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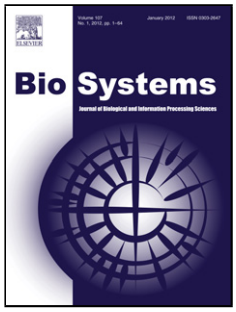

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Mathematical Fundamentals for the Noise Immunity of the Genetic Code

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Abstract. Symmetry is one of the essential and most visible patterns that can be seen in nature. Starting from the left-right symmetry of the human body, all types of symmetry can be found in crystals, plants, animals and nature as a whole. Similarly, principals of symmetry are also some of the fundamental and most useful tools in modern mathematical natural science that play a major role in theory and applications. As a consequence, it is not surprising that the desire to understand the origin of life, based on the genetic code, forces us to involve symmetry as a mathematical concept. The genetic code can be seen as a key to biological self-organisation. All living organisms have the same molecular bases - an alphabet consisting of four letters (nitrogenous bases): adenine, cytosine, guanine, and thymine. Linearly ordered sequences of these bases contain the genetic information for synthesis of proteins in all forms of life. Thus, one of the most fascinating riddles of nature is to explain why the genetic code is as it is. Genetic coding possesses noise immunity which is the fundamental feature that allows to pass on the genetic information from parents to their descendants. Hence, since the time of the discovery of the genetic code, scientists have tried to explain the noise immunity of the genetic information. In this chapter we will discuss recent results in mathematical modelling of the genetic code with respect to noise immunity, in particular error-detection and error-correction. We will focus on two central properties: Degeneracy and frameshift correction.

Degeneracy: Different amino acids are encoded by different quantities of codons and a connection between this degeneracy and the noise immunity of genetic information is a long standing hypothesis. Biological implications of the degeneracy have been intensively studied and whether the natural code is a frozen accident or a highly optimised product of evolution is still controversially discussed. Symmetries in the structure of degeneracy of the genetic code are essential and give evidence of substantial advantages of the natural code over other possible ones. In the present chapter we will present a recent approach to explain the degeneracy of the genetic code by algorithmic methods from bioinformatics, and discuss its biological consequences.

Frameshift correction: The biologists recognised this problem immediately after the detection of the non-overlapping structure of the genetic code, i.e, coding sequences are to be read in a unique way determined by their reading frame. But how does the reading head of the ribosome recognises an error in the grouping of codons, caused by e.g. insertion or deletion of a base, that can be fatal during the translation process and may result in nonfunctional proteins? In this chapter we will discuss possible solutions to the frameshift problem with a focus on the theory of so-called circular codes that were discovered in large gene populations of prokaryotes and eukaryotes in the early 90s. Circular codes allow to detect a frameshift of one or two positions and recently a beautiful theory of such codes has been developed using statistics, group theory and graph theory.

Key words and phrases. genetic code, degeneracy of the genetic code, circular codes, evolution of the genetic code, symmetric group, graph theory, frameshift problem.

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