The Code Model of Semiosis: The First Steps Toward a Scientific Biosemiotics

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Abstract: Biosemiotics asserts the idea that *semiosis* is fundamental to life, and that all living creatures are therefore semiotic systems. The idea itself is strongly supported by the evidence of the genetic code — but thus far it has made little impact in the scientific world, and is largely regarded as the basis for a philosophy of meaning, rather than a basis for science a meaning. This is regrettable, but perhaps understandable from the scientists' point of view. Scientists know that the cell is the necessary unit of all life. I will argue here, then, that Biosemiotics can become a science only if it can prove that the cell is, in fact, a semiotic system — i.e., that semiosis exists at the cellular level. To do this, we first need to define what *is* semiosis, so that we can be explicit about what exactly constitutes a semiotic system. So far, we have had two main answers to this question. One is the model proposed by Saussure, who defined a semiotic system as a duality of 'signifier and signified'. The other is the model of Peirce, who pointed out that interpretation is an essential component of semiosis and defined a semiotic system as a triad of 'sign, object and interpretant'. After the discovery of the genetic code, each of these two models have been applied to biology and have given rise to two distinct schools of biosemiotics. One is the school of Marcel Florkin (1974), which is based on the model of Saussure, and the other is the school of Thomas Sebeok (1972, 2001), which is based on the model of Peirce. Unfortunately, neither of them can be applied to the cell, and that is why most biologists continue to be skeptical about biosemiotics. There is however a third model of semiosis that is actually applicable to the cell. It is based on the theory that the cell is a trinity of genotype, phenotype and ribotype (Barbieri 1981, 1985, 2003). Here, the ribotype is the ribonucleoprotein system of the cell and represents its 'codemaker', i.e., the seat of the genetic code. This model assumes that *semiosis* is defined by *coding*, not by *interpretation*, and is therefore referred to as *the code model* of semiosis. This paper is dedicated to illustrating this third model and, above all, to showing that the cell is a true semiotic system.

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Introduction

At the heart of biosemiotics is the idea that all living creatures are semiotic systems — but thus far, this idea has made little impact in the scientific world, and is largely regarded as a philosophical view rather than a ground for science. There are many reasons for this, but the most important, in my opinion, is the fact that *biosemiotics has not yet proven that the cell is a semiotic system*. The cell is the necessary unit of all of life, and there is no chance that biosemiotics can become a science if it does not prove that signs exist in the cell at the molecular level. This is the first and the most important challenge of biosemiotics: can it prove that the cell is a semiotic system?

In this enterprise, the starting point must be a definition of *semiosis* — and to this purpose, it is natural to turn to the classical models of Saussure and Peirce, especially as modified by their biosemiotic followers. The difference between these two models is often described by saying that Saussure proposed a *dualistic* model of the sign (made up of *signifier-signified*), whereas Peirce proposed a *triadic* model (made up of *sign-object-interpretant*). Yet in reality, even the model of Saussure is a triadic one, because the link between signifiers and signified is provided by the rules of a cultural code, i.e., by the rules of language. These rules come from a community and therefore from outside the individual systems — whereas the process of interpretation is necessarily produced within the individual system.

In short, according to Saussure, a semiotic system consists of *signifiers, signified and conventions*, where the conventions of a code come from a codemaker which is outside the system. According to Peirce, a semiotic system consists of *signs, objects and interpretants*, where the interpretants come from an interpreter which is inside the system and takes an active part in semiosis. The real difference between Saussure and Peirce, therefore, is not between a dyadic and a triadic model of semiosis. It is between a model based on coding and a model based on interpretation. More precisely, between a model based on *external coding* and a model based on *internal interpretation*.

These two models have been applied in biology, and have given rise to two distinct schools of biosemiotics. One is the school of Marcel Florkin (1974), which is based on the model of Saussure, and the other is the school of Thomas Sebeok (1972, 2001), which is based on the model of Peirce. Unfortunately, none of these models turns out to provide a good description of the cell because, they can account only for some of its characteristics. The cell contains a genetic code, and in this respect it is like a Saussurean system because it has a codemaker, not an interpreter. The cellular codemaker, on the other hand, is

inside the system, not outside it, and in that respect the cell is like a Peircean system. This suggests that a realistic model of the cell belongs to yet a third category. A semiotic system is always made of signs and meanings that are linked together by the components of a third party, but this party can be of three different types: (1) an *external codemaker*, (2) an *internal interpreter* and (3) an *internal codemaker*. We have therefore three distinct models of semiosis, and here it is shown that the third model does allow us to prove that the cell is a semiotic system.

The Code Model of Semiosis

Semiotics is usually referred to as the study of signs (from the Greek *semeion* = sign) but I want to propose that this definition is too restrictive, because signs are always associated with other entities. A sign, to start with, is always linked to a *meaning*. As living beings, we have a built-in drive to make sense of the world, to give meanings to things, and when we give a meaning to something, that something becomes a sign for us. Sign and meaning, in other words, cannot be taken apart, because they are the two sides of the same coin. Semiotics, therefore, is not just the study of signs; it is the study of signs and meanings together. The result is that a system of signs, i.e., a *semiotic system*, is always made of at least two distinct worlds: a world of entities that we call *signs* and a world of entities that represent their *meanings*.

The link between sign and meaning, in turn, calls attention to a third entity, i.e., to their *relationship*. A sign is a sign only when it stands for something that is *other than itself*, and this *otherness* implies at least some degree of independence. It means that there is no deterministic relationship between sign and meaning. Different languages, for example, give different names to the same object, precisely because there is no necessary connection between names and objects. A semiotic system, therefore, is not just any combination of two distinct worlds. It is must be *a combination of two worlds between which there is no necessary link*, and this realization has extraordinary consequences. It implies that a *bridge* between the two worlds can be established only by conventional rules, i.e., by the rules of a *code*. This is what defines the semiotic systems, and what makes them different from everything else: *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 three distinct entities: *signs*, *meanings* and *code*.

Here at last we have a definition where it is stated explicitly that a code is an essential component of a semiotic system. It is the rules of a code that create a correspondence between signs and meanings, and we can say therefore that an

act of semiosis is always an act of coding, i.e., it is always a convention. More precisely, we can say that an elementary act of semiosis is a triad of '*sign, meaning and convention*', whereas a semiotic system is the whole set of signs and meanings that are linked together by all the various conventions that make up a code.

Signs, meanings and conventions, however, do not come into existence of their own. There is always an 'agent' that produces them, and that agent can be referred to as a *codemaker* because it is always an act of coding that gives origin to semiosis. In the case of culture, for example, the codemaker is the human mind, since it is the mind that produces the mental objects that we call signs and meanings and the conventions that link them together. We come in this way to a general conclusion that can be referred to as 'the code model of semiosis': *a semiotic system is a triad of signs, meanings and code that are all produced by the same agent, i.e., by the same codemaker*.

This conclusion is highly relevant to biology because it tells us precisely what we need to prove in order to show that the cell is a semiotic system. We need to prove that in every living cell there are four distinct entities: signs, meanings, code and codemaker.

The Cell as a Trinity

The idea that life is based on genes and proteins is often expressed by saying that every living system is a duality of genotype and phenotype. This model was first proposed by Wilhelm Johannsen in 1909, but came to prominence only in the 1940s and 1950s, when molecular biology discovered that genes are chemically different from proteins — and, above all, when it became clear that genes carry *linear information* whereas proteins function by virtue of their *three-dimensional structures*. The genotype-phenotype duality is therefore a dichotomy that divides not only two different biological functions (heredity and metabolism), but also two different physical quantities (information and energy). It is the simplest and most general way of defining a living system, and has become the foundational paradigm of modern biology, the scheme that transformed the energy-based biology of the nineteenth century into the information-based biology of the twentieth century.

In the 1950s and 1960s, however, the study of protein synthesis revealed that genes and proteins are not formed spontaneously in the cell, but are manufactured by a system of molecular machines based on RNAs. In 1981, the components of this manufacturing system were called *ribosoids*, and the system itself was given the collective name of *ribotype* (Barbieri 1981, 1985). The cell was described in this way as a structure made of genes, proteins and ribosoids, i.e., as a trinity of genotype, phenotype and ribotype.

This model is based on the conclusion that the ribotype had historical priority over the genotype and the phenotype. In the model, spontaneous genes and spontaneous proteins did appear on the primitive Earth — but these proto-structures could not give origin to cells because they did not have biological specificity. Rather, they gave origin to copymakers and codemakers, respectively, and it was these molecular machines, made of ribosoids, that evolved into the first cells.

The RNAs and the proteins that appeared spontaneously on the primitive Earth produced a wide variety of ribosoids, some of which were synthetizing ribosoids whereas others were ribogenes and others were riboproteins (or ribozymes). The systems produced by the combination of all these molecules, therefore, had a ribotype, a ribogenotype and a ribophenotype. Eventually, evolution replaced the ribogenes with genes and the riboproteins with proteins but the synthetising ribosoids of the ribotype have never been replaced. This shows not only that the ribotype is a distinct category of the cell, but also that it is a category without which the cell simply cannot exist.

The ribosoids of the ribotype are the oldest phylogenetic molecules that exist on Earth (Woese 2000) and they firmly remain at the heart of every living cell. Genes, proteins and ribosoids are all manufactured molecules, but only the ribosoids themselves become makers of such molecules. This concept can perhaps be illustrated by comparing the cell to a city where proteins are the material objects, genes are the instructions and ribosoids are the 'makers' of genes and proteins, i.e., the inhabitants of the city.

It is an experimental fact, at any rate, that every cell contains a system of RNAs and ribonucleoproteins that makes proteins according to the rules of a code. That system can therefore be described as a 'code-and-template-dependent-protein-maker', i.e., as a 'codemaker'. This 'codemaker' is the third party that makes of every living cell a trinity of genotype, phenotype and ribotype. The genotype is the seat of heredity, the phenotype is the seat of metabolism, and the ribotype is the codemaker of the cell — the seat of the genetic code.

The Defining Feature of Signs and Meanings

A semiotic system is made of signs, meanings, a code and a codemaker, and as biologists, we know that there is a genetic code to protein synthesis. We also know that proteins, in turn, are made by a system of ribonucleoproteins and that this system is the physical seat of the genetic code and that functions therefore as the 'codemaker' of the cell. This tells us that every living cell does have a genetic code and a codemaker. But what about the other two entities? Can we say that there are also signs and meanings at the molecular level? Can

such entities exist in the cell? In order to answer this question, let us examine first the traditional signs and meanings of culture to see if they have a qualifying feature that can be extended to the molecular level.

The signs and meanings that we are most familiar with are often the mental representations of objects and events in the physical world. A sign, for example, can be a spoken word and its meaning can be a mental image. The mental image of an object may be normally evoked by different words in different languages, and this clearly shows that sounds and mental images are separable. When they are separated, however, they no longer function as signs and meanings. To a non-English speaker, for example, a word like 'twitch' may have no linguistic meaning and in this case it would be just a sound, not a sign. There is no contradiction therefore in saying that signs and meaning are distinct mental objects and that they cannot be taken apart, because when they are taken apart they simply stop functioning as signs and meanings.

This exemplifies an extremely important feature of semiosis. It shows us that a mental sign, or a mental meaning, is never an *intrinsic* property of a mental object. It is something that the mind can give to a mental object and that the mind can take away from it. It is the mind, and more precisely the mental codemaker, that brings signs and meanings into existence.

Mental signs and mental meanings simply do not exist without a code maker, or outside of a codemaking process. The codemaker is the *agent* of semiosis, whereas signs and meanings are its instruments. We conclude therefore that signs and meanings are totally dependent on codemaking, i.e., they are codemaker-dependent entities. This is the qualifying feature that we were looking for, because it is completely general and can be applied to all systems. We can therefore establish that signs and meanings exist at the molecular level, and in particular in protein synthesis, only if we prove that in protein synthesis there are such codemaker-dependent entities.

The Sequences of Genes and Proteins

All biochemistry textbooks confirm that there is a genetic *code* in protein synthesis, but none of them mentions the existence of *signs* and *meanings*. At first sight, in fact, these entities do not seem to exist at the molecular level. The genetic translation apparatus can be regarded as a 'codemaker' because it is the seat of the code that creates a correspondence between genes and proteins — but these molecules appear to have only 'objective' chemical properties, and not the 'codemaker-dependent' properties that define signs and meanings. A messenger RNA, for example, appears to be a unique and objective sequence of molecules, but let us take a closer look.

A messenger RNA is certainly a unique and objective chain of *nucleotides*, but in no way it is a unique *sequence* of *codons*, because different codemakers can and do scan it in different ways. If the nucleotides were scanned two-by-two, for example, (or even three-by-three, as usual, but starting from one additional nucleotide to the left or right) the *sequence of codons* would be totally different; while the objectively observable chain of the nucleotide would remain exactly the same. The same chain of nucleotides, in other words, can give origin to many sequences of codons — and it is always the codemaker that determines the sequence, because it is the codemaker that *defines* the codons *as* codons. A linear sequence of *codons*, in short, does not exist without a codemaker, nor outside of a codemaking process. It is totally dependent on codemaking and is therefore a *codemaker-dependent entity*, which is precisely what we have defined a sign as.

In the same way, the linear sequence of amino acids that is produced by the translation apparatus is *also* a codemaker-dependent entity, because only a codemaker can produce *it*. Just any spontaneous assembly of amino acids would not make linear chains — and, above all, it would not arrange the amino acids to a specific order. Specific linear sequences of amino acids can be produced *only* by codemakers — and again, different codemakers would arrange the amino acids in different ways — which shows that the resulting *sequence* of a protein is only one of the many possible 'meanings' that could be given to an objective string of nucleotides.

The sequence of a gene and the sequence of a protein, in conclusion, are not objective properties of those molecules. They are codemaker-dependent properties, both because they do not exist without a codemaking process, and because they would be different if the codemaker had a different structure. The sequences of genes and proteins, in short, have precisely the characteristics that define signs and meanings. They are codemaker-dependent entities made of organic molecules and are therefore organic signs and organic meanings. All we need to keep in mind is that signs and meanings are mental entities when the codemaker is the mind, but they are organic entities when the codemaker is an organic system (Barbieri 2003). We reach in this way the conclusion that every living cell contains all four components of semiosis (signs, meanings, code and codemaker) and is therefore a genuinely semiotic system.

Two Types of Signs

Since antiquity, signs have been divided into two great classes that are traditionally represented by *symbols* and *symptoms*. Augustine (A.D. 389) called them *signa data* and *signa naturalia*, a distinction that continues to these days

under the terms of *conventional signs* and *natural signs* (Deely 2006; Favareau 2007). The conventional signs are those where there is no *physical* relationship between signifiers and meanings and a connection between them can be established only by arbitrary rules, i.e., by conventions. Words, for example, are signs (because they 'stand for' the named entities) and are conventional signs because they are not determined by the characteristics of the named entities. In the same way, there is no necessary connection between symbols and the entities that they stand for (between a flag and a country, for example).

In natural signs, by contrast, a physical link is always present between the signifier and the signified. Typical examples are the *symptoms* that doctors use to diagnose illnesses (spots on the skin, a fever, a swollen area, etc.), as well as a variety of *cues* (smoke as sign of fire, odours as signs of food, footprints as signs of organisms, etc.). In all these cases, there is a physical relationship between the visible signs and the invisible entities that they point to — and yet the relationship is *underdetermined*, so much so that it takes a process of learning and an act of interpretation to establish it. The diagnosis of an illness from symptoms, for example, is always an interpretative exercise, and even simple associations, such as those between clouds and rain, depend upon the processes of learning and memory.

At the molecular level, we have seen that in protein synthesis, a sequence of nucleotides is used as a sign by a codemaker to produce a sequence of amino acids, according to the rules of the genetic code. In that case, there is no necessary connection between the components of the two molecules, and the sequence of nucleotides is used therefore as a *conventional* organic sign, i.e., as an *organic symbol*.

A sequence of nucleotides, however, can also be used by a copymaker to produce a complementary copy of itself, and in that case the relationship between the two sequences is no longer established by a code, but by direct physical interactions between complementary surfaces. These interactions, however, occur between very small regions of the molecules, and that means that the first sequence provides only a limited number of physical determinants for the second. The first sequence, in other words, does have a physical relationship with the second, but such relationship is undetermined and represents therefore only a 'cue', i.e., a *natural sign*, for the second.

We conclude that the distinction between natural and conventional signs exists also at the molecular level, and represents in fact a divide between two very different types of molecular processes. Sequences of nucleotides are used as natural signs in molecular copying, and as conventional signs in molecular coding. The replication of genes, in other words, is based on *natural* organic signs, whereas the synthesis of proteins is based on *conventional* organic signs.

The Two Versions of the Code Model in Biosemiotics

The discovery of the genetic code took place between 1961 and 1966 (Niremberg and Matthaei 1961; Khorana et al. 1966; Niremberg et al. 1966), and almost immediately inspired a version of biosemiotics that is profoundly different from the Peirce-Sebeok approach. It is a version that can be referred to a *code-based biosemiotics* — because it assumes that semiosis is defined by coding, and not by interpretation. The evidence for this is that the rules of the genetic code have been virtually the same in all living systems and in all environments ever since the origin of life, which clearly shows that such rules do not depend on interpretation.

The manifesto of the code-based biosemiotics was written by George and Muriel Beadle in 1966 in a single simple sentence: "the deciphering of the genetic code has revealed our possession of a language much older than hieroglyphics, a language as old as life itself, a language that is the most living language of all — even if its letters are invisible and its words are buried in the cells of our bodies" (Beadle and Beadle 1966: 207).

In 1974, Marcel Florkin coined the term 'biosemiotics' for the study of this molecular language, and proposed, as a theoretical framework, the dualistic model of Saussure. He gave the names *biosemes* and *biosyntagms* to the basic units of molecular semiosis, but strongly emphasized that linguistic signs are arbitrary whereas molecular signs are not: "A bioseme carries no 'beteutung', no 'meaning', because its signifier is a molecular structure and its signified is a biological function" (Florkin 1974: 13).

Florkin's conclusion was the logical consequence of the idea that the cell is a duality of genotype and phenotype — a biological computer made of genetic software and protein hardware. The crucial point is that a computer contains codes, but is not a 'semiotic' system because its codes come from a codemaker which is outside the system. This makes it legitimate to say that the components of the cell do not carry real 'meaning' because the genetic code was assembled by natural selection, i.e., by a codemaker that was outside the cell just as the human mind is outside the computer it designs. The Saussure-Florkin model, in short, is a version of the code model where the code comes from an external codemaker, and can therefore be referred to as *external code model*.

Such a theoretical framework regards the cell as a biological computer that is not capable of autonomous semiosis — and this is why the first model of true molecular semiosis was the idea that every cell is a trinity of genotype, phenotype and ribotype, i.e., the idea that the cell contains an internal codemaker (Barbieri 1981, 1985, 2003). This latter approach is a version of the

code model where the code is assembled by an internal codemaker, and can therefore be referred to as *internal code model*.

One may point out that even the ribotype could have been assembled by natural selection, and that would bring us back to the conclusion that the ultimate codemaker is always outside living systems. This is why a model of true molecular semiosis requires also the idea that coding is not completely accounted for by natural selection — i.e., the idea that natural selection and natural conventions are two distinct mechanisms of evolution (Barbieri 1985, 2003).

There are, in conclusion, two very different versions of the code model of semiosis, and the failure to distinguish them has seriously confused the issue in recent debates, because it has led people to identify the code model with the Saussurean model — i.e., with the version where semiosis is produced by an external codemaker, whereas, as I have attempted to make clear here, it is explicitly a model that is dependent upon the existence of an *internal* codemaker. That this internal codemaker is not synonymous with an internal *interpreter* , is what I wish similarly to make clear next.

On the Peirce Model

The most authoritative treatise of semiotics, published in four volumes between 1997 and 2003 by Roland Posner, Klaus Robering and Thomas Sebeok, defines semiosis in unmistakably Peircean terms:

> We stipulate that the following is a necessary and sufficient condition for something to be a semiosis: A interprets B as representing C. In this relational characterization of semiosis, A is the Interpretant, B is some object, property, relation, event, or state of affairs, and C is the meaning that A assigns to B. (Posner et al. 1997: 4)

By the 1990s, much of the Peircean approach to biosemiotics had become almost universally accepted, and today too semiotics is still synonymous with Peircean-semiotics, which means that the concept of sign is still squarely based on interpretation. As a result, it has been taken almost for granted that the extension of semiosis to the animal world and to the entire living world, is nothing but the extension of Peircean-semiosis to all of life. Sebeok expressed this concept in no uncertain terms: "*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: 68).

We have seen, however, that the Peircean model cannot be applied to the cell because the genetic code does not depend on interpretation. But is this an insurmountable obstacle? Couldn't we say, for example, that the seat of the genetic code, i.e., the 'codemaker' of the cell, is an 'interpreter'? Why shouldn't

we generalize the concept of interpretation and say that an act of coding is also an act of interpretation?

In principle, of course, we could, but there is a caveat. If we generalize the concept of interpretation in order to include coding, why don't we go the whole way and generalize it even further? Why don't we say, following Edwina Taborsky, that any function

$$f(x) = y$$

is an act of interpretation whereby the function '*f* interprets '*x*' as representing '*y*'? (Taborsky 1999: 601). In this way all physical laws expressed by functions like *f* would be processes of interpretation and therefore acts of semiosis.

The point is that Peirce himself took this view and concluded that semiosis exists everywhere in the universe. We realize in this way that if we generalize the concept of interpretation, thusly, the Peircean model would become a 'pansemiotic' model, not a biosemiotic one. If we want to keep the biosemiotic idea that semiosis started with life, therefore, we must also keep the traditional concept of interpretation, and in this case we can no longer apply the Peircean model to the cell. This does not mean that the Peirce model is wrong. It means that it is valid only for those living systems that are capable of interpretation in the traditional sense of the word, i.e., for organisms that have a nervous system. It also mean that we need a definition of semiosis that does not depend on interpretation, and luckily we can easily obtain it by generalizing the definition proposed by Posner, Robering and Sebeok (1997: 4) reported earlier. Our modified formulation thus becomes:

> We stipulate that the following is a necessary and sufficient condition for something to be a semiosis: A establishes a *conventional correspondence* between B and C. In this relational characterization of semiosis, A is the *Adaptor*, B is some object, property, relation, event, or state of affairs that is *taken* as a *sign* and C is the *meaning* that A assigns to B.

The Evolution of Semiosis

The genetic code was the first code in the history of life and the apparatus of protein synthesis was the first semiotic system that appeared on Earth. But what happened afterwards? The evidence suggests that many other organic codes came into being, particularly in eukaryotic cells, and accounted for many great biological innovations that appeared in those cells in the first three billion years of evolution (Barbieri 1985, 2003).

The complexity of the genome, however, could not increase indefinitely and there was a limit to the number of codes that could be programmed in the genes. This is particularly evident in the case of animal behaviour. The most primitive

behaviors were almost entirely determined by genes, but the number of hard-wired responses could not grow indefinitely, and animals started resorting to processes of learning in order to increase their behavioral repertoire.

Learning how to respond to a signal, on the other hand, means learning how to *interpret* that signal, and this amounts to the construction of a behavioral code whose rules are *context-dependent*. At the same time, learning requires a *memory* where the results of experience are accumulated, and this means that interpretation is also a *memory-dependent* process. A process of *interpretation*, in short, is a new type of semiosis because it is dependent on *learning*, *memory* and *context*.

Systems capable of interpretation, in turn, evolved in many different ways and eventually a third type of semiosis appeared — a semiosis that was based on symbolic codes shared by all members of a community, i.e., on *language*. The evolution of semiosis is characterized therefore by three great innovations: (1) the origin of organic semiosis (the *semiotic threshold*), (2) the origin of interpretation (the *hermeneutic threshold*), and (3) the origin of language (the *symbolic threshold*).

The origin of semiosis and the origin of interpretation were separated by almost three billion years of cellular evolution, because interpretation is dependent on learning, memory and context, and probably evolved only in multicellular systems. The origin of language came after another five hundred million years and apparently evolved only in our species. The history of semiosis, in conclusion, was a process that started with context-free codes and produced codes that were more and more context-dependent. Today, our cultural codes are so heavily dependent on context that we can hardly imagine semiosis without interpretation, and yet these are distinct processes and we need to keep them apart if we want to understand their origin and their evolution in the history of life.

Toward a Scientific Biosemiotics

Biosemiotics can become a science only if we can prove that the cell — the necessary and sufficient unit of all life — is a semiotic system. But in order to achieve this goal, we cannot rely on the models of Saussure and Peirce, because they are not applicable to the molecular level. We need a third model of semiosis, and luckily such a model does exist.

It has been suggested that the Peircean model can be extended to the cell simply by generalizing the concept of interpretation, but this is not a satisfactory solution because the issue is not about words, it is about real processes and real objects. We need three distinct types of semiosis because there are

three distinct types of objects in life: there are *organic objects*, *mental objects* and *cultural objects*. The origin and the evolution of life was the origin and the evolution of the different entities that make up the three worlds of life: the organic world, the mental world and the world of culture.

In order to prove that the cell is a semiotic system, in short, we need a model of organic semiosis, not a model of mental semiosis extended to the organic world. But that is not all. We also need to realize that the cell is not a duality of genotype and phenotype, but a trinity of genotype, phenotype and ribotype, because a semiotic system is necessarily made of three distinct categories, one of which is a codemaker and the other two of which are signs (genotypes) and their meanings (phenotypes) (Barbieri 1981). Finally, we need to realize that evolution took place not only by natural selection, but also by *natural conventions* because all types of semiosis are based on conventions (Barbieri 1985, 2003).

Thus, in order to build a scientific biosemiotics, we need new concepts both in semiotics, and in biology. More precisely, we need a new model of semiosis, a new theory of the cell and a new mechanism of evolution. All these ideas have already been proposed, and we can therefore start building a scientific biosemiotics on the basis of the following foundational concepts:

(1) Semiosis is defined by coding, not by interpretation
(2) The agents of semiosis are the codemakers, not the signs
(3) Signs and meanings are codemaker-dependent entities
(4) Genetic sequences are codemaker-dependent entities and are the organic signs of protein synthesis
(5) Protein sequences are codemaker-dependent entities and are the organic meanings of protein synthesis
(6) The translation apparatus is a semiotic system made of organic signs, organic meanings and the genetic code
(7) The cell is a semiotic system made of genes, proteins and codemaker (genotype, phenotype and ribotype)
(8) The basic mechanisms of life are copying and coding
(9) The basic mechanisms of evolution are natural selection (from copying) and natural conventions (from coding).

We conclude that a scientific biosemiotics is possible, but we only if we go beyond the models of Saussure and Peirce. These models are still valid, but only in the worlds of cultural semiosis and mental semiosis. Now we need a model also for the greater world of organic semiosis. This is not a denial of Saussure and Peirce. On the contrary, it is the real continuation of their work, for it is the step that allows us to prove that semiosis is fundamental to the whole of life and that the cell is a true semiotic system.

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