

An Informational Approach to Biological Complexity

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This work explores a new understanding of physiological phenomena by revisiting the informational organization of the living cell. There is a presupposition that, contemporarily, the new fields of genomics, proteomics, transcriptomics, metabolomics, degradomics, signaling science etc. are in demand of a new information synthesis -the “systems biology” advocated by numerous parties. The approach followed here starts out from the *molecular recognition* field, which provides a unitary framework to analyze any further complexification of molecular-biological processes. In the living cell, the recognition encounters, or *hits*, between molecular partners embedded in informational architectures of sequential nature (DNA and RNA worlds) versus amorphous ones (diluted, amorphous assemblies of enzymes and proteins) are at the very center of cellular functioning. Properly establishing the functionality of the active elements -enzymes and proteins, the amorphous architecture- is in itself a “principled” matter that largely conditions the analysis of enzyme networks and the cellular cycle. How the stochastic function of the enzyme and its whole molecular-recognition circumstances (not only the probability of the “how”, but also the “when”, “where”, “how fast”, “with whom”, and for “how long”) have been coded together into the eukaryotic genome bears the hallmark of *problem-solving universality* at the molecular realm. In this sense, there emerges a striking parallel between the working cycle of the enzymic function and the eukaryotic cellular cycle, respectively understood as elementary functional components of cellular systems and of complex multicellular organisms. Finally, it will be argued that an old evolutionary dispute between allometric exponents in the species distribution of metabolic regimes ($2/3$ versus $3/4$) may correspond not only to the search of energy/transportation optima, but could also correspond to direct optimization in an informational setting: the allegiance of organisms to the “partitional canon” in the progressive addition of further organismic parts taken as sub-summands in the distribution total of arithmetic partitions.