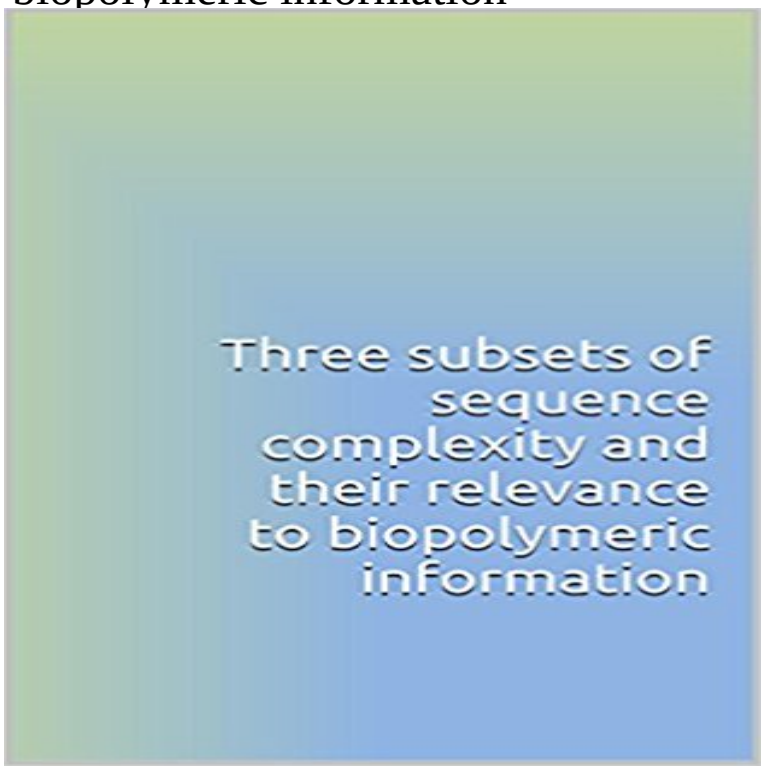
Three subsets of sequence complexity and their relevance to biopolymeric information



Genetic algorithms instruct sophisticated biological organization. Three qualitative kinds of sequence complexity exist: random (RSC), ordered (OSC), and functional (FSC). FSC alone provides algorithmic instruction. Random and Ordered Sequence Complexities lie at opposite ends of the same bi-directional sequence complexity vector. Randomness in sequence space is defined by a lack of Kolmogorov algorithmic compressibility. A sequence is compressible because it contains redundant order and patterns. Law-like cause-and-effect determinism produces highly compressible order. Such forced ordering precludes both information retention and freedom of selection so critical to algorithmic programming and control. Functional Sequence Complexity requires this added programming dimension of uncoerced selection at successive decision nodes in the string. Shannon information theory measures the relative degrees of RSC and OSC. Shannon information theory cannot measure FSC. FSC is invariably associated with all forms of complex biofunction, including biochemical pathways, cycles, positive and negative feedback regulation, and homeostatic metabolism. The algorithmic programming of FSC, not merely its aperiodicity, accounts for biological organization. No empirical evidence exists of either RSC of OSC ever having produced a single instance of sophisticated biological organization. Organization invariably manifests FSC rather than successive random events (RSC) or low-informational self-ordering phenomena (OSC).

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References 1. **Thermodynamic Inversion: Origin of Living Systems - Google Books Result** Abel (David) & Jack Trevors, Three Subsets of Sequence Complexity and Their Relevance to Biopolymeric Information, Theoretical Biology and Medical **complexity, self-organization, and emergence at the edge of - jstor** July 3, 2011, Posted by kairosfocus under Intelligent Design paper on Three subsets of sequence complexity and their relevance to biopolymeric information:. **Functional Sequence Complexity (FSC) Measured in Fits** Three subsets of sequence complexity and their relevance to biopolymeric information. A key figure (NB: in the public domain) in the article was their Fig. 4:. Abel and Trevors have defined three types of sequence complexity, .. The value ? is a measure of the FSC, or functional information, of any .. Trevors, J.T. 2005, Three subsets of sequence complexity and their relevance to biopolymeric. **5. Functional Sequence Complexity in Biopolymers Introduction** References Abel DL (2000) Is life reducible to complexity? Last accessed Jan 2012 Abel DL (2009a) The biosemiosis of prescriptive information. Three subsets of sequence complexity and their relevance to biopolymeric information. **Bao cao y h?c: Three subsets of sequence complexity and their** Three subsets of sequence complexity and their relevance to biopolymeric information. David L Abel and Jack T TrevorsEmail author. Theoretical Biology and **Three subsets of sequence complexity and their relevance to** (under Definitions)(Last accessed May 2006). http://www. lifeorigin. info. Abel, D. L. Three subsets of sequence complexity and their relevance to biopolymeric **Three subsets of sequence complexity and their relevance to Models and Applications of Chaos Theory in Modern Sciences - Google Books Result** Theoretical Biology and Medical Modelling Three subsets of sequence

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