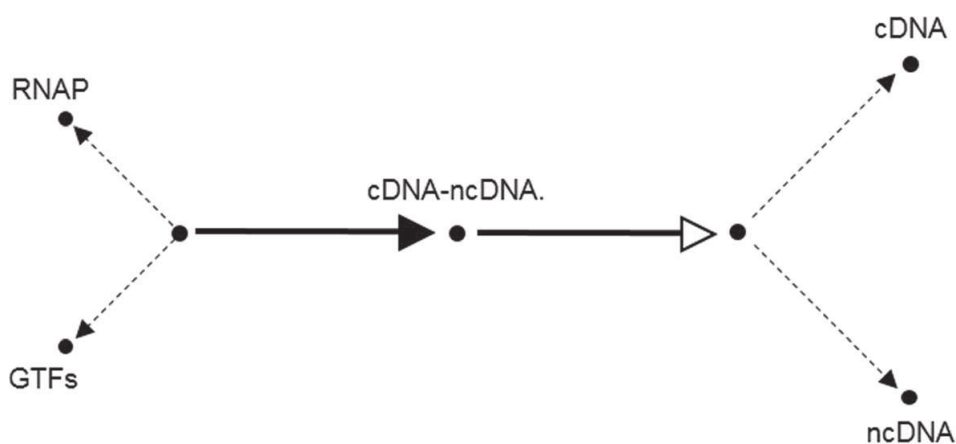
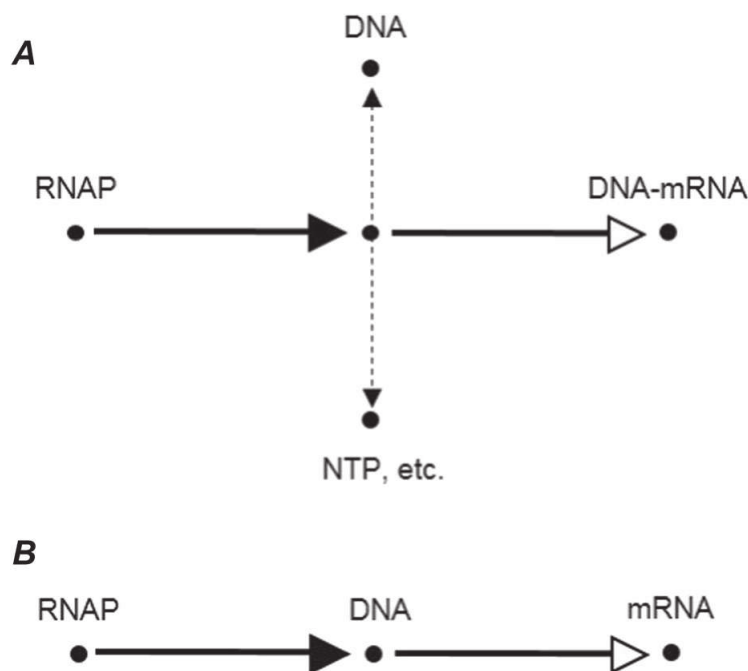


Fig. 6 A Separation of the two strands of the DNA helix



**Fig. 7** **A** Transcription of a DNA nucleotide. **B** Transcription of a DNA nucleotide

In this case, the RNAP is the efficient cause that produces an mRNA from a DNA and the final cause of mRNA is the contribution of this molecule to the closure of the system.

On the other hand, with the same arguments used above, it is concluded that the mRNA determines the DNA but the DNA does not determine the RNAP, so that the transition of a nucleotide DNA does not correspond to a semiotic action.

### Elongation

The elongation of transcription is represented in Fig. 8A, in which the mappings representing the transcription of two consecutive DNA nucleotides and the union of the two resulting mRNAs have been composed.

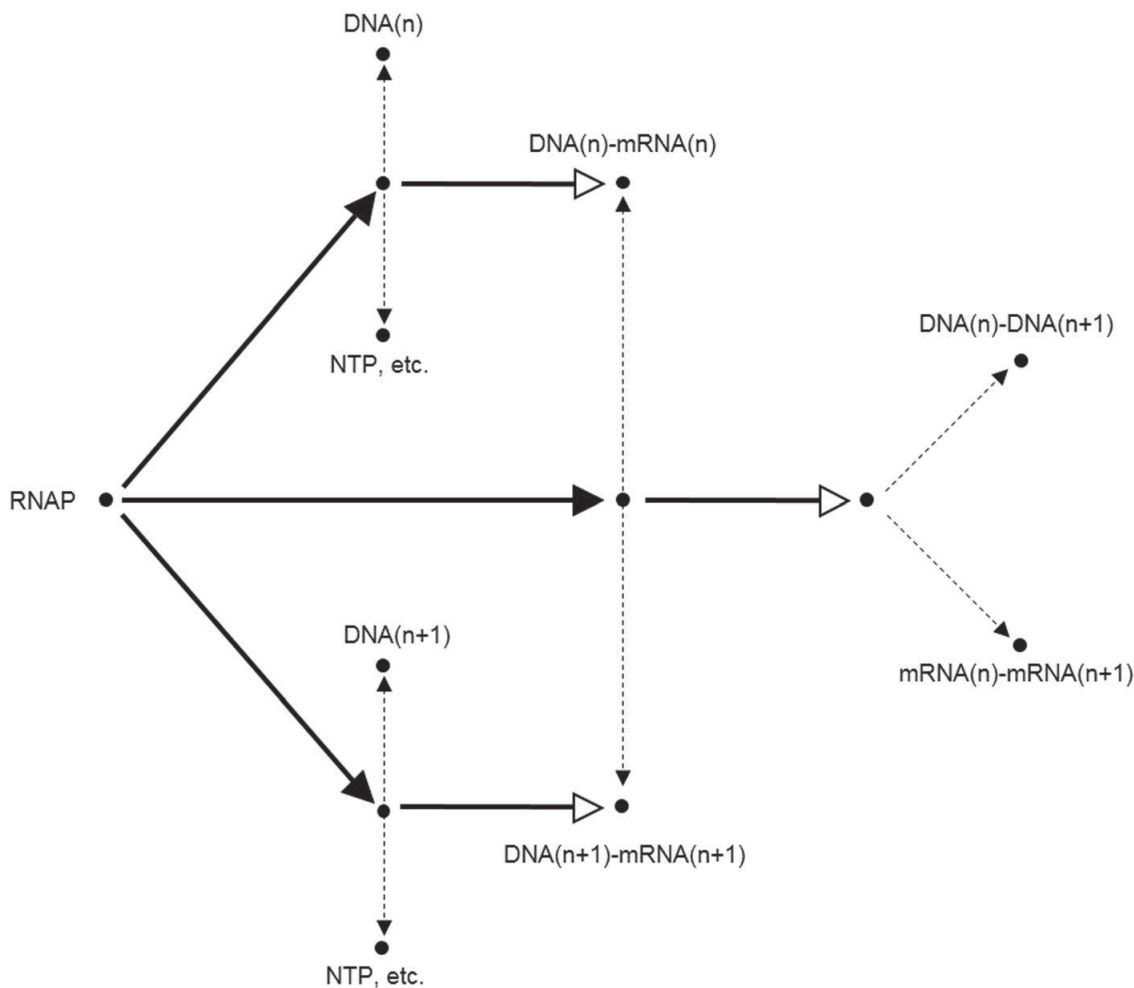
As the RNA moves through the DNA strand, the mRNA nucleotides that are produced form a chain that is complementary to the DNA chain that is transcribed.

As a summary, it must be stated that transcription is not a semiotic process.

### Regulation of Transcription

Protein synthesis in eukaryotes can be controlled in transcription, translation, and post-translation. The regulation of transcription is analyzed here, based on the representation in Fig. 9A.

The process depicted can be described as follows. A region of DNA called enhancer (ENH), to which an activator protein (ACT) –a specific transcription factor– has joined, bends the DNA strand bringing the activator near a gene promoter (PROM), also joining other proteins that act as general transcription factors (GTFs), a multiprotein complex called a mediator (MED) that functions as a transcriptional coactivator, and a RNAP.



**Fig. 8** A Elongation of transcription

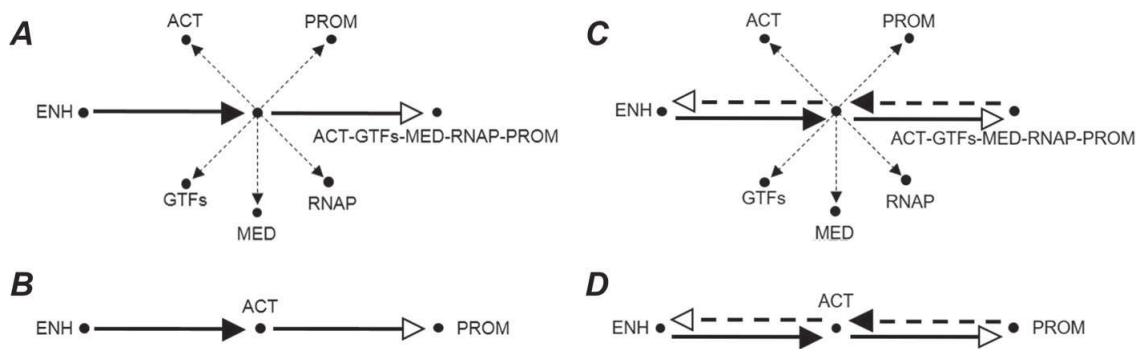
As a result, the transcription of the gene corresponding to the promoter selected by the enhancer is ready to begin. The process described corresponds to the association of an activator and a promoter of a gene to be transcribed, which can be represented by the mapping in Fig. 9.

A relational description similar to those presented previously can be made of this process. In this case, it is interesting to highlight that the output of the component is the preparation of the transcription of a specific gene and the final cause is the contribution of said gene to the self-maintenance of the metabolism, self-repair and organizational invariance of the system.

It is now convenient to analyze whether the regulation of transcription corresponds to the interpretation of a sign; whether an enhancer interprets an activator as a sign of a (promoter of a) gene, and whether the enhancer, the activator and the promoter form a triadic relation that corresponds to a semiotic action.

In the first place, the transcription preinitiation complex formed by the union of all the proteins represented in Fig. 9A and the promoter to which they have been linked determines the set of elements that form it. Equivalently, it can be said that the promoter determines the activator that has served as the basis for its selection.

The question to be solved is whether the set of proteins and the promoter in Fig. 9A determine the enhancer. Taking into account that RNA polymerase, the mediator and



**Fig. 9** **A** Regulation of transcription. **B** Regulation of transcription. **C** The semiotic relation: interpretant = ENH; sign = (ACT, PROM, GTFs, MED, RNAP); object = ACT-PROM-GTFs-MED-RNAP. **D** The semiotic relation: interpretant = ENH; sign = ACT; object = PROM

the general transcription factors perform similar functions for all genes, this is equivalent to questioning whether the activator determines the enhancer.

It can be stated that an activator determines an enhancer if aspects of the activator that are suitable to represent the promoter determine the enhancer. This is indeed the case. An activator is a sequence-specific DNA-binding factor that binds to a specific DNA sequence that belongs to the enhancer of a specific gene. The DNA binding domain of the activator that is suitable to represent the promoter determines the enhancer. Only specific enhancers can lead to the formation of the transcription preinitiation complex around specific promoters from specific activators.

Consequently, it must be stated that the regulation of transcription corresponds to a semiotic action, to a semiotic relation that is represented in Fig. 9C and D.

### Gene Expression is an Indexical Semiotic Action

In previous arguments, two signs have been identified that correspond, respectively, to the formation of the aatRNAs, which define the genetic code, and to the regulation of the initiation of the transcription of a gene, one of the processes by which the expression of genes is regulated in eukaryotes.

It should be noted that, from the point of view of relational biology, the components that correspond to these semiotic relations contribute to the same closure to efficient cause (the closure that realizes the cell) acting at two different levels. In both cases, the inputs and outputs are proteins and nucleotides. However, the second component affects all elements that make up the gene and the protein it synthesizes.

Similarly, from the point of view of semiotics, they are also two semiotic actions that act at different levels. The interpretation of the sign that regulates the start of the transcription of a gene subsequently triggers the interpretations of each of its mRNA nucleotides.

On the other hand, as explained, a promoter determines an activator that determines an enhancer because there is a relation between those three elements that cannot be explained by the laws of physics alone. As stated above, there is nothing in these laws preventing any other set of promoter-enhancer pairs from having been established. Accordingly, an enhancer, an activator and a promoter form a triadic relation that cannot be reduced to dyadic relations and that consequently corresponds to a semiotic relation.

Furthermore, the component in Fig. 9B corresponds to the interpretation of a sign that conforms to Short's definition of interpretation:

An enhancer interprets an activator a sign of a promoter (as a sign of a gene) if and only if (a) the enhancer is or is a feature of a response to the activator for a purpose, (b) the enhancer is based on a relation, actual or past or apparent or supposed, of the activator to the promoter or of things of the type of the activator to things of the type of the promoter, and (c) obtaining the promoter has some positive bearing on the appropriateness of the enhancer to the purpose.

Again, the question of which agent performs the interpretation has two complementary answers. On the one hand, the interpretation is realized by a part of the organism; on the other hand, the interpretation is realized by the complete system defined by the closure. The interpretation of an activator as a sign of a promoter corresponds to the realization of a local biological function that contributes to the self-maintenance of the whole cell.

Regarding the type of sign, the relation between an activator and a promoter is not based on complementarities or correspondences between said elements, so it is not an icon.

In this case, it can be affirmed that there is a real relation between the sign and the object, a relation that is established, on the one hand, by the DNA binding domain that joins the enhancer and the activator, and on the other, by the configuration of the DNA strand that associates the enhancer and the promoter. The enhancer-activator and enhancer-promoter associations are not completely independent but are determined by the synthesis of the activator and the structure of the DNA strand that can, in principle, be explained by adding the genetic code to the laws of physics. Thus, the relation between an activator and a promoter does not correspond to a symbol but to an index. The set of indices that correspond to the regulation of transcription are explained from the laws of physics and the set of symbols that define the genetic code.

A final comment on the contribution of these indexical signs to the cell. The genetic code has been seen to provide the specificity that increases the cell's capacity for development, self-maintenance and contribution to open evolution. The same, but multiplied, can be said of the set of signs that regulate transcription.

The genetic code includes 64 semiotic relations, implemented by 20 aaRSs, which interpret the 64 aa-tRNA anticodons as 20 amino acids.<sup>14</sup> On the other hand, in the human genome there are hundreds of thousands of enhancers<sup>15</sup> that can interpret about 1,600 different activators<sup>16</sup> as signs of promoters of different genes. A single activator may bind to many enhancers and hence control the expression of many genes. A few arbitrary, conventional rules, the symbols of the genetic code, contribute to the formation of a multiplicity of indices that multiply the specificity of the organism.

<sup>14</sup> According to the proposed definition, each semiotic relation of the genetic code is the union of a component (aaRS: ACtRNA → aa) and the relation by which the aa determines that the ACtRNA determines the aaRS.

<sup>15</sup> Pennacchio et al. (2013).

<sup>16</sup> Lambert et al. (2018).

## A Critical Analysis of Two Alternative Accounts

### Code Biology

Code biology is the theoretical framework for the study of biology developed by Marcello Barbieri, whose main postulates can be summarized as follows (Barbieri, 2008, 2009, 2015).

In general, a semiotic system is a system formed by two independent worlds connected by the conventional rules of a code; a system that is necessarily made up of at least three different entities: signs, meanings and code.

Barbieri analyzes the presence of codes in an organism (organic codes), in which the worlds to be connected are two different sets of molecules. In this case, a third type of molecular structures (codemakers) act as adapters, independently binding the molecules of both sets.

Barbieri provides the following definitions. The sequence used by a codemaker during a coding process is an organic sign. The sequence produced by a codemaker during a coding process is an organic meaning. An organic code is a set of rules of correspondence between signs and meanings.

The correspondence established by codemakers does not respond to the physical properties of the molecules of the connected sets but to conventional rules. Only an authentic code guarantees biological specificity. Furthermore, he identifies three different types of organic codes in life –manufacturing (as in translation), signaling (as in signal transduction) and regulatory codes (as in regulation of transcription) – and it is the combination of these codes that accounts for the complexity and evolutionary potential of organisms.

According to Barbieri, it is possible to affirm the existence of organic signs and meanings if the existence of organic codes is demonstrated and, therefore, he proposes as a biological research goal the identification of organic codes at all levels as an integral part of life.

At the cellular level, he rejects semiosis based on interpretation, arguing that it leads to the abandonment of scientific objectivity and the conversion of biology into a division of the humanities.

Finally, Barbieri argues that, in addition to natural selection, the explanation of evolution requires a second mechanism, natural conventions, corresponding to the emergence of new codes.

An analysis of code biology must necessarily begin by recognizing Barbieri's very outstanding contribution to defining a framework for the study of biology that includes semiosis. Code biology naturalizes the concepts of sign and meaning in an organism and opens up a path to biological research: the identification of codemakers that define codes.

However, some observations must be made.

Barbieri rejects the concept of interpretation at the cellular level, for understanding that this concept necessarily opens the door to nonscientific approaches to biology. However, he proposes a naturalization of the concept of meaning and, as has been stated quoting Hoffmeyer, interpretation corresponds to the production of meaning; both concepts are inseparable. In Vega (2018) the limitations of Barbieri's concept of interpretation are criticized and the possibility of including it in a scientific study of life

is upheld. Furthermore, Vega (n.d.) proposes a definition of a semiotic relation and an application of Short's definition of interpretation to the case of the organism.

On the other hand, the definition of organic meaning presents the problem of not distinguishing between the object of a sign (in Peirce's terminology) and its meaning, or (in relational terms) between the output of a component and the function it performs in the organism. It should be noted that, for example, the meaning of a chain of mRNA codons is not the protein produced in translation, but its contribution to the closure of the system, to the self-maintenance of the organism.

To deepen the analysis, it is convenient to ask whether an organic code is a semiotic relation and, if so, to what type of sign it corresponds.

From the point of view of relational biology, the codemaker, the organic sign and the organic meaning correspond to the efficient cause, the input and the output of a component of the organism. The aforementioned definition of a semiotic relation in an organism, applied to an organic code, is equivalent to affirming that the codemaker, the organic sign and the organic meaning are respectively the interpretant, the sign and the object; the organic meaning determines the organic sign that determines the codemaker; and the action of this component corresponds to the interpretation of a Peirce sign.<sup>17</sup>

Code biology gives priority to the codemaker. It is the codemaker that creates signs and meanings, which do not exist (as such) outside a codemaking process. However, as an integrated account of Rosen's relational biology and Peirce's semiosis shows (Vega, n.d.), the entities that play the role of codemaker, organic sign and organic meaning are defined as such by their mutual interdependence. The determination of a codemaker is not the production of an entity that acts as such but its selection from among the entities produced by the closure of the system. Moreover, it is the closure that is established between the interpretation and the determination of the interpretant that defines the semiotic relation.

On the other hand, applying Short's definition of interpretation to the organic code, the following is obtained: a codemaker interprets an organic sign as a sign of an organic meaning if and only if (a) the codemaker is or is a feature of a response to the organic sign for a purpose, (b) the codemaker is based on a relation, actual or past or apparent or supposed, of the organic sign to the organic meaning or of things of the type of the organic sign to things of the type of the organic meaning, and (c) obtaining the organic meaning has some positive bearing on the appropriateness of the codemaker to the purpose. Also in this case, the integrated account of the theories of Rosen and Peirce supports the application of the concept of interpretation to code biology.

In conclusion, an organic code corresponds to a Peirce sign. It then remains to elucidate what type of sign it is. According to Barbieri, organic codes are organic symbols. This statement should be revised in view of the analysis carried out in the cases of translation and the regulation of transcription.

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<sup>17</sup> This paper answers the questions posed by Brier and Joslyn in their analysis of code semiosis: (1) what can "interpretation" mean, if it is not code following? And (2) what do code-semioticians call code following, since it's clearly not "interpretation" (2013, p. 153). Furthermore, it is shown that these authors confuse the concepts of interpreter (the agent who performs the interpretation) and interpretant. For example, they claim that a ribosome is an interpreter. However, as seen above, translation is a semiotic process in which a chain of messenger RNA codons is the sign, a chain of amino acids is the object, and a ribosome and a set of aminoacyl tRNA synthetases form the interpretant.

As explained above, the translation apparatus, made up of a ribosome and a set of aaRSs, produces an amino acid chain from an mRNA codon chain. According to code biology, the organic sign is the mRNA codon chain, the organic meaning is the amino acid chain and the codemaker is the translation apparatus. As stated above, the relationship between an amino acid and a tRNA anticodon in an aaRNA is not based on complementarities or correspondences between said elements, nor can it be said that the anticodon tRNA refers to the amino acid by virtue of being really affected by it. Translation corresponds to a symbolic action, which coincides with what is defended by code biology. The genetic code is a set of rules that cannot be explained by the laws of physics, the only norms applicable at the time of its emergence. These are arbitrary rules that define a symbol.

On the other hand, in terms of code biology, the explanation of gene expression would lead to the assertion that the enhancer is the codemaker, the activator is the organic sign and the promoter corresponds to the organic meaning. Furthermore, as has been explained, the regulation of transcription must also be explained as a semiotic action. However, it has been stated that there is a real relation between the activator and the promoter. The enhancer-activator and enhancer-promoter associations are conditioned by the synthesis of the activator and the structure of the DNA. At the time of the emergence of the regulation of transcription, in addition to the laws of physics, the rules of the genetic code are also applicable. The specificity provided by the code that regulates gene expression is supported by the specificity provided by the genetic code, and significantly broadens it. The code that corresponds to the regulation of transcription is specified in a set of rules constrained by the genetic code.

One final comment on the concept of natural conventions: the difference stated between the genetic code and that which regulates transcription leads to two complementary statements. On the one hand, the appearance of new codes supposes qualitative changes in evolution, as Barbieri maintains. However, this does not necessarily imply the need to introduce an additional explanatory principle. The regulation of transcription corresponds to a semiotic relation that, in principle, can be explained with the laws of physics, the genetic code and natural selection.

### **Protosemiosis**

Sharov and Vehkavaara (2015) consider that Peirce's semiosis is not applicable at the most basic level of an organism, and they propose a primitive type of semiosis, which they call protosemiosis, in which agents (i.e., active systems guided by natural self-interest) associate signs directly with actions without considering objects.

They argue that the most primitive signs (proto-signs) are signs because they produce a specific response from the agents that contributes to their natural self-interest (i.e., increase the rates of survival and self-reproduction), and therefore play a functional role that is not the same as its physical nature. However, protosemiosis differs from Peirce's semiotics because it is not based on object categorization and tracking. The association of signs with categories of objects would require the agent to



have a “minimal mind” and a capacity for representation, which would not be present in the most primitive forms of life. Consequently, a proto-sign is not a triadic relation between sign, object and interpretant, but a dyadic relation between sign and action.

On the other hand, while Peirce classifies the signs into icons, indices and symbols by the type of relationship that exists between the sign and the object, Sharov and Vehkavaara classify proto-signs according to their immediate interactions with partner agents, that is, according to the type of mechanism by which the functional effect of the sign is produced: proto-icons signal via single specific interaction, proto-indexes combine several functions, and proto-symbols are processed by a universal subagent equipped with a set of heritable adapters.

The following comments should be made about the concept of protosemiosis.

The concept of a semiotic relation in an organism introduced in Vega (n.d.) avoids the problems that lead Sharov and Vehkavaara to propose a semiosis different from that of Peirce. In the aforementioned paper, the concept of semiotic relation is naturalized, which includes the formation of the semiotic relation and the interpretation of the sign.

For example, as seen above, to explain protein synthesis as a semiotic action, the concepts of minimal mind, representation and categorization of objects, similar to those used to explain the interpretation of signs by the human being, are not necessary. Instead, the concepts of closure and final cause have been used to account for the functional role that signs play in the self-interest of the agent who interprets them.

Continuing with this example, it should also be noted that when a ribosome and a set of aminoacyl tRNA synthetases produce an amino acid chain from an mRNA codon chain, the rules of a code that respond to the closure to efficient cause of the organism and to the local closures that defines the semiotic relations are applied. These are rules defined by evolution; rules that are arbitrary at the time of their definition but not at the time of their application. Each amino acid is an object that forms a triadic relation with a CmRNA codon and the junction of a ribosome and an aaRS; a previously defined triadic relation that realizes at the time of translation.

On the other hand, the classification of proto-signs should be commented considering two examples proposed by Sharov and Vehkavaara. Following their classification criteria, these authors conclude that the formation of an aminoacyl tRNA by an aaRS from an amino acid and a tRNA corresponds to the action of a proto-index. Conversely, it has been argued above that an aatRNA is the realization of a rule of the genetic code and that it is an arbitrary rule that corresponds to a symbol.

Additionally, Sharov and Vehkavaara argue that the translation of mRNA sequences is an action corresponding to proto-symbols because they are members of a family of similarly-structured molecular signs that are processed uniformly by the same kind of subagents (ribosomes) and the same set of heritable adapters (aatRNAs, which are proto-indexes). On the contrary, this paper argues that the symbolic character of translation is based on the symbolic character of the formation of each aatRNA and that the genetic code is made up of a set of symbols (not indices).

Finally, it should be noted that Sharov and Vehkavaara propose protosemiosis as a necessary intermediate step between a (simple) world without semiosis and the appearance of Peirce's (complex) semiosis. However, as has been argued, the semiotic relations that are at the base of current living beings, the genetic code, must already be explained as Peirce signs, not as proto-signs. As Hoffmeyer (2008) indicates, increasingly useful dyadic relation systems must have preceded the emergence of life,

which would only have emerged with the formation of the first triadic (semiotic) relations, giving rise to a new type of causality. Subsequently, on the first signs, others would have arisen, generating the different layers and relations that correspond to the semiotic scaffolding that is now observed. The application of the concepts and the method proposed in this paper to the translation and regulation of transcription suggests that, although there are different semiotic actions that perform important functions in an organism, all of them must have been built from the genetic code. Furthermore, once it has been admitted that the genetic code corresponds to Hoffmeyer's first triadic (semiotic) relations, the search for alternative explanations for the genesis of triadic semiosis within natural systems does not seem necessary.

## Conclusions

In Vega (n.d.), an integrated account of Rosen's relational biology and Peirce's semiosis has been posited, in which relational biology and Peirce's semiosis have complemented each other by including them in a common framework. Naturalized definitions, applicable to a simple organism, for the concepts of semiotic relation, semiotic action and sign have been put forward, and the application of Short's definition of interpretation has been extended to that context. Finally, a method to identify and analyze signs in an organism has been proposed.

In this paper, protein synthesis has been analyzed, in accordance with the theoretical approach of the quoted work, obtaining the following results.

First, both the concepts that naturalize semiosis in an organism, as well as the method of identification and analysis of signs at that level, have been shown to be consistent and useful for the study of processes such as transcription and translation that occur inside a cell. Descriptions of standard biology, relational biology and semiotics have been integrated in the analysis carried out.

Second, two groups of signs have been identified. Those of the first type are present in the formation of the amino acyl tRNA molecules, correspond to the realization of the genetic code, and are the basis of the explanation that translation is a semiotic action. Those of the second type correspond to the regulation of transcription. It has been argued that the former are symbols and the latter are indices. The indexical nature of the regulation of transcription is due to the fact that, in this case, there is a real relation between the sign and the object that can, in principle, be explained from the laws of physics and the set of symbols that define the genetic code. The existence of the symbols of the genetic code is a necessary condition for the existence of the indices that regulate transcription. The application of the concepts and the method proposed here seem to suggest that, although there are different semiotic actions that perform important functions in the organism, the only symbolic actions are those of the genetic code.

Finally, the proposals defended here have been opposed to those of code biology and protosemiosis, concluding against what is defended in said theories, that Peirce's semiosis (integrated with Rosen's relational biology) is adequate for the study of signs in an organism.

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## CONCLUSIONES

Como resultado de esta tesis, se confirman las hipótesis planteadas: (i) la biología relacional y la biosemiótica son propuestas válidas para fundamentar una nueva ciencia de la biología, (ii) el carácter científico de la biosemiótica puede sustentarse en la biología relacional y (iii) la aplicación de ambas teorías en la práctica científica puede sustentarse en la integración de ambas.

En los tres artículos publicados, se han desarrollado las bases de un marco teórico para el estudio científico de la biología que integra la semiosis de Peirce y la biología relacional de Rosen, una biosemiótica relacional en la que (i) se ha dado cabida a la causa final, (ii) se han naturalizado los conceptos de relación semiótica, signo, significado, acción semiótica e interpretación y (iii) se ha definido y aplicado un método de identificación y análisis de signos en un organismo.

Estas conclusiones se desarrollan a continuación en los resúmenes de los artículos publicados.

## RESÚMENES DE LAS PUBLICACIONES

### **A Critique of Barbieri's Code Biology through Rosen's Relational Biology: Reconciling Barbieri's Biosemiotics with Peircean Biosemiotics.**

La semiótica estudia los sistemas de signos, su producción y funcionamiento. Charles Sanders Peirce argumentó que la semiosis requiere una relación triádica entre un signo, un objeto y un *interpretant*.

La biosemiótica es la unión de la biología y la semiótica. Sostiene que la vida y la semiosis son coextensivas, y que los signos y los significados son entidades naturales en los que debe basarse la explicación de los seres vivos. La biosemiótica peirceana es el marco en el que se han desarrollado las propuestas de gran parte de los expertos, agrupados principalmente en las escuelas de Copenhague y Tartu. Se basa en la semiosis de Peirce, que combina con conceptos como los de autoorganización, auto mantenimiento y cierre.

Marcello Barbieri ha desarrollado un marco teórico que también se centra en el papel de los signos y significados en la explicación de la biología. Sin embargo, la biosemiótica de Barbieri se ha desarrollado fuera de la corriente principal, apoyándose en el concepto de código. Luego de una etapa de colaboración con otras escuelas, Barbieri se apartó del campo común de la biosemiótica, considerando que la biosemiótica peirceana abre la puerta a enfoques no científicos a través del concepto de interpretación.

Este artículo muestra que el rechazo de Barbieri a la biosemiótica peirceana se basa en una concepción limitada de la ciencia y una comprensión incorrecta de la biosemiótica peirceana, que malinterpreta el ámbito de aplicación de la semiosis de Peirce y no toma en cuenta el resto de las teorías en las que se basa la biosemiótica peirceana.

El trabajo de Barbieri se estudia aquí con herramientas tomadas de la biología relacional de Robert Rosen. La biología de Rosen proporciona un concepto de ciencia que permite superar la identificación de Barbieri de ciencia con perspectiva mecanicista y, por otro lado, puede verse como una base para la biosemiótica peirceana.

Las tres primeras secciones del artículo reúnen los elementos necesarios de las teorías a analizar. Primero, se enuncian brevemente los conceptos básicos de la semiosis de Peirce y la biosemiótica peirceana. De acuerdo con Peirce, para estudiar la naturaleza, además de las acciones físicas, se deben tener en cuenta las acciones semióticas, en las que un signo (o *representamen*), un objeto y un interpretant se unen en una relación triádica que no puede reducirse a relaciones diádicas. Una acción asociada a un signo se realiza por medio de la interpretación del signo. La biosemiótica peirceana fue creada por Thomas Sebeok a partir de la semiosis de Peirce y los estudios de Jacob von Uexküll sobre la comunicación animal, y posteriormente combinada con diversas influencias de

la teoría general de sistemas. Según la biosemiótica, es el uso de signos lo que caracteriza a los seres vivos.

En segundo lugar, se presenta el marco de Barbieri para el estudio de la biología. Para Barbieri, un sistema semiótico es un sistema formado por dos mundos independientes conectados por las reglas convencionales de un código, un sistema que se compone de signos, significados y código. En el caso de los códigos orgánicos, se distinguen tres conjuntos de moléculas, que corresponden a signos, significados y creadores de códigos. La secuencia utilizada por un creador de códigos durante un proceso de codificación es un signo orgánico. La secuencia producida por un creador de códigos durante un proceso de codificación es un significado orgánico. Un código orgánico es un conjunto de reglas de correspondencia entre signos y significados. La codificación no puede reducirse a la copia, por lo que la evolución requiere dos mecanismos independientes: la selección natural y las convenciones naturales, correspondiente este último mecanismo a la aparición de nuevos códigos.

Barbieri (2015) analiza dos marcos para el estudio de la biología: la Síntesis Moderna y la biología de sistemas. La Síntesis Moderna pone el foco en los aspectos poblacionales y se basa en el mecanismo de la selección natural. Según este autor, es necesario otro mecanismo adicional para explicar la evolución: las convenciones naturales. Por su parte, para la biología de sistemas, un organismo es un sistema que se autofabrica y se explica por medio de la autopoiesis. En su lugar, Barbieri propone explicar el organismo por la *codepoiesis*. Después del surgimiento del primer código orgánico, el código genético, la evolución posterior de las células se explicaría con dos procesos complementarios que, en conjunto, constituyen la codepoiesis: la generación de nuevos códigos orgánicos y la conservación de los existentes.

A nivel celular, rechaza la semiosis basada en la interpretación por considerarla no-científica. Identifica ciencia con perspectiva mecanicista.

Y tercero, se analiza la biología relacional de Rosen. Según este autor, el concepto de ley natural se basa en la afirmación de que existe, y puede establecerse, una relación entre la causalidad de los sistemas naturales y las implicaciones de los sistemas formales. Un sistema formal  $F$  es un modelo de un sistema natural  $N$  si se obtiene el mismo resultado en los dos casos siguientes: (i) paso de un fenómeno a otro en  $N$ , y (ii) codificación de  $N$  en  $F$ , aplicación de  $F$  y decodificación de  $F$  en  $N$ . Un sistema natural puede tener varios modelos.

Rosen introduce los conceptos de analogía y metáfora entre dos sistemas naturales, que permiten aprender de uno de los sistemas estudiando el otro. Entre dos sistemas naturales  $N_1$  y  $N_2$  que pueden codificarse en un mismo sistema formal se establece una analogía, en la que  $N_2$  contiene un modelo de  $N_1$  y  $N_1$  contiene un modelo de  $N_2$ . Por otra parte, en el caso de dos sistemas formales  $F_1$  y  $F_2$  correspondientes a dos sistemas naturales  $N_1$  y  $N_2$ , si entre  $F_1$  y  $F_2$  existe una relación matemática, pero no existe una

función entre las proposiciones en ambos sistemas formales que preserve la estructura de implicaciones, no puede establecerse una analogía entre  $N_1$  y  $N_2$ , pero si puede afirmarse que  $N_1$  es una metáfora de  $N_2$  y viceversa. Rosen (2012) aplica el concepto de analogía en el estudio de los sistemas anticipatorios, y explica metafóricamente los conceptos de eficacia biológica (fitness), adaptación, selección natural y evolución.

En las figuras 1 y 3 del artículo se representan respectivamente los conceptos de ley natural y modelo, y de analogía entre dos sistemas naturales.

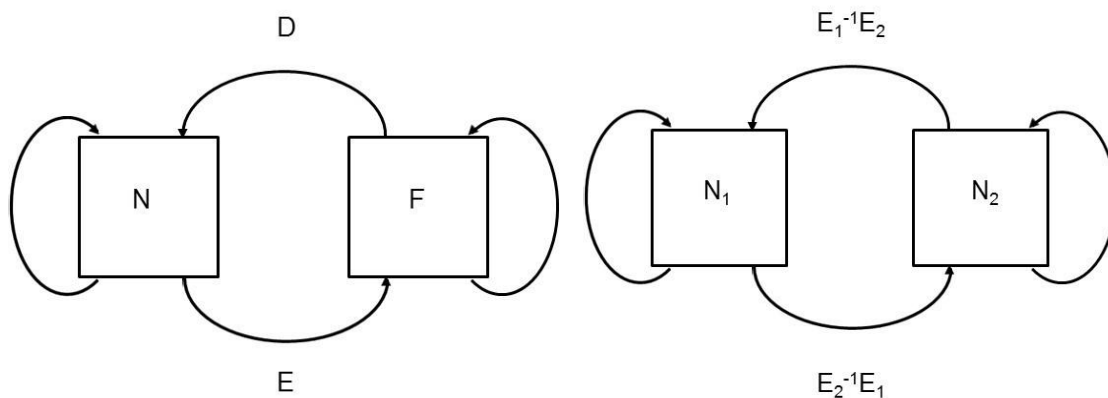


Fig. 1 Ley natural y modelo

Fig. 3 Analogía entre dos sistemas naturales

Adicionalmente, precisa el concepto de simulación entre dos sistemas formales. Si  $F_2$  es un modelo de  $F_1$ , entonces  $F_1$  es simulado por  $F_2$ . En este caso,  $F_1$  se incorpora dentro de  $F_2$  y el formalismo simulado se convierte en el efecto del formalismo simulador. No se establece una relación de congruencia entre ambos formalismos, por lo que no puede aprenderse nada sobre  $F_1$  a partir de su simulación. De acuerdo con Rosen, una función es simulable (o computable) si es definible por un algoritmo, es decir, si es evaluable por una máquina matemática (de Turing).

Rosen afirma que un sistema natural es un mecanismo si y solo si todos sus modelos son simulables y concluye que un organismo es diferente de un mecanismo. Un mecanismo es una construcción puramente sintáctica, que corresponde a un sistema simple. Un organismo es un sistema complejo. Un organismo puede tener modelos mecanicistas, pero el límite de sus modelos mecanicistas no es un mecanismo, no puede existir un mecanismo que corresponda a un modelo completo del organismo. Un organismo es un sistema congruente con un modelo impredicativo, un modelo en el que la definición de cada componente hace referencia al componente que se define o a otro que le contiene. Un sistema vivo debe tener modelos no computables. La física es la ciencia de los mecanismos y debe considerarse una ciencia especial, mientras que la biología es una ciencia más general que estudia sistemas complejos que requieren más tipos de modelos, algunos de los cuales no son simulables.

Rosen estudia los sistemas anticipatorios. Un sistema anticipatorio es un sistema que contiene un modelo predictivo de sí mismo y/o de su entorno, que le permite cambiar de estado en un instante de acuerdo con las predicciones del modelo correspondientes a un instante posterior. Puede, por tanto, afirmarse que un sistema anticipatorio interpreta. El estudio de los sistemas anticipatorios se basa en el concepto de analogía.

Los sistemas formales propuestos por Rosen para como modelos de los sistemas naturales son modelos relacionales, definidos por sus componentes y las relaciones establecidas entre ellos. Siguiendo la clasificación aristotélica, Rosen analiza las causas de un componente y concluye que un sistema material es un organismo si y solo si es un sistema cerrado bajo causación eficiente.

Finalmente, propone el sistema (M, R) como modelo de un organismo. En este tipo de sistema se produce el cierre entre tres clases de funciones, que denomina metabolismo, reparación y replicación. Un sistema (M, R) presenta un carácter anticipatorio intrínseco, que va más allá de los mecanismos e implica una semiosis que incluye y sobrepasa la semiosis basada en códigos.

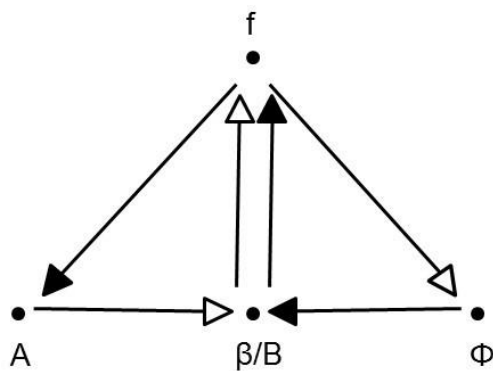


Fig. 7 Un sistema (M, R)

Estas tres secciones explican que existen enfoques y objetivos diferentes, pero también conceptos compartidos, que son aceptados o rechazados, con igual o diferente significado, e implican por sí mismos una primera comparación de la biología de códigos, la biosemiótica peirceana y la biología relacional.

En la sección cuarta, se critican dos propuestas clave la biología de códigos con argumentos tomados de la biología relacional de Rosen. En primer lugar, se discute la relación entre ciencia y mecanismo. Barbieri sostiene que el método científico se basa en la definición de modelos, e identifica modelos con mecanismos, lo que le lleva a identificar el método científico y la perspectiva mecanicista. Sin embargo, como se ha expuesto anteriormente, Rosen argumenta que los mecanismos no son suficientes para la ciencia de la biología.



En segundo lugar, se analiza la crítica de Barbieri al concepto de interpretación y, con ella, su rechazo a la biosemiótica peirceana. Barbieri (2015) descarta la semiosis basada en la interpretación porque (i) la interpretación se basa en la abducción, (ii) lo que se interpreta no es el mundo sino representaciones del mundo; y (iii) el resultado de la interpretación depende del entorno y la experiencia previa (la interpretación requiere memoria).

Sin embargo, el sistema anticipatorio de Rosen contienen un modelo de sí mismo y/o de su entorno, de modo que cambia su estado en un instante de acuerdo con las predicciones del modelo sobre un tiempo posterior. Parece adecuado afirmar que el sistema interpreta lo que indica su modelo sobre lo que puede ocurrir en el futuro, a partir de su estado y del entorno en el presente. Por otra parte, el sistema (M, R), que propone como modelo del organismo, tiene un carácter anticipatorio inherente construido en su organización. Su capacidad predictiva depende también del entorno y de la experiencia previa (aprendizaje, memoria) del sistema. Finalmente, Rosen argumenta que (i) la selección y la adaptación generan modelos predictivos; (ii) el aprendizaje puede verse como parte de la adaptación o como una metáfora de la misma; y (iii) los procesos de aprendizaje generan modelos predictivos.

En la sección quinta, como resultado adicional de la investigación realizada, se esbozan algunas líneas de un estudio de la biología de Rosen como teoría biosemiótica compatible con la biología de códigos y la biosemiótica peirceana. La analogía entre dos sistemas naturales  $N_1$  y  $N_2$  se basa en una relación de modelado entre ambos sistemas, en la que las cualidades de  $N_1$  se codifican en las cualidades de  $N_2$ .  $N_1$  y  $N_2$  son dos sistemas independientes unidos por reglas de codificación, lo cual es formalmente similar a los dos mundos independientes conectados por un código propuesto por Barbieri; y el concepto de analogía, es la base de la definición de un sistema anticipatorio. Además, los componentes de Rosen corresponden a dos conjuntos independientes relacionados por un mapping, donde la causa eficiente conduce de cada elemento del primer conjunto a un elemento del segundo. Sin embargo, no todos los mappings de un modelo relacional representan procesos sujetos a causas eficientes arbitrarias. Solo aquellos mappings en los que las relaciones entre las entradas y las salidas corresponden a reglas arbitrarias son comparables a los códigos de Barbieri.

Se concluye que: (i) la biología de códigos proporciona las herramientas teóricas adecuadas para el desarrollo de la investigación biológica; (ii) es posible desarrollar otras biosemióticas científicas en el marco de la biosemiótica peirceana; (iii) la biología de códigos y la biosemiótica peirceana, a pesar de sus diferentes enfoques, pueden formar parte de un marco común para la biología; y (iv) también se puede realizar una lectura biosemiótica de la biología de Rosen.

## An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part I: Components and Signs, Final Cause and Interpretation

En este artículo, se propone un relato integrado de la biología relacional de Rosen y la semiosis de Peirce.

En biología relacional, los organismos se analizan como sistemas formados por componentes que están relacionados entre sí, produciendo un cierre del sistema bajo causación eficiente. Es este cierre lo que define al ser vivo; lo que establece entre las partes de un sistema natural unas relaciones que adquieren una realidad diferenciada con características propias, más allá de las de las partes que participan en ellas; lo que convierte dichas partes en los componentes que realizan funciones biológicas que surgen al realizarse el cierre.

Por otro lado, la biosemiótica sostiene que es el uso de signos lo que caracteriza al ser vivo. A diferencia de las acciones dinámicas, las acciones semióticas corresponden a relaciones triádicas entre los sujetos que componen la relación semiótica (signo, objeto e interpretant) que no pueden reducirse a relaciones diádicas.

La sección "Components, Signs, Mappings and Triadic Relations" comienza con la presentación de los conceptos de Rosen de ley natural, modelo<sup>1</sup>, componente y mapping, y su análisis de las causas aristotélicas. En un modelo relacional, un componente -la unidad básica del sistema- se representa con un mapping entre dos conjuntos,  $f: A \rightarrow B$ , que puede expandirse  $f \longrightarrow (a \longrightarrow f(a))$ , para cada  $a \in A$ , con  $f(a) = b \in B$ , que puede leerse "f implica que a implica b". La representación gráfica de un componente puede verse en las figuras 1A y 1B del artículo, en las que las flechas de punta hueca representan el flujo de a a b, y las flechas de punta sólida simbolizan el efecto del componente.



Fig. 1A Representación de un componente

Fig. 1B Acción de un componente sobre una entrada

Siguiendo la clasificación de las causas aristotélicas, cabe preguntarse por qué se realiza la cualidad del sistema representada por b. De acuerdo con Rosen, el componente f es la causa eficiente y la entrada a es la causa material. Según Louie (2009), la causa formal corresponde a la estructura del mapping, a la unión ordenada de las dos flechas. Pero ¿cuál es la causa final? Se responde a esta pregunta en una sección posterior.

<sup>1</sup> Ver el resumen del artículo anterior.

A continuación, considerando la definición de signo de Peirce, se discute la posibilidad de representar relaciones semióticas con mappings y se hace una propuesta. Citando a Peirce:

A sign, or representamen (...) addresses somebody, that is, creates in the mind of that person an equivalent sign, or perhaps a more developed sign. That sign which it creates I call the interpretant of the first sign (Peirce as quoted in Favareau (2009, p. 122)).

I define a sign as anything which is so determined by something else, called its Object, and so determines an effect upon a person, which effect I call its interpretant, that the latter is thereby mediately determined by the former" (Peirce 1998, p. 478).

Una acción semiótica conduce de un signo a un objeto, creando un interpretant en el intérprete. En un sistema relacional que representa un organismo, donde todas las acciones son realizadas por los componentes del sistema, se puede considerar que la interpretación del signo corresponde a la acción de un componente, en el que el interpretant es la causa eficiente, el signo es la causa material, y el objeto es la salida, como se muestra en la Fig. 5 del artículo, donde I, S y O representan respectivamente al interpretant, el signo y el objeto. El concepto de interpretación en un organismo se explica en una sección posterior.

Por otra parte, la afirmación de que, en una relación semiótica, el objeto determina que el signo determina al interpretante, equivale a afirmar que el objeto implica que el signo implica el determinante, por lo que también sería conveniente representarlo con un mapping. Sin embargo, la determinación del interpretante no corresponde a un componente, por lo que se utilizan líneas discontinuas, como se muestra en la Fig. 4.



Fig. 4 Determinación del interpretant

Fig. 5 Interpretación del signo

La unión de la determinación del interpretant y la interpretación del signo (el cierre entre ambas) define la relación semiótica como una relación triádica, irreductible a relaciones diádicas. Su representación requiere los dos mappings antes mencionados. La relación semiótica se representa en la Fig. 6 del artículo.

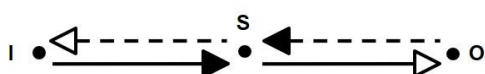


Fig. 6 Una relación semiótica

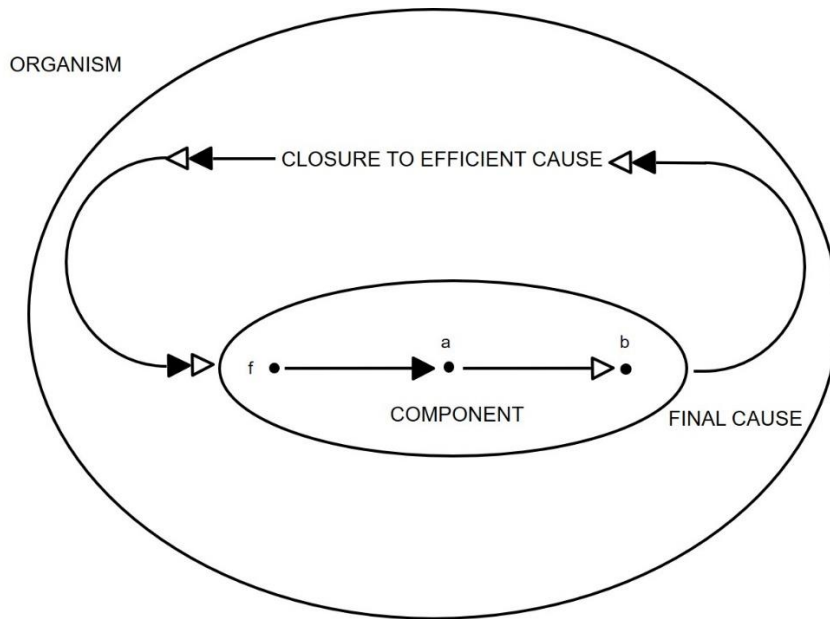
En la sección “Causa final”, se analiza el papel de la causa final en la selección natural, la biología relacional y la semiosis de Peirce.

Como explica Short (2002), mientras que la causa eficiente conduce a resultados particulares, la causa final es un tipo de resultado que se puede realizar de diferentes maneras. Además, un tipo de resultado es una causa final solo si explica por qué suele haber instancias de este tipo. La reintroducción del concepto de causa final en la ciencia moderna es necesaria porque hay preguntas que las causas eficientes no pueden responder, hay explananda que no admiten explicaciones mecanicistas. Además, para explicar un explanandum de este tipo, la causa final también debe proporcionar una forma diferente de explicación; una forma en que el explanandum figura en el explanans. La tendencia a que ocurran resultados de cierto tipo se explica por lo que ese tipo es.

El desarrollo de adaptaciones, y la evolución y diversidad de las especies constituye el explanandum distintivo de la selección natural. Además, el explanandum figura en el explanans: las consecuencias que explican la existencia de rasgos adaptativos son las consecuencias que tienen estos rasgos, y las consecuencias preceden al efecto que explican. Sin embargo, la causalidad final no es *retrocausalidad* porque el tipo de resultado no es un resultado particular: no hay un resultado particular que tenga influencia sobre una entrada particular que lo preceda en el tiempo.

En biología relacional, el explanandum que requiere la introducción de la causa final es lo que diferencia a los seres vivos de la materia inanimada. Según Rosen, la definición de vida requiere la introducción de un nuevo principio explicativo: el cierre de causa eficiente. Un sistema material es un organismo si y sólo si está cerrado bajo causación eficiente, es decir, si sus componentes tienen causas eficientes generadas dentro del sistema y efectos que contribuyen a la producción de otras causas eficientes. Además, las funciones de los componentes contribuyen a la producción de otras funciones y a la organización y mantenimiento del sistema. El cierre de causa eficiente genera un conjunto de funciones: la funcionalidad es una propiedad emergente del cierre. La pregunta “¿por qué b?” puede responderse “porque b contribuye al cierre de causa eficiente del sistema del que forma parte el componente”, o, de manera equivalente, “porque b realiza una función en el sistema”.

En consecuencia, se propone representar la causa final como se muestra en la figura 7 del artículo. En un modelo relacional, la representación de la causa final de un componente no se encuentra dentro del mapping que representa el componente, sino en la relación de dicho mapping con los que representan otros componentes con los que contribuye al cierre del sistema.



*Fig. 7 Representación de la causa final*

Conviene también preguntarse por la causa final de un organismo completo: ¿por qué hay un sistema cerrado bajo causación eficiente? El cierre de causa eficiente es un tipo de organización que explica por qué tienden a existir sistemas que ejemplifican ese tipo. La realización de un cierre de causa eficiente se explica por las relaciones que se establecen entre las funciones realizadas por los componentes de un organismo, pero también cada función se explica por su contribución al cierre de causa eficiente.

Finalmente, la semiosis de Peirce es un estudio lógico y científico de la acción de los signos en la naturaleza en el que, para desarrollar una teoría de la lógica y estudiar la naturaleza, también se deben considerar un tipo de acciones que no pueden caracterizarse como acciones físicas ordinarias, las acciones semióticas. Las acciones semióticas constituyen el explanandum que plantea la teoría de los signos de Peirce; un explanandum que no se puede explicar sólo con las leyes de la física; un explanandum que requiere un nuevo explanans. Y también en este caso el explanandum forma parte del explanans. La acción semiótica se explica por la interpretación de un signo que forma una relación triádica junto con un objeto y un interpretant. Pero, por otro lado, es la relación semiótica que corresponde a la acción semiótica lo que define al interpretant, al signo y al objeto como tales. La semiosis de Peirce descansa en el concepto de causa final. El análisis de la causa final de una acción semiótica se puede descomponer en dos cuestiones que corresponden a la determinación del interpretant ya la interpretación del signo. ¿Por qué el interpretant? Porque conduce al agente del signo al objeto. ¿Por qué el objeto? Porque determina que el signo determine el interpretant.

Las similitudes y diferencias establecidas en los apartados anteriores entre las teorías de Rosen y Peirce, así como el análisis del papel que juega la causa final en ellas, constituyen una herramienta adecuada para discutir la existencia de signos que se realizan y se interpretan en los organismos.

La sección "Signs in an organism" comienza con el análisis de la definición de interpretación de Short, construida sobre la explicación naturalizada del propósito:

An interpretant interprets a representamen as a sign of an object if and only if (a) the interpretant is or is a feature of a response to the representamen for a purpose, (b) the interpretant is based on a relation, actual or past or apparent or supposed, of the representamen to the object or of things of the type of the representamen to things of the type of the object, and (c) obtaining the object has some positive bearing on the appropriateness of the interpretant to the purpose. (Short 2007, 158).

Como explica Short, cuando se dice "el interpretant interpreta", no debe entenderse que el interpretant es el agente que realiza la interpretación. El interpretant es solo uno de los tres sujetos que forman parte de la relación triádica que define una relación semiótica. Y, un propósito tiene que serlo de algún agente (el intérprete), que selecciona para ese tipo de resultado; o tiene que ser algún medio, es decir, algo que se selecciona por tener resultados de ese tipo.

Sin embargo, este autor sostiene que solo en el reino animal se puede hablar de signo, interpretación y significado. Para superar esta limitación y extender el uso de estos conceptos al nivel del organismo más simple, se revisa la conceptualización de "intencionalidad" en biosemiótica, eligiendo la siguiente definición:

It is the cyclical organization of metabolism which makes it meaningful to speak of 'intention' (whether conscious or not), because the directedness of intention, be it inside the organism or directed outwards into the niche is governed by the cyclical attractor of metabolism...(Stjernfelt citado en Favareau and Gare (2017, pp. 227-228)).

Para captar adecuadamente el concepto de intencionalidad, "la organización cíclica del metabolismo" debe ser reemplazada por "el cierre de causa eficiente del sistema", que explica el auto mantenimiento, la auto reparación y la replicación del sistema

En consecuencia, la definición de Short puede extenderse al organismo y, considerando lo argumentado anteriormente, también se puede afirmar que:

En un organismo, una relación semiótica es la unión de un componente del sistema y una relación entre las entidades que forman parte de ese componente, por la cual la salida determina que la entrada determina la causa eficiente. En este caso, la causa eficiente, la causa material y la salida del componente

corresponden respectivamente al interpretant, el signo y el objeto de la relación semiótica, y la acción del componente corresponde a la interpretación del signo.

La realización de una acción semiótica en un organismo, la formación e interpretación de un signo, requiere dos tipos de cierres; primero, el cierre de causa eficiente que define el organismo, al que contribuye el componente que forma parte de la relación semiótica, y segundo, el cierre que se establece entre la interpretación y la determinación del interpretant, que define la relación semiótica. Un organismo que incluye un signo puede representarse como se muestra en la Fig. 8 del artículo.

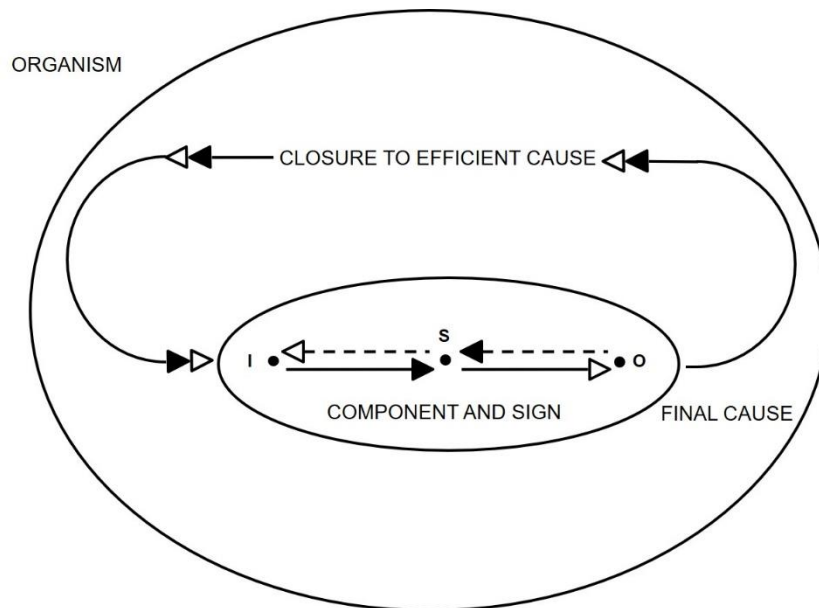


Fig. 8 An organism that includes a sign

Para explicar la existencia de signos en un organismo, la cuestión que queda por abordar es cuál es el agente crea e interpreta estos signos. En primer lugar, considerando lo anterior, debe señalarse que si un organismo incluye un signo cuya interpretación corresponde a la acción de un componente del organismo, entonces el propósito del signo es el auto mantenimiento del sistema, y el agente que realiza la interpretación es el organismo mismo. Por otro lado, según Hoffmeyer (2010, p. 371), “The act of interpretation (...) seems to be a key to the production of meaning when this word is used in a situated local sense”.

Para aclarar esta aparente contradicción, conviene tener en cuenta que (i) en un organismo, la acción de un componente se realiza localmente, pero responde al auto mantenimiento global del sistema, es decir, a su cierre de causa eficiente, y (ii) la realización de un signo en un organismo implica la realización de dos cierres, uno local que define la relación semiótica, y uno global, que define el organismo. En consecuencia, en un organismo, la interpretación de un signo se realiza localmente pero sólo porque se

realiza el cierre sistémico: la interpretación de un signo en un organismo es un proceso tanto local como sistémico.

Finalmente, el apartado "Un método de análisis", presenta los pasos a seguir para identificar la presencia de signos en un organismo:

1. Identificar aquellos procesos que la biología explica utilizando conceptos como señales, códigos o información, aunque no les atribuye ningún carácter semiótico.
2. Realizar un análisis relacional, identificando el proceso candidato a acción semiótica con la acción de un componente del organismo.
3. Establecer una correspondencia de las entidades identificadas como causa eficiente, entrada y salida con los conceptos de interpretant, signo y objeto, y analizar si el objeto determina que el signo determina el interpretant.

Se pueden resumir tres conclusiones específicas del artículo. Primero, en un organismo, una relación semiótica es la unión de un componente del sistema y una relación entre las entidades que forman parte de él, por la que la salida determina que la entrada (la causa material) determina la causa eficiente. En este caso, la causa eficiente, la causa material y la salida del componente corresponden respectivamente al interpretant, el signo y el objeto de la relación semiótica, y la acción del componente corresponde a la interpretación del signo. Una relación semiótica se puede representar con dos *mappings* correspondientes a la determinación de un interpretant y la interpretación de un signo.

En segundo lugar, la existencia de un signo en un organismo requiere la realización de dos cierres, uno local, que define la relación semiótica, y otro sistémico, que define el organismo. La acción de un componente corresponde a la interpretación de un signo solo si la causa eficiente está determinada por la entrada del componente, que está, a su vez, determinada por la salida. La definición de interpretación de Short se aplica en este artículo al nivel de un organismo. En dicha definición, como este autor aclara, cuando se dice "el interpretant interpreta" no debe entenderse que el interpretant es el agente que realiza la interpretación. La interpretación en un organismo es un proceso tanto local como sistémico y, por lo tanto, requiere dos explicaciones complementarias. Una local – la interpretación la realiza una parte del organismo–, pero también una global –la interpretación la realiza el organismo completo definido por el cierre bajo causa eficiente. En otras palabras, la interpretación tiene lugar localmente, pero solo porque a nivel global se produce el cierre del sistema por causa eficiente. La interpretación corresponde así a la realización de una función biológica local que contribuye al auto mantenimiento de todo el organismo.

Y tercero, y aplicando los conceptos expuestos, se define un método de identificación de signos en un organismo y su clasificación en iconos, índices y símbolos, que se aplica en el siguiente artículo al análisis de la síntesis de proteínas, integrando las descripciones de la biología estándar, la biología relacional y la semiótica.



## **An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part II: Analysis of Protein Synthesis**

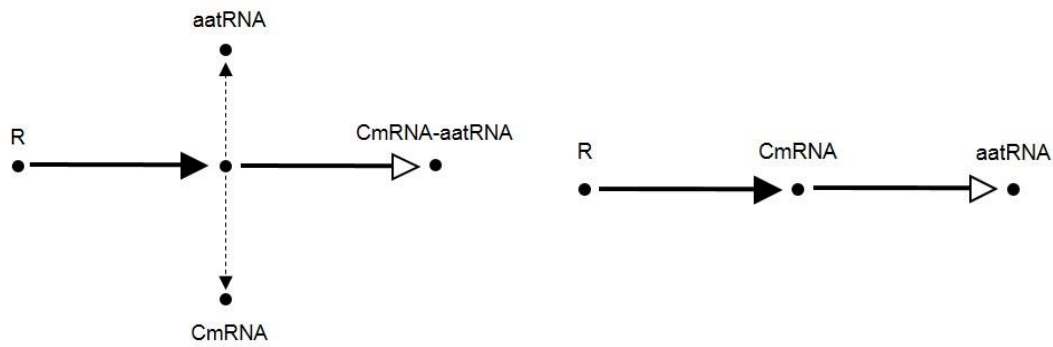
Siguiendo las propuestas teóricas del artículo anterior, este trabajo analiza cuáles de los principales procesos biológicos implicados en la síntesis de proteínas –transcripción y traducción– corresponden a acciones semióticas.

El método para identificar y analizar la presencia de signos en un organismo consta de los siguientes pasos. Primero, identificar y describir un proceso que sea candidato a ser una acción semiótica. En segundo lugar, realizar el análisis relacional e identificar la causa eficiente, la entrada y la salida del componente, que corresponderían al interpretant, el signo y el objeto de una relación semiótica. Y tercero, analizar si la salida implica que la entrada implica la causa eficiente. De ser así, las tres entidades que componen el componente corresponden a los tres sujetos de una relación semiótica. Luego, una vez identificado un signo, se debe determinar qué tipo de signo es según la clasificación de iconos, índices y símbolos de Peirce, es decir, estudiando el tipo de relación que existe entre el signo y el objeto.

La traducción es el proceso en el que un ribosoma (R) y un conjunto de aminoacil tRNA sintetasas (aaRS) producen una cadena de aminoácidos (aa) siguiendo el patrón de una cadena de codones de ARN mensajero (CmRNA). Para estudiar el proceso de traducción, se ha dividido su relato en tres partes: (i) la unión de un CmRNA y un aminoacil tRNA (aatRNA), (ii) la traducción de dos codones consecutivos y la unión del par de aminoácidos resultante, y (iii) el papel de las aminoacil tRNA sintetasas.

El primer paso se representa en la Fig. 2A del artículo y se puede explicar resumidamente de la siguiente manera. Un ribosoma se mueve a lo largo de una cadena de codones de mRNA. El ribosoma coloca un codón de la cadena de mRNA en su interior y luego recibe el aatRNA adecuado, cuyo anticodón se une al CmRNA. La colocación del CmRNA en la posición adecuada puede explicarse estudiando el movimiento del ribosoma y la correspondencia del codón y el sitio que ocupa. La unión de CmRNA-aatRNA se explica por la correspondencia del aatRNA y el sitio que ocupa, y la complementariedad entre las bases del codón del mRNA y el anticodón del aatRNA.

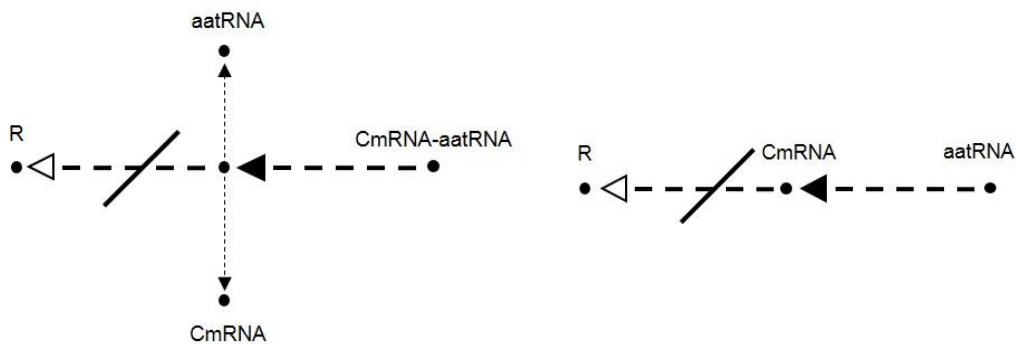
Desde el punto de vista de la biología relacional, la figura 2A representa un componente en el que el ribosoma es la causa eficiente, el par (CmRNA, aatRNA) es la entrada (la causa material), la unión CmRNA-aatRNA es la salida y la estructura del mapping es la causa formal. La causa final es la contribución de la producción del componente al cierre de causa eficiente del organismo del que forma parte. Cabe señalar que la unión de un CmRNA y un aatRNA establece una relación entre ambas moléculas que se representa en la figura 2B.



**Fig. 2A** Unión de un codón de mRNA y un aminoacil tRNA

**Fig. 2B** Asociación de un CmRNA con un aatRNA

Finalmente, se analiza si el primer paso de la traducción debe explicarse como una acción semiótica; si el proceso realizado por el componente corresponde a la interpretación de un signo; si el ribosoma interpreta un par (CmRNA, aatRNA) como un signo de CmRNA-aatRNA. Ciertamente, una unión CmRNA-aatRNA determina un par (CmRNA, aatRNA) porque solo la unión de un par específico de CmRNA y aatRNA produce un CmRNA-aatRNA específico. Por el contrario, no se puede afirmar que los aspectos de un par (CmRNA, aatRNA) que son adecuados para representar un CmRNA-aatRNA determinen el ribosoma. El resultado de este análisis se muestra en las figuras 2C y 2D. En consecuencia, se debe concluir que la unión de un codón de mRNA y un aminoacil tRNA no corresponde a una acción semiótica.



**Fig. 2C** La unión de un codón de mRNA y un aminoacil tRNA no determina el ribosoma

**Fig. 2D** La asociación de un CmRNA con un aatRNA no determina el ribosoma

A continuación, se analiza la traducción de dos codones y la unión de los aminoácidos correspondientes. Un nuevo aatRNA entra en el ribosoma y se une al siguiente codón. La unión de los CmRNA-aatRNA de orden  $n$  y  $n+1$  facilita la unión de los aa  $n$  y  $n+1$ . Como resultado, salen del ribosoma las cadenas de mRNA y de aminoácidos, y las moléculas tRNAs. También aquí, las salidas determinan las entradas, pero las entradas no determinan el ribosoma. El resultado de este análisis, que no se desarrolla en este resumen, se representa en las figuras 3D and 3E del artículo.

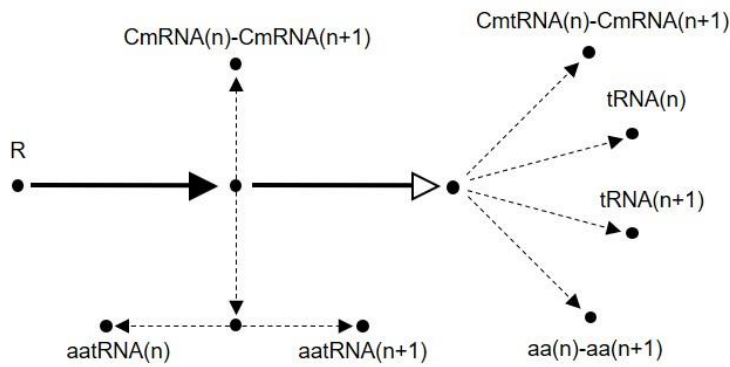


Fig. 3D Traducción de dos codones mRNA y unión de los dos aminoácidos resultantes

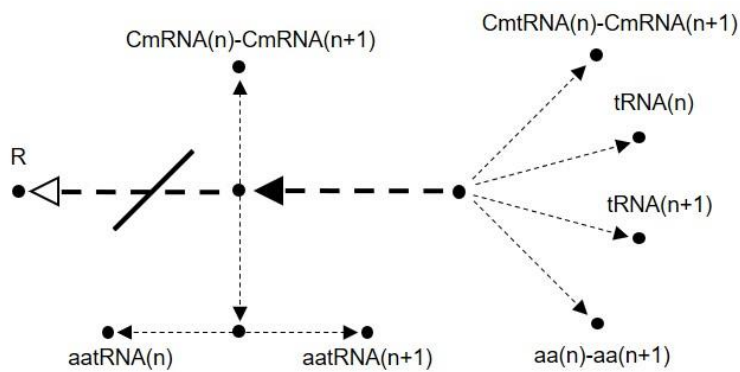


Fig. 3E La traducción de dos codones mRNA y la unión de los dos aminoácidos resultantes no determina el ribosoma

Finalmente, se estudia la formación de un aminoacil tRNA que entra en el ribosoma y se une a un CmRNA. La investigación ha demostrado que las enzimas denominadas aminoacil tRNA sintetasas (aaRS) son responsables de la síntesis de aatRNA a partir de aminoácidos y tRNAs. Hay 20 aaRSs. Cada una de ellas está asociada con un aminoácido y uno o más tRNAs. El reconocimiento de un aminoácido por el aaRS es independiente del reconocimiento de un anticodón de tRNA. De hecho, el anticodón no juega ningún papel en la entrada de tRNA en el aaRS, ni en su unión al aa.

Según la biología relacional, la figura 4A representa un componente en el que la aaRS es la causa eficiente, el par (tRNA, aa) es la entrada (la causa material) y el aatRNA es la salida. La unión de un tRNA específico y un aminoácido establece una relación entre el anticodón del tRNA (ACtRNA) y el aminoácido, que se representa en la Fig. 4B.

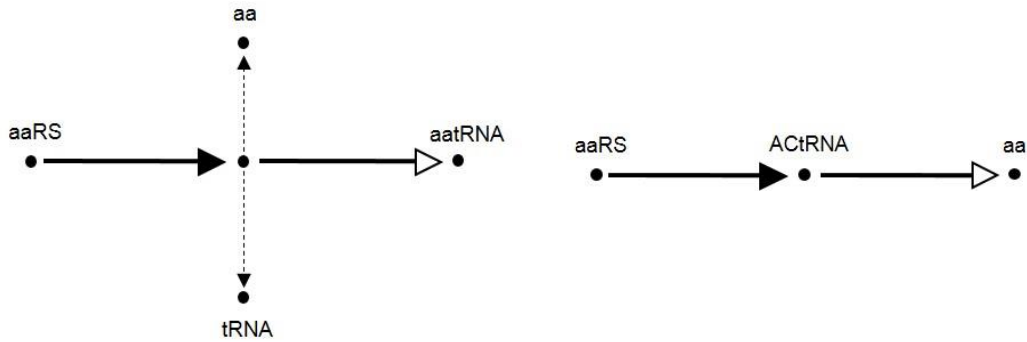


Fig. 4A Formación de un aminoacil tRNA

Fig. 4B Asociación de un anticodón tRNA con un aminoácido

Se discute ahora si el proceso que estamos analizando corresponde a la interpretación de un signo; si el aaRS interpreta el anticodón de un tRNA como un signo de un aminoácido; si un aaRS, el anticodón de un tRNA y un aminoácido forman una relación triádica que corresponde a una relación semiótica. Primero, un aatRNA determina el par correspondiente (tRNA, aa), ya que esos tRNA y aa específicos son las únicas moléculas que pueden formar ese aatRNA específico. Además, los aspectos del par de moléculas que son adecuados para representar su unión determinan el aaRS. Del mismo modo, también se puede afirmar que un aminoácido determina que un ACtRNA determina un aaRS en la medida en que solo ese aaRS puede asociar el anticodón con el aminoácido correspondiente. La determinación de un aaRS se muestra en las Figs. 4C y 4D.

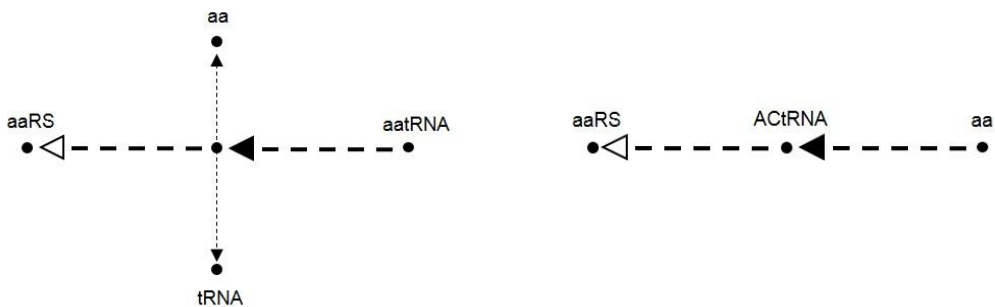


Fig. 4C El aminoacil tRNA determina el par (tRNA, aa) que determina el aaRS

Fig. 4D El aminoácido determina el ACtRNA que determina el aaRS

En consecuencia, debe señalarse que la formación de un aminoacil tRNA es una acción semiótica que corresponde a la relación semiótica que se representa en las figuras. 4E y 4F. Aplicando la definición de Short, se puede afirmar que una aminoacil tRNA sintetasa interpreta un anticodón de tRNA como un signo de un aminoácido.

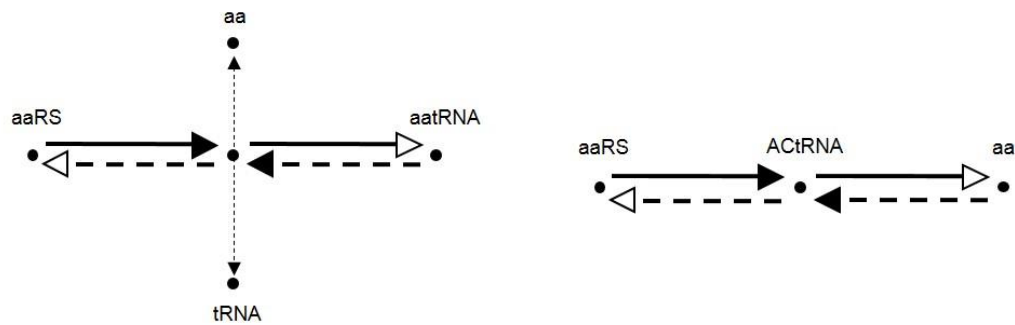


Fig. 4E La relación semiótica: interpretant = aaRS, signo = (tRNA, aa), objeto = aatRNA

Fig. 4F La relación semiótica: interpretant = aaRS, signo = ACtRNA, objeto = aa

Por otra parte, analizando de qué tipo de signo se trata, se llega a las siguientes conclusiones. No es un icono: el anticodón no tiene ninguna cualidad que lo relacione con el aminoácido. No es un índice: no se puede decir que el anticodón se refiera al aminoácido en virtud de estar realmente afectado por él. Es un símbolo: las aaRSs implementan en los aatRNAs las reglas que unen los aminoácidos y los anticodones tRNA. La síntesis de los aatRNAs corresponde a la definición de un sistema de relaciones semióticas convencionales (arbitrarias): el código genético.

Se concluye, por tanto, que la traducción es una acción semiótica simbólica y que su carácter semiótico es consecuencia del carácter semiótico de la formación de los aatRNAs. La determinación del aparato de traducción (formado por un ribosoma y un conjunto de aaRSs) como el interpretant de una relación semiótica es consecuencia de la determinación de las aminoacil tRNA sintetasas. El código genético hace que la traducción sea una acción simbólica. La correspondiente relación semiótica se representa en la figura 5H del artículo.

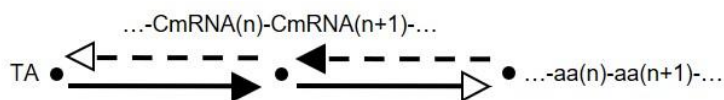


Fig. 5H La relación semiótica: interpretant = aparato de traducción; signo = cadena de CmRNAs; objeto = cadena de aminoácidos

Por otra parte, realizando análisis similares, se concluye que el proceso de transcripción no es un proceso semiótico. Sí lo es, sin embargo, la regulación de la transcripción. En este proceso, una región de DNA llamada potenciador (enhancer), a la que se ha unido una proteína activadora, dobla la hebra de DNA acercando el activador al promotor de un gen, uniéndose también a otras proteínas que actúan como factores de transcripción, a un complejo multiproteico llamado mediador que funciona como un coactivador transcripcional, y a una RNA polimerasa. Como resultado, la transcripción del gen correspondiente al promotor seleccionado por el potenciador está lista para comenzar.

El potenciador implica que el activador implica el promotor, pero también, el promotor determina que el activador que determina el potenciador. Solo potenciadores específicos pueden conducir a la formación del complejo de preiniciación de la transcripción alrededor de promotores específicos a partir de activadores específicos. Un potenciador interpreta un activador como un signo de un promotor (de un gen). La relación semiótica se muestra en las figuras 9C y 9D.

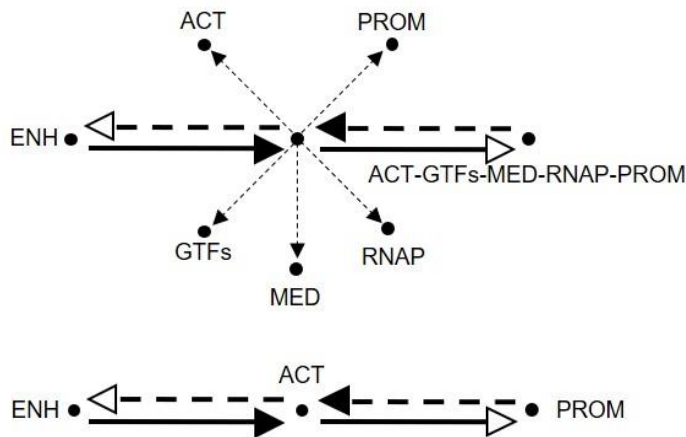


Fig. 9C La relación semiótica: interpretant = ENH; signo = (ACT, PROM, GTFs, MED, RNAP); objeto = ACT-PROM-GTFs-MED-RNAP

Fig. 9D La relación semiótica: interpretant = ENH; signo = ACT; objeto = PROM

Por último, se argumenta que las asociaciones potenciador-activador y potenciador-promotor no son completamente independientes, sino que están determinadas por la síntesis del activador y la estructura de la hebra de ADN que, en principio, pueden explicarse añadiendo el código genético a las leyes de la física. La relación entre un activador y un promotor no corresponde a un símbolo sino a un índice.

La existencia de los símbolos del código genético es una condición necesaria para la existencia de los índices que regulan la transcripción. La aplicación de los conceptos y el método aquí propuestos parecen sugerir que, si bien existen diferentes acciones semióticas que desempeñan funciones importantes en un organismo, las únicas acciones simbólicas son las del código genético.

Finalmente, las propuestas defendidas se utilizan para analizar críticamente dos teorías alternativas que niegan la posibilidad de explicar la presencia de signos en un organismo utilizando la semiosis de Peirce. En primer lugar, se muestra que las definiciones aportadas en el artículo anterior para los conceptos de relación semiótica, acción semiótica e interpretación, y su aplicación en este artículo a la síntesis de proteínas contradicen el carácter de no-científico que Barbieri atribuye a la aplicación de la semiosis de Peirce al nivel del organismo. Además, se argumenta que, aplicando la definición de Barbieri, un código orgánico corresponde a una relación semiótica

simbólica. Sin embargo, el análisis realizado de la transcripción y la traducción apuntan a que, salvo el código genético, el resto de los códigos de la biología de códigos corresponderían a relaciones semióticas indexicales. Esto no disminuye la importancia de las relaciones semióticas en la explicación de un organismo, pero pone en cuestión la necesidad de añadir las convenciones naturales propuestas por Barbieri como mecanismo para explicar la evolución.

En segundo lugar, el concepto de relación semiótica en un organismo, introducido en el artículo anterior y aplicado aquí, evita los problemas que llevan a Sharov y Vehkavaara (2015) a proponer la protosemiosis como una semiosis diferente a la de Peirce. Por ejemplo, para explicar la síntesis de proteínas como una acción semiótica no son necesarios los conceptos de mente mínima, representación y categorización de objetos, similares a los que se utilizan para explicar la interpretación de signos por parte del ser humano. En cambio, los conceptos de cierre y causa final se han utilizado para dar cuenta del papel funcional que juegan los signos en el interés propio del agente que los interpreta.

Los resultados de este trabajo demuestran la consistencia teórica y la utilidad práctica de integrar las teorías de Rosen y Peirce, ofrecen una forma de identificar signos en un organismo y respaldan un análisis crítico de la biología de códigos y la protosemiosis, dos relatos que niegan la posibilidad de explicar los signos en un organismo a partir de la semiosis de Peirce.

## SUMMARIES OF PUBLICATIONS

### **A Critique of Barbieri's Code Biology through Rosen's Relational Biology: Reconciling Barbieri's Biosemiotics with Peircean Biosemiotics.**

Semiotics studies the systems of signs, their production and operation. Charles Sanders Peirce argued that semiosis requires a triadic relation among a sign, an object, and an interpretant.

Biosemiotics is the union of biology and semiotics. He maintains that life and semiosis are coextensive, and that signs and meanings are natural entities on which the explanation of living beings must be based. Peircean biosemiotics is the framework in which the proposals of a large part of the experts have been developed, mainly grouped in the Copenhagen and Tartu schools. It is based on Peirce's semiosis, which it combines with concepts such as self-organization, self-maintenance and closure.

Marcello Barbieri has developed a theoretical framework that also focuses on the role of signs and meanings in the explanation of biology. However, Barbieri's biosemiotics has developed outside the mainstream, leaning on the concept of code. After a period of collaboration with other schools, Barbieri moved away from the common field of biosemiotics, considering that Peircean biosemiotics opens the door to non-scientific approaches through the concept of interpretation.

This paper shows that Barbieri's rejection of Peircean biosemiotics is based on a limited conception of science and an incorrect understanding of Peircean biosemiotics, which misunderstands the scope of application of Peirce's semiosis and does not take into account the rest of the theories on which Peircean biosemiotics is based.

Barbieri's work is studied here with tools taken from Robert Rosen's relational biology. Rosen's biology provides a concept of science that allows to overcome Barbieri's identification of science with mechanistic perspective and on the other hand, can be seen as a basis for Peircean biosemiotics.

The first three sections of the article gather the necessary elements of the theories to be analyzed. First, the basic concepts of Peirce's semiosis and Peircean biosemiotics are briefly stated. According to Peirce, to study nature, in addition to physical actions, semiotic actions must be considered, in which a sign (or representamen), an object, and an interpretant come together in a triadic relation that cannot be reduced to dyadic relations. An action associated with a sign is performed through the interpretation of the sign. Peircean biosemiotics was created by Thomas Sebeok from Peirce's semiosis and Jacob von Uexküll's studies of animal communication, and later combined with various influences from general systems theory. According to biosemiotics, it is the use of signs that characterizes living beings.



Second, Barbieri's framework for the study of biology is presented. For Barbieri, a semiotic system is a system made up of two independent worlds connected by the conventional rules of a code, a system that is made up of signs, meanings and code. In the case of organic codes, three sets of molecules are distinguished, corresponding to signs, meanings and codemakers. The sequence used by a codemaker during a coding process is an organic sign. The sequence produced by a codemaker during a coding process is an organic meaning. An organic code is a set of rules of correspondence between signs and meanings. Coding cannot be reduced to copying, so evolution requires two independent mechanisms: natural selection and natural conventions, the latter mechanism corresponding to the appearance of new codes.

Barbieri (2015) discusses two frameworks for the study of biology: Modern Synthesis and systems biology. The Modern Synthesis focuses on population aspects and is based on the mechanism of natural selection. According to this author, another additional mechanism is necessary to explain evolution: natural conventions. For its part, for systems biology, an organism is a system that is self-manufactured and is explained by autopoiesis. Instead, Barbieri proposes to explain the organism by codepoiesis. After the emergence of the first organic code, the genetic code, the subsequent evolution of cells would be explained by two complementary processes that, together, constitute codepoiesis: the generation of new organic codes and the conservation of existing ones.

At the cellular level, he rejects interpretation-based semiosis as unscientific. He identifies science with a mechanistic perspective.

And third, Rosen's relational biology is analyzed. According to this author, the concept of natural law is based on the assertion that there is, and can be established, a relation between the causality of natural systems and the implications of formal systems. A formal system  $F$  is a model of a natural system  $N$  if the same result is obtained in the following two cases: (i) passage from one phenomenon to another in  $N$ , and (ii) encoding of  $N$  in  $F$ , application of  $F$  and decoding from  $F$  to  $N$ . A natural system can have several models.

Rosen introduces the concepts of analogy and metaphor between two natural systems, which allow learning from one of the systems by studying the other. An analogy is established between two natural systems  $N_1$  and  $N_2$  that can be codified in the same formal system, in which  $N_2$  contains a model of  $N_1$  and  $N_1$  contains a model of  $N_2$ . On the other hand, in the case of two formal systems  $F_1$  and  $F_2$  corresponding to two natural systems  $N_1$  and  $N_2$ , if there is a mathematical relation between  $F_1$  and  $F_2$ , but there is no function between the propositions in both formal systems that preserves the structure of implications, an analogy between  $N_1$  and  $N_2$  cannot be established, but it can be stated that  $N_1$  is a metaphor for  $N_2$  and vice versa. Rosen (2012) applies the concept of analogy in the study of anticipatory systems, and explains metaphorically the concepts of fitness, adaptation, natural selection, and evolution.

Figs. 1 and 3 of the article represent the concepts of natural law and model, and analogy between two natural systems, respectively.

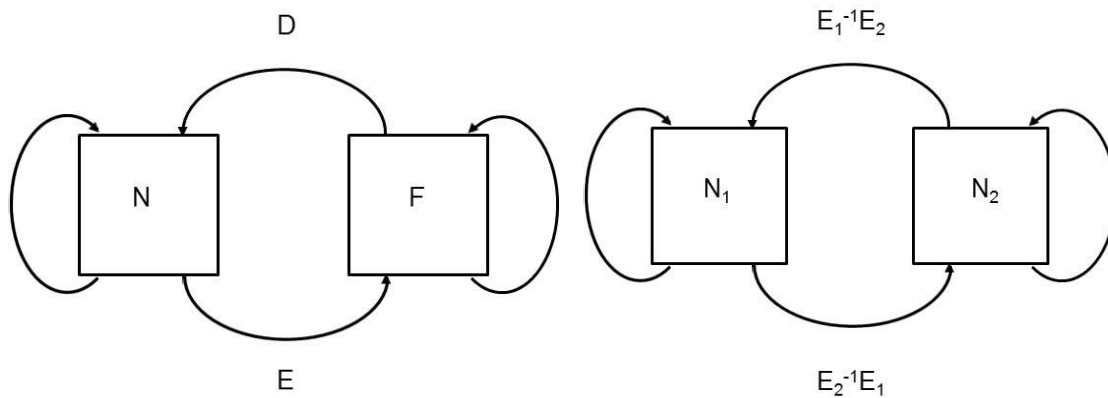


Fig.1 Natural law and model

Fig. 3 Analogy between two natural systems

Additionally, he specifies the concept of simulation between two formal systems. If  $F_2$  is a model of  $F_1$ , then  $F_1$  is simulated by  $F_2$ . In this case,  $F_1$  is incorporated into  $F_2$  and the simulated formalism becomes the effect of the simulator formalism. No congruence relation is established between the two formalisms, so nothing can be learned about  $F_1$  from its simulation. According to Rosen, a mapping is simulable (or computable) if it is definable by an algorithm, i.e., if it is evaluable by a mathematical (Turing) machine.

Rosen asserts that a natural system is a mechanism if and only if all its models are simulable and concludes that an organism is different from a mechanism. A mechanism is a purely syntactic construct, corresponding to a simple system. An organism is a complex system. An organism can have mechanistic models, but the limit of its mechanistic models is not a mechanism, there cannot be a mechanism that corresponds to a complete model of the organism. An organism is a system consistent with an impredicative model, a model in which the definition of each component refers to the component that is defined or to another that contains it. A living system must have non-computable models. Physics is the science of mechanisms and should be considered a special science, while biology is a more general science that studies complex systems that require more types of models, some of which are not simulable.

Rosen studies anticipatory systems. An anticipatory system is a system that contains a predictive model of itself and/or its environment, which allows it to change state at an instant according to the model's predictions for a later instant. It can, therefore, be affirmed that an anticipatory system interprets. The study of anticipatory systems is based on the concept of analogy.

The formal systems proposed by Rosen as models of natural systems are relational models, defined by their components and the relations established between them.

Following the Aristotelian classification, Rosen analyzes the causes of a component and concludes that a material system is an organism if and only if it is a system closed to efficient cause.

Finally, he proposes the (M, R) system as a model of an organism. In this type of system, closure realizes between three classes of functions, which he calls metabolism, repair, and replication. An (M, R) system has an intrinsic anticipatory character, which goes beyond mechanisms and implies a semiosis that includes and surpasses code-based semiosis.

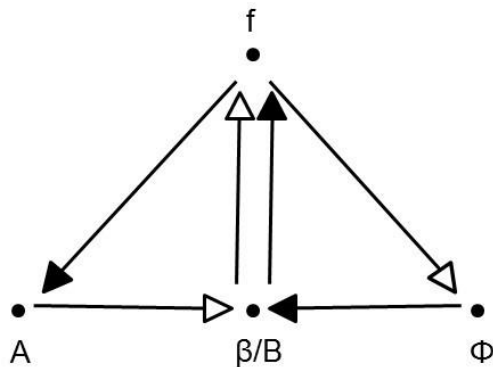


Fig. 7 An (M, R) system

These three sections explain that there are different approaches and objectives, but also shared concepts, that are accepted or rejected, with the same or different meaning, and imply by themselves a first comparison of Code Biology, Peircean biosemiotics and relational biology.

In the fourth section, two key proposals of Code Biology are criticized with arguments taken from Rosen's relational biology. First, the relationship between science and mechanism is discussed. Barbieri upholds that the scientific method is based on the definition of models, and identifies models with mechanisms, which leads him to identify the scientific method and the mechanistic perspective. However, as discussed above, Rosen argues that mechanisms are not enough for the science of biology.

Second, Barbieri's critique of the concept of interpretation is analyzed and, with it, his rejection of Peircean biosemiotics. Barbieri (2015) discards interpretation-based semiosis because (i) interpretation is based on abduction, (ii) what is interpreted is not the world but representations of the world; and (iii) the result of the interpretation depends on the environment and previous experience (the interpretation requires memory).

However, Rosen's anticipatory system contains a model of itself and/or its environment, so that it changes its state at an instant according to the model's predictions at a later time. It seems appropriate to state that the system interprets what its model indicates

about what may happen in the future, based on its current state and environment. On the other hand, the (M, R) system, which he proposes as a model of the organism, has an inherent anticipatory character built into its organization. Its predictive capacity also depends on the environment and previous experience (learning, memory) of the system. Finally, Rosen argues that (i) selection and adaptation generate predictive models; (ii) learning can be seen as a part of adaptation or as a metaphor for it; and (iii) learning processes generate predictive models.

In section five, as an additional result of the research carried out, some lines of a study of Rosen's biology as a biosemiotic theory compatible with Code Biology and Peircean biosemiotics are sketched. The analogy between two natural systems  $N_1$  and  $N_2$  is based on a modeling relation between both systems, in which the qualities of  $N_1$  are encoded into the qualities of  $N_2$ .  $N_1$  and  $N_2$  are two independent systems joined by coding rules, which is formally similar to the two independent worlds connected by a code proposed by Barbieri; and the concept of analogy, is the basis of the definition of an anticipatory system. Furthermore, Rosen's components correspond to two independent sets related by a mapping, where the efficient cause leads from each element of the first set to an element of the second. However, not all the mappings of a relational model represent processes subject to arbitrary efficient causes. Only those mappings in which the relationships between inputs and outputs correspond to arbitrary rules are comparable to Barbieri codes.

It is concluded that: (i) code-based biology provides the appropriate theoretical tools for the development of biological research; (ii) it is possible to develop other scientific biosemiotics within the framework of Peircean biosemiotics; (iii) Code Biology and Peircean biosemiotics, despite their different approaches, can be part of a common framework for biology; and (iv) a biosemiotic reading of Rosen's biology can also be conducted.

## An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part I: Components and Signs, Final Cause and Interpretation

In this paper, an integrated account of Rosen's relational biology and Peirce's semiosis is proposed.

In relational biology, organisms are analyzed as systems made up of components that are related to each other, producing system closure to efficient cause. It is the closure that defines the living being; that establishes relationships between the parts of a natural system that acquire a differentiated reality with its own characteristics, beyond those of the parts that participate in them; that turns these parts into the components that perform biological functions that arise when closure is realized.

On the other hand, biosemiotics maintains that it is the use of signs that characterizes the living being. Unlike dynamic actions, semiotic actions correspond to triadic relations between the subjects that make up the semiotic relation (sign, object and interpretant) that cannot be reduced to dyadic relations.

Section "Components, signs, mappings and triadic relations" begins with the presentation of Rosen's concepts of natural law, model<sup>2</sup>, component and mapping, and his analysis of Aristotelian causes. In a relational model, a component -the basic unit of the system - is represented by a mapping between two sets,  $f: A \rightarrow B$ , which can be expanded  $f \longrightarrow (a \longrightarrow f(a))$ , for every  $a \in A$ , with  $f(a) = b \in B$ , which can be read "f entails that a entails b". The graphical representation of a component can be seen in Figs. 1A and 1B of the article, where the hollow arrows represent the flow from a to b, and the solid arrows symbolize the effect of the component.



Fig. 1A Representation of a component

Fig. 1B Action of a component on an input

Following the classification of Aristotelian causes, it is worth asking why the quality of the system represented by  $b$  is realized. According to Rosen, the component  $f$  is the efficient cause and the input  $a$  is the material cause. According to Louie (2009), the formal cause corresponds to the structure of the mapping, to the ordered union of the two arrows. But what is the final cause? This question is answered in a later section.

Next, considering Peirce's definition of a sign, the possibility of representing semiotic relations with mappings is discussed and a proposal is made. Quoting Peirce:

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<sup>2</sup> See the summary of the previous article.

A sign, or representamen (...) addresses somebody, that is, creates in the mind of that person an equivalent sign, or perhaps a more developed sign. That sign which it creates I call the interpretant of the first sign (Peirce as quoted in Favareau (2009, p. 122)).

I define a sign as anything which is so determined by something else, called its Object, and so determines an effect upon a person, which effect I call its interpretant, that the latter is thereby mediately determined by the former” (Peirce 1998, p. 478).

A semiotic action leads from a sign to an object, creating an interpretant in the interpreter. In a relational system that represent an organism, where all actions are performed by the components of the system, it can be considered that the interpretation of the sign corresponds to the action of a component, where the interpretant is the efficient cause, the sign is the material cause, and de object is the output, as shown in Fig. 5 of the article, where I, S, and O stand respectively for the interpretant, the sign and the object. The concept of interpretation in an organism is explained in a later section.

On the other hand, the claim that, in a semiotic relation, the object determines that the sign determines the interpretant, is equivalent to stating that the object entails that the sign entails the determinant, so it would also be convenient to represent it with a mapping. However, the determination of the interpretant does not correspond to a component, so dashed lines are used, as shown in Fig. 4.



Fig. 4 Determination of the interpretant

Fig. 5 Interpretation of the sign

The union of the determination of the interpretant and the interpretation of the sign (the closure between the two) define the semiotic relation as a triadic relation, irreducible to dyadic relations. Its representation requires the two aforementioned mappings. The semiotic relation is represented in Fig. 6 of the article.

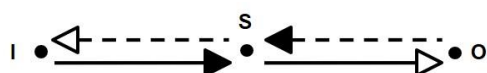


Fig. 6 A semiotic relation

In the “Final Cause” section, the role of final cause in natural selection, relational biology, and Peirce's semiosis is discussed.

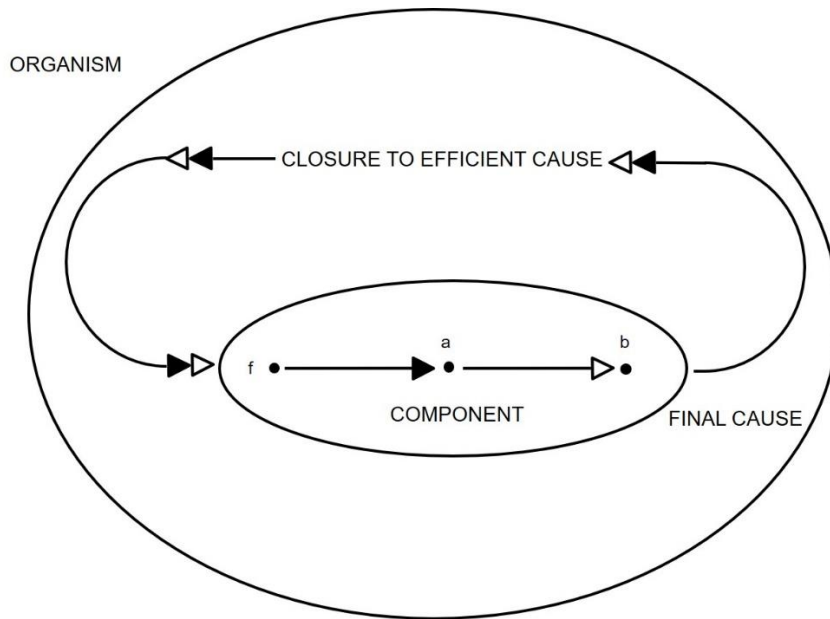
As Short (2002) explains, while the efficient cause leads to particular outcomes, the final cause is a type of result that can be realized in different ways. Furthermore, a type of

outcome is a final cause only if it explains why there tend to be instances of this type. The reintroduction of the concept of final cause in modern science is necessary because there are questions that efficient causes cannot answer, there are explananda that are not mechanistically explainable. Furthermore, to explain an explanandum of this type, the final cause must also provide a different form of explanation; a way in which the explanandum figures in the explanans. The tendency for outcomes of a certain type to occur is explained by what that type is.

The development of adaptations, and the evolution and diversity of species constitutes the distinctive explanandum of natural selection. Moreover, the explanandum figures in the explanans: the consequences that explain the existence of adaptive traits are the consequences that these traits have, and the consequences precede the effect they explain. However, the final causation is not a *backwards causation* because the type of outcome is not a particular outcome: there is no particular outcome that has influence on a particular income that precedes it in time.

In relational biology, the explanandum that requires the introduction of the final cause is what differentiates living beings from inanimate matter. According to Rosen, the definition of life requires the introduction of a new explanatory principle: closure to efficient cause. A material system is an organism if and only if it is closed to efficient cause, i.e., if its components have efficient causes generated within the system, and effects that contribute to the production of other efficient causes. Furthermore, the functions of the components contribute to the production of other functions, and to the organization and maintenance of the system. Closure to efficient cause generates a set of functions: functionality is an emergent property of closure. The question "why **b**?" can be answered "because **b** contributes to closure to efficient cause of the system to which the component is part", or, equivalently, "because **b** performs a function in the system".

Consequently, it is proposed to represent the final cause as shown in Fig. 7 of the article. In a relational model, the representation of the final cause of a component is not found within the mapping that represents the component, but in the relation of said mapping with those that represent other components with which it contributes to the closure of the system.



*Fig. 7 Representation of the final cause*

It is also worth to ask about the final cause of a whole organism: why is there a system closed to efficient cause? Closure to efficient cause is a type of organization that explains why there tend to be systems that exemplify that type. The realization of a closure to efficient cause is explained by the relations established between the functions performed by the components of an organism, but also each function is explained by its contribution to the closure to efficient cause.

Finally, Peirce's semiosis is a logical and scientific study of signs action in nature in which, in order to develop a theory of logic and to study nature, a type of actions that cannot be characterized as ordinary physical actions must also be considered, semiotic actions. Semiotic actions constitute the explanandum posed by Peirce's theory of signs; an explanandum that cannot be explained with the laws of physics alone; an explanandum that requires a new explanans. And in this case too, the explanandum is part of the explanans. The semiotic action is explained by the interpretation of a sign which forms a triadic relation together with an object and an interpretant. But, on the other hand, it is the semiotic relation that corresponds to the semiotic action that defines the interpretant, the sign and the object as such. Peirce's semiosis rests on the concept of final cause. The analysis of the final cause of a semiotic action can be broken down into two questions that correspond to the determination of the interpretant and the interpretation of the sign. Why the interpretant? Because it leads the agent from the sign to the object. Why the object? Because it determines that the sign determines the interpretant.



The similarities and differences established in the previous sections between the theories of Rosen and Peirce, as well as the analysis of the role that the final cause plays in them constitute an adequate tool to discuss the existence of signs that realize and are interpreted inside organisms.

Section "Signs in an organism" begins with the analysis of Short's definition of interpretation, built on the naturalized account of purpose:

An interpretant interprets a representamen as a sign of an object if and only if (a) the interpretant is or is a feature of a response to the representamen for a purpose, (b) the interpretant is based on a relation, actual or past or apparent or supposed, of the representamen to the object or of things of the type of the representamen to things of the type of the object, and (c) obtaining the object has some positive bearing on the appropriateness of the interpretant to the purpose. (Short 2007, 158).

As Short explains, when "the interpretant interprets" is said, it should not be understood that the interpretant is the agent that performs the interpretation. The interpretant is just one of the three subjects that are part of the triadic relation that defines a semiotic relation. And, a purpose has to be some agent's (the interpreter), that selects for that type of outcome; or it has to be some mean's, that is, something that is selected for its having results of that type.

However, this author maintains that only in the animal realm can one speak of sign, interpretation and meaning. To overcome this limitation and extend the use of these concepts to the level of the simplest organism, the conceptualization of "intentionality" in biosemiotics is reviewed, choosing the following definition:

It is the cyclical organization of metabolism which makes it meaningful to speak of 'intention' (whether conscious or not), because the directedness of intention, be it inside the organism or directed outwards into the niche is governed by the cyclical attractor of metabolism... (Stjernfelt as quoted in Favareau and Gare (2017, pp. 227-228)).

According to what is stated in the paper that is summarized, to properly grasp the concept of intentionality, "the cyclical organization of metabolism" should be replaced by "the closure to efficient cause of the system", which explains the self-maintenance, the self-repair and the replication of the system

As a result, Short's definition can be extended to the organism and, considering what was argued above, it can also be stated that:

In an organism, a semiotic relation is the union of a component of the system and a relation between the entities that are part of that component, by which the output determines that the input determines the efficient cause. In this case, the efficient cause, the material cause and the output of the component

correspond respectively to the interpretant, the sign and the object of the semiotic relation, and the action of the component corresponds to the interpretation of the sign.

The realization of a semiotic action in an organism, the formation and interpretation of a sign, requires two types of closures; first, the closure to efficient cause that defines the organism, to which the component that forms part of the semiotic relation contributes, and second, the closure established between the interpretation and the determination of the interpretant, which defines the semiotic relation. An organism that include a sign can be represented as shown in Fig. 8 of the paper.

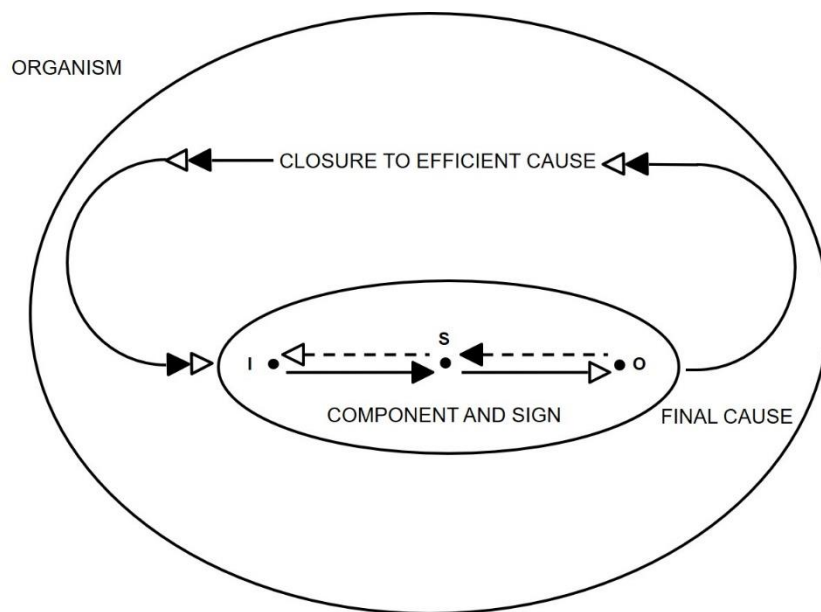


Fig. 8 An organism that includes a sign

To explain the existence of signs in an organism, the question that remains to be addressed is which agent creates and interprets these signs. First, considering the above, it must be stated that if an organism includes a sign whose interpretation corresponds to the action of a component of the organism, then the purpose of the sign is the self-maintenance of the system, and the agent performing interpretation is the organism itself. On the other hand, according to Hoffmeyer (2010, p.371), “The act of interpretation (...) seems to be a key to the production of meaning when this word is used in a situated local sense”.

To clarify this apparent contradiction, it should be borne in mind that (i) in an organism, the action of a component is locally performed but responds to the global self-maintenance of the system, i.e. to its closure to efficient cause, and (ii) the realization of a sign in an organism implies the realization of two closures, a local one that defines the semiotic relation, and a global one, that defines the organism. Accordingly, in an organism, the interpretation of a sign is locally realized but only because the systemic

closure is realized: the interpretation of a sign in an organism is both a local and a systemic process.

Finally, the section "A method of analysis", presents the steps to follow to identify the presence of signs in an organism:

1. Identify those processes that biology explains using concepts such as signals, codes or information, although it does not attribute any semiotic character to them.
2. Carry out a relational analysis, identifying the candidate process for semiotic action with the action of a component of the organism.
3. Establish a correspondence of the entities identified as efficient cause, input and output with the concepts of interpretant, sign and object, and analyze whether the object determines that the sign determines the interpretant.

Three specific conclusions from the paper can be summarized. First, in an organism, a semiotic relation is the union of a component of the system and a relation between the entities that are part of it, by which the output determines that the input (the material cause) determines the efficient cause. In this case, the efficient cause, the material cause and the output of the component correspond respectively to the interpretant, the sign and the object of the semiotic relation, and the action of the component corresponds to the interpretation of the sign. A semiotic relation can be represented with two mappings corresponding to the determination of an interpretant and the interpretation of a sign.

Second, the existence of a sign in an organism requires the realization of two closures, a local one, that defines the semiotic relation, and a systemic one, that defines the organism. The action of a component corresponds to the interpretation of a sign only if the efficient cause is determined by the input of the component, which is, in turn, determined by the output. Short's definition of interpretation is applied in this article at the level of an organism. In this definition, as this author clarifies, when "the interpretant interprets" is said, it should not be understood that the interpretant is the agent who performs the interpretation. The interpretation in an organism is both a local and a systemic process and therefore requires two complementary explanations. A local one -the interpretation is realized by a part of the organism-, but also a global one -the interpretation is realized by the complete organism defined by the closure. In other words, the interpretation takes place locally, but only because the system closure to efficient cause occurs. The interpretation thus corresponds to the realization of a local biological function that contributes to the self-maintenance of the whole organism.

And third, and applying the concepts expounded, a method of identifying signs in an organism and their classification into icons, indices and symbols is defined, which is applied in the following article to the analysis of protein synthesis, integrating the descriptions of standard biology, relational biology and semiotics.

## **An Integrated Account of Rosen's Relational Biology and Peirce's Semiosis. Part II: Analysis of Protein Synthesis**

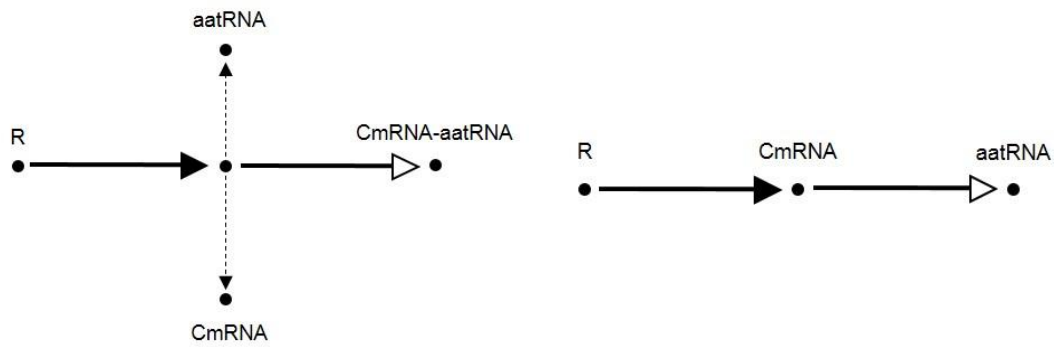
Following the theoretical proposals of the previous article, this paper analyzes which of the main biological processes involved in protein synthesis –transcription and translation–correspond to semiotic actions.

The method for identifying and analyzing the presence of signs in an organism consists of the following steps. First, to identify and describe a process that is a candidate to be a semiotic action. Second, to carry out the relational analysis and identify the efficient cause, the input and the output of the component, which would correspond to the interpretant, the sign and the object of a semiotic relation. And third, to analyze whether the output entails that the input entails the efficient cause. If so, the three entities that make up the component correspond to the three subjects of a semiotic relation. Then, once a sign has been identified, it should be determined what type of sign it is according to Peirce's classification of icons, indices and symbols, that is, studying the type of relationship that exists between the sign and the object.

Translation is the process in which a ribosome (R) and a set of aminoacyl tRNA synthetases (aaRS) produce a chain of amino acids (aa) following the pattern of a chain of messenger RNA codons (CmRNA). To study the translation process, its account has been broken down into three parts: (i) the binding of a CmRNA and an aminoacyl tRNA (aatRNA), (ii) the translation of two consecutive codons and the binding of the resulting pair of amino acids, and (iii) the role of the aminoacyl tRNA synthetases.

The first step is represented in Fig. 2A of the article and can be summarily explained as follows. A ribosome moves along a chain of mRNA codons. The ribosome places a codon of the mRNA chain inside it and, then receives the adequate aatRNA, whose anticodon binds to the CmRNA. The placing of the CmRNA in the adequate position can be explained by studying the movement of the ribosome and the correspondence of the codon and the site it occupies. The CmRNA-aatRNA binding is explained by the correspondence of the aatRNA and the site it occupies, and the complementarity between the bases of the mRNA codon and the anticodon of the aatRNA.

From the point of view of relational biology, Fig. 2A represents a component in which the ribosome is the efficient cause, the pair (CmRNA, aatRNA) is the input (the material cause), the CmRNA-aatRNA junction is the output, and the mapping structure is the formal cause. The final cause is the contribution of the output of the component to the closure to efficient cause of the organism of which it is a part. It should be noted that the union of a CmRNA and an aatRNA establishes a relation between both molecules that is represented in Fig. 2B.

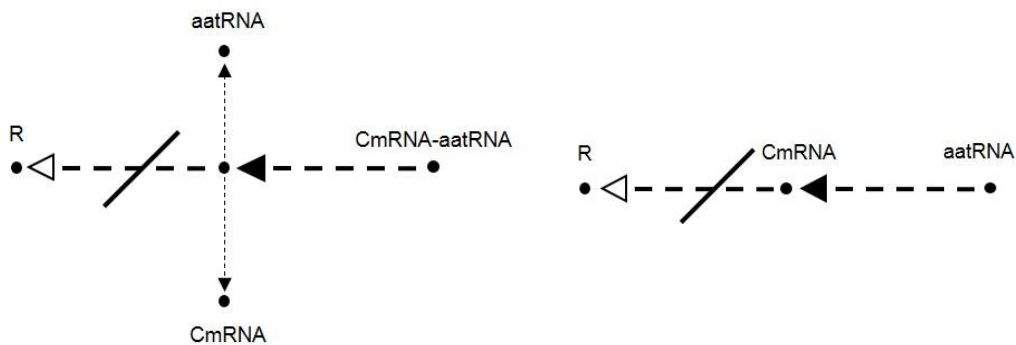


*Fig. 2A Binding of an mRNA codon and an aminoacyl tRNA*

*Fig. 2B Association of a CmRNA with an aatRNA*

Finally, It is analyzed if the first step of translation must be explained as a semiotic action; if the process carried out by the component corresponds to the interpretation of a sign; if the ribosome interprets a pair (CmRNA, aatRNA) as a sign of a CmRNA-aatRNA. Certainly, a union CmRNA-aatRNA determines a pair (CmRNA, aatRNA) because only the binding of a specific pair of CmRNA and aatRNA produces a specific CmRNA-aatRNA. Conversely, it cannot be stated that the aspects of a pair (CmRNA, aatRNA) that are suitable to stand for a CmRNA-aatRNA determine the ribosome. The result of this analysis is shown in Figs. 2C and 2D.

Consequently, it must be concluded that the binding of an mRNA codon and an aminoacyl tRNA does not correspond to a semiotic action.



*Fig. 2C The binding of an mRNA codon and an aminoacyl tRNA does not determine the ribosome*

*Fig. 2D The association of a CmRNA with an aatRNA does not determine the ribosome*

Next, the translation of two codons and the binding of the corresponding amino acids are analyzed. A new aatRNA enters the ribosome and binds to the next codon. The binding of CmRNA-aatRNA of order  $n$  and  $n+1$  facilitates the binding of aa  $n$  and  $n+1$ . As a result, mRNA and amino acid chains, and tRNAs molecules leave the ribosome. Here too, the outputs determine the inputs, but the inputs do not determine the

ribosome. The result of this analysis, which is not developed in this summary, is represented in Figs. 3D and 3E of the article.

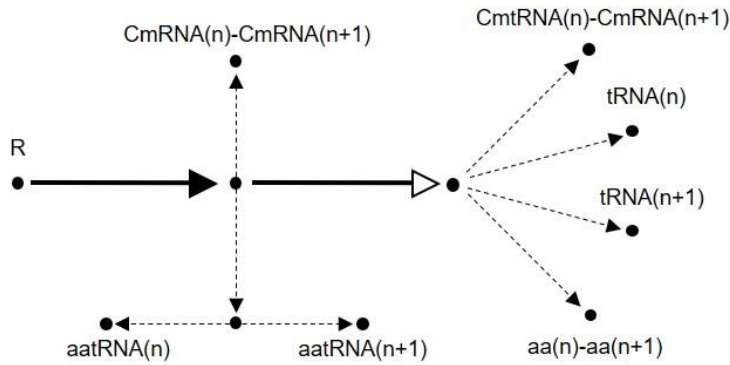


Fig. 3D Translation of two mRNA codons and binding of the two resulting amino acids

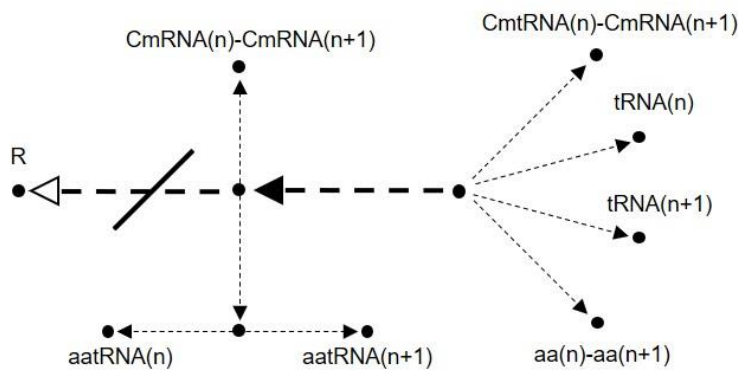


Fig. 3E The translation of two mRNA codons and the binding of the two resulting amino acids does not determine the ribosome

Finally, the formation of an aminoacyl tRNA that enters the ribosome and binds to a CmRNA, is studied. Research has shown that enzymes called aminoacyl tRNA synthetases (aaRSs) are responsible for the synthesis of aatRNAs from amino acids and tRNAs. There are 20 aaRSs. Each of them is associated with an amino acid and one or more tRNAs. The recognition of an amino acid by the aaRS is independent of the recognition of an anticodon of tRNA. In fact, the anticodon does not play any role in the entry of tRNA into the aaRS, nor in its binding to the aa.

According to relational biology, Fig. 4A represents a component in which the aaRS is the efficient cause, the pair (tRNA, aa) is the input (the material cause) and the aatRNA is the output. The union of a specific tRNA and an amino acid establishes a relation between the anticodon of the tRNA (ACTRNA) and the amino acid, which is represented in Fig. 4B.

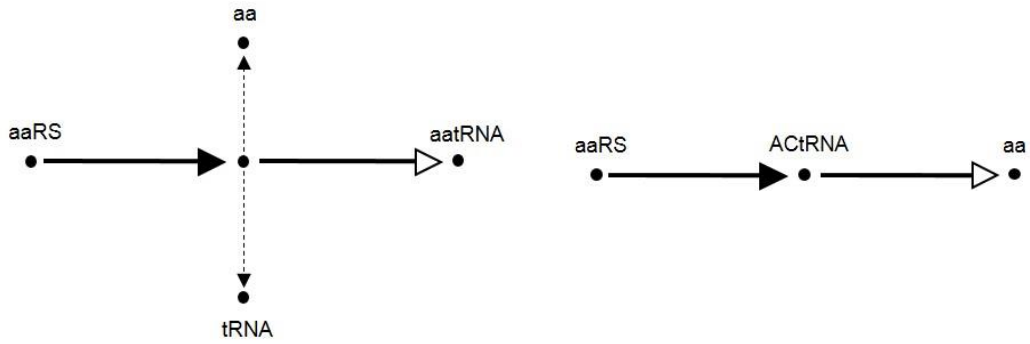


Fig. 4A Formation of an aminoacyl tRNA

Fig. 4B Association of a tRNA anticodon with an amino acid

It is discussed now if the process we are analyzing corresponds to the interpretation of a sign; if the aaRS interprets the anticodon of a tRNA as a sign of an amino acid; if an aaRS, the anticodon of a tRNA and an amino acid form a triadic relation that corresponds to a semiotic relation. First, an aatRNA determines the corresponding pair (tRNA, aa) since those specific tRNA and aa are the only molecules that can form that specific aatRNA. Furthermore, the aspects of the pair of molecules that are suitable to represent their union determine the aaRS. Similarly, it can also be stated that an amino acid determines that an ACtRNA determines an aaRS insofar as only that aaRS can associate the anticodon with the corresponding amino acid. The determination of an aaRS is shown in Figs. 4C and 4D.

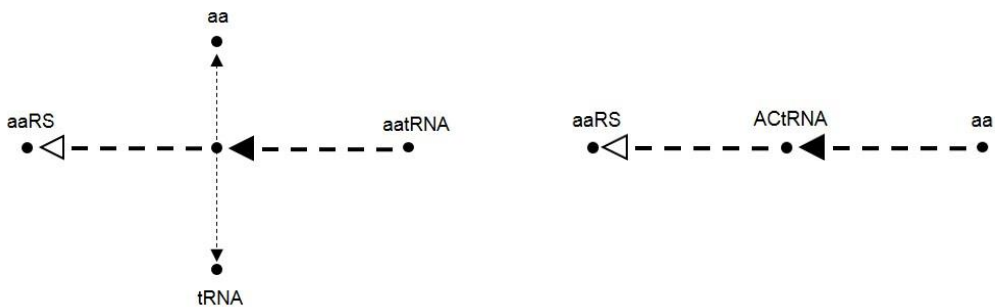


Fig. 4C The aminoacyl tRNA determines the pair (tRNA, aa) that determines the aaRS

Fig. 4D The amino acid determines the ACtRNA that determines the aaRS

Consequently, it must be stated that the formation of an aminoacyl tRNA is a semiotic action that corresponds to the semiotic relation that is represented in Figs. 4E and 4F. Applying Short's definition, it can be stated that an aminoacyl tRNA synthetase interprets a tRNA anticodon as a sign of an amino acid.

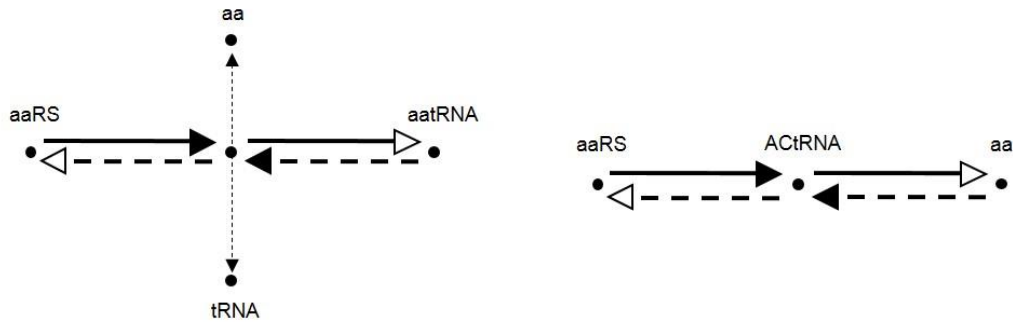


Fig. 4E The semiotic relation: interpretant = aaRS, sign = (tRNA, aa), object = aatRNA

Fig. 4F The semiotic relation: interpretant = aaRS, sign = ACtRNA, object = aa

On the other hand, analyzing what type of sign it is, the following conclusions are reached. It is not an icon: the anticodon does not have any quality that relates it to the amino acid. It is not an index: the anticodon cannot be said to refer to the amino acid by virtue of actually being affected by it. It is a symbol: the aaRSs implement in the aatRNAs the rules that link amino acids and tRNA anticodons. The synthesis of the aatRNAs corresponds to the definition of a system of conventional (arbitrary) semiotic relations: the genetic code.

It is concluded, therefore, that translation is a symbolic semiotic action and that its semiotic character is a consequence of the semiotic character of the formation of aatRNAs. The determination of the translation apparatus (made up of a ribosome and a set of aaRSs) as an interpretant of a semiotic relation is a consequence of the determination of the aminoacyl tRNA synthetases. The genetic code makes translation a symbolic action. The corresponding semiotic relation is represented in figure 5H of the article.

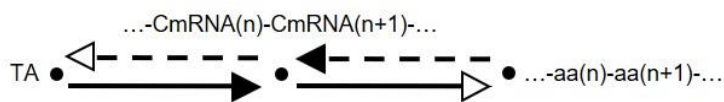


Fig. 5H The semiotic relation: interpretant = translation apparatus; sign = chain of CmRNAs; object = chain of amino acids

On the other hand, carrying out similar analyses, it is concluded that the transcription process is not a semiotic process. It is, however, the regulation of transcription. In this process, a region of DNA called enhancer, to which an activator protein has joined, bends the DNA strand, bringing the activator close a gene promoter, also joining other proteins that act as transcription factors, a multiprotein complex called a mediator that functions as a transcriptional coactivator, and an RNA polymerase. As a result, the



transcription of the gene corresponding to the promoter selected by the enhancer is ready to start. The semiotic relation is shown in Figs. 9C and 9D.

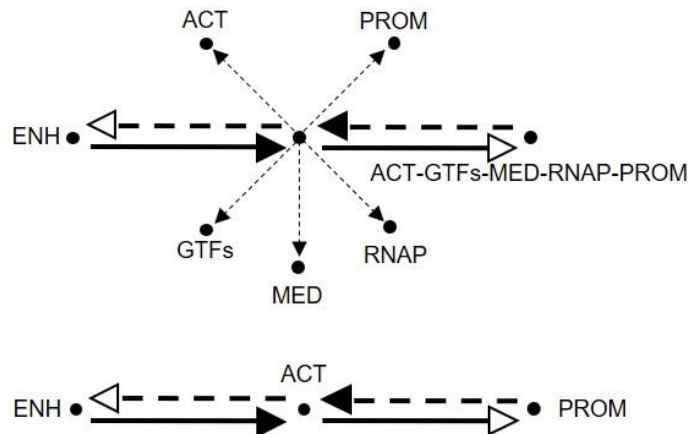


Fig. 9C The semiotic relation: interpretant = ENH; sign = (ACT, PROM, GTFs, MED, RNAP); object = ACT-PROM-GTFs-MED-RNAP

Fig. 9D The semiotic relation: interpretant = ENH; sign = ACT; object = PROM

The enhancer entails that the activator entails the promoter, but also, the promoter determines that the activator that determines the enhancer. Only specific enhancers can lead to the formation of the transcription preinitiation complex around specific promoters from specific activators. An enhancer interprets an activator as a sign of a promoter (of a gene).

Finally, it is argued that enhancer-activator and enhancer-promoter associations are not completely independent but are determined by the synthesis of the activator and the structure of the DNA strand, which can, in principle, be explained by adding the genetic code to the laws of physics. The relation between an activator and a promoter does not correspond to a symbol but to an index.

The existence of the symbols of the genetic code is a necessary condition for the existence of the indices that regulate transcription. The application of the concepts and the method proposed here seem to suggest that, although there are different semiotic actions that perform important functions in an organism, the only symbolic actions are those of the genetic code.

Finally, the proposals defended are used to critically analyze two alternative theories that deny the possibility of explaining the presence of signs in an organism using Peirce's semiosis. First, it is shown that the definitions provided in the previous paper for the concepts of semiotic relation, semiotic action and interpretation, and their application in this paper to protein synthesis contradict the unscientific character that Barbieri attributes to the application of Peirce's semiosis at the level of the organism. Furthermore, it is argued that, applying Barbieri's definition, an organic code

corresponds to a symbolic semiotic relation. However, the analysis carried out on transcription and translation suggest that, except for the genetic code, the rest of the Code Biology codes correspond to indexical semiotic relations. This does not diminish the importance of semiotic relations in explaining an organism, but it does call into question the need to add natural conventions proposed by Barbieri as a mechanism to explain evolution.

Second, the concept of a semiotic relation in an organism, introduced in the previous article and applied here, avoids the problems that lead Sharov and Vehkavaara to propose protosemiosis as a semiosis different from that of Peirce. For example, to explain protein synthesis as a semiotic action, the concepts of minimal mind, representation and categorization of objects, similar to those used to explain the interpretation of signs by the human being, are not necessary. Instead, the concepts of closure and final cause have been used to account for the functional role that signs play in the self-interest of the agent who interprets them.

The results of this work demonstrate the theoretical consistency and the practical utility of integrating the theories of Rosen and Peirce, offer a way to identify signs in an organism, and support a critical analysis of Code Biology and protosemiosis, two accounts that deny the possibility of explaining the signs in an organism from Peirce's semiosis.

## INFORMACIÓN DE LAS REVISTAS DE PUBLICACIÓN

A continuación, se justifica la idoneidad de las revistas en las que se ha realizado las publicaciones para el trabajo que constituye la tesis que se presenta.

### **Biosemiotics**

Según la propia revista declara, Biosemiotics se dedica a construir un puente entre la biología, la filosofía, la lingüística y las ciencias de la comunicación. La investigación biosemiótica se ocupa del estudio de signos y significados en organismos y sistemas vivos. Su principal desafío es naturalizar el significado y la información biológicos basándose en la creencia de que los signos son componentes fundamentales y constitutivos del mundo viviente. La revista está afiliada a la Sociedad Internacional de Estudios Biosemióticos (ISBS).

El Journal Citations Report incluye Biosemiotics en las categorías de “Historia y Filosofía de la Ciencia” y “Humanidades, Multidisciplinario”. Considerando los años 2017 a 2020 en la categoría “Historia y Filosofía de la Ciencia, Biosemiotics se clasifica los cuatro años en el primer cuartil del Journal Citation Indicator (JCI), y el en el Journal Impact Factor (JIF) se encuadra un año en el tercer cuartil, uno en el segundo y dos en el primero.

Por otra parte, en el indicador SCImago Journal Rank (SJR) de 2020, Biosemiotics está incluida en el segundo cuartil de la categoría “Artes y Humanidades: Lengua y Lingüística”.

### **Biological Theory**

Biological Theory declara que se dedica a los avances teóricos en los campos de la evolución y la cognición con énfasis en la integración conceptual que brindan los enfoques evolutivos y de desarrollo. La revista atrae a una amplia audiencia de científicos, científicos sociales y académicos de las humanidades, en particular filósofos e historiadores de la biología.

Dado que el objetivo de esta tesis es aportar un marco teórico que extienda la biología actual, como complemento de Biosemiotics, se ha seleccionado Biological Theory, perteneciente al Instituto Konrad Lorenz para la investigación de la evolución y la cognición, por su relevancia en lo relativo a la selección natural.

Esta revista no está incluida en los índices de clasificación habituales, pero sí aparece en Emergence Source Citation Index y tiene un ICDS de 7.7 en la Matriz de Información para el Análisis de Revistas (MIAR).

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