

# Chapter 4

## On Biological Computing, Information and Molecular Networks

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### ABSTRACT

*The author will focus this chapter on studying the set of special characteristics molecular networks which constitute living systems might have. In order to do that, he will study them from the perspective which allows us to visualize the most basic element constituting that which is living. This approach should lead us to uncover the essential properties which form any dynamic entity that could be called a living system. It will furthermore permit us to understand the intrinsic relationship produced between the handling of biological information and the start-up of something completely new that is revealed in the set of aspects which bear natural computations within living systems.*

### 1. INTRODUCTION

The term biological computing is also called natural computing, and we employ these two terms to refer to a sort of computation that nature carries out.

On the other hand, we also use them to refer to nature-inspired computational models.

For example, evolutionary algorithms and neural network-based algorithms are being implemented on conventional computers.

Thus, it is not possible to disregard contributions coming from the field of computer science since it has revealed that complex natural processes can be seen as computational processes.

The same can be stated concerning biology when we observe the fact it has pushed forward the understanding of processes within its field, with ongoing assistance from applications created through information science that have coalesced into more sophisticated programs and advanced computers.

However, there is one branch of research that possesses a long list of questions investigators have

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yet to pose on account of newly found data, and that is research into the question on whether certain forms, which we could call “computations”, are spontaneously produced in nature.

The following discussion will form our attempt to shine some light on this electrifying topic.

Our chapter is structured the following way. In the section “*Origin of Biological Information*”, we shall briefly go over different alternatives that could be used for biological information and their possible relationship to signs.

In the section “*Looking at Biological Networks*”, we shall begin presenting our proposals in relation to the topics, moving backwards in time to the pre-biotic world. Here, we contend the pre-biotic era ushered in a protocell that contained very new properties.

In our last section, “*Insights into Biological Computing*”, we shall provide an examination of the consequences that are derived from the previous sections.

Once concluded, we should have our first glimpse of what our protocell may have generated: the appearance or emergence of a primary capacity of what we shall call biological computation.

## 2. ORIGIN OF BIOLOGICAL INFORMATION

The first issue which strongly calls our attention is the fact there is no clear acceptance of the term biological information. Moreover, many times that term is even considered equivalent to the term “genetic information”. This is perhaps owing to the very fact that the notion of information in biology is deeply connected to the birth of molecular biology. The first time we read about the notion of information forming part of a biological study’s explanation is in Watson and Crick’s second work in 1953:

*“...It follows that in a long molecule many different permutations are possible, and it therefore seems*

*likely that the precise sequence of the bases is the code which carries the genetical information...”*  
(Watson & Crick, 1953, p. 965).

Later in (Crick, 1958; Crick, 1970), we can see what he called the “central dogma of molecular biology” characterized as follows:

*“...Because these were all the possible transfers from protein, the central dogma could be stated in the form ‘once (sequential) information has passed into protein it cannot get out again’...”*  
(Crick, 1970, p. 562).

Here, we must point out that the crux of this chapter is not an exploration of the different uses of the notion of information in the history of molecular biology (if the reader is so interested, please consult the following: Darden, 2006; Kay, 1993; Kay, 2000; Watson et al., 1988).

Nevertheless, what we are definitely interested in underscoring is that different researchers have begun to use the notion of information, codes, signs, and similar ideas to discuss other aspects that make up the biological dynamic and that are not necessarily related to genetic information (Jablonka, 2002; Jablonka & Lamb, 2005; Kauffman et al., 2008; Maynard, 2000).

On the other hand, we do want to stress that our approach to the notion of information, signs, and the like is set within the perspective of evolution.

For us, this implies we draw upon no assumptions, characteristics, or properties coming from humans or the world of human products. In truth, we hold that the notions we are studying need to be clarified from a naturalist point of view.

In other words, we need to avoid extrapolations coming from the human world, like ascriptional interpretations or epiphenomenal ones.

In agreement with Bickhard’s (2004) proposals, we are confident that normative emergence is necessary for any naturalistic account of biology.

An interesting spin upon research carried out on the nature of the living and its difference to

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