eJBio

Electronic Journal of Biology, 2023, Vol. 19(1):1-2

Brief Note on Biological Systems and Quantum Biology

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Citation: Willium J (2023) Brief Note on Biological Systems and Quantum Biology. Electronic J Biol, 19(1): 1-2

Received date: January 11, 2023, Manuscript No. IPEJBIO-23-16031; **Editor assigned date:** January 13, 2023, PreQC No. IPEJBIO-23-16031 (PQ); **Reviewed date:** January 24, 2023, QC No. IPEJBIO-23-16031; **Revised date:** February 04, 2023, Manuscript No. IPEJBIO-23-16031 (R); **Published date:** February 11, 2023, DOI: 10.36648/1860-3122.19.1.070

Description

Biological systems are fundamentally computational in that they process information in an apparently purposeful fashion rather than just transferring bits of it in a purely syntactical manner. Biological information, such has genetic information stored in DNA sequences, has semantic content. It carries meaning that is defined by the molecular context of its cellular environment.

Biological Systems

Information processing in biological systems displays an inherent reflexivity, a tendency for the computational information-processing to be “about” the behaviour of the molecules that participate in the computational process. This is most evident in the operation of the genetic code, where the specificity of the reactions catalysed by the aminoacyl-tRNA synthetase enzymes is required to be self-sustaining. A cell’s suite of aaRS enzymes completes a reflexively autocatalytic set of molecular components capable of making themselves through the operation of the code. This set requires the existence of a body of reflexive information to be stored in an organism’s genome. The genetic code is a reflexively self-organised mapping of the chemical properties of amino acid sidechains onto codon “tokens”.

The unprecedented development in novel and high throughput techniques to understand biology at multiple dimensions has opened unique challenges and opportunities for computational methodologies to harness “big data in biology” and extract actionable insights. New models and methodologies are need for systems biology-based approaches to reconcile data from different spatio-temporal scales, connecting diverse set of computational techniques towards a systems-level understand of living organisms. Current tools and techniques in computational systems biology have demonstrated their usage in various application areas. At the same time, paradigm shifts in experimental techniques, powerful data analytics, modeling and visualization methodologies, have resulted in empowering computational systems biology models and methodologies. These developments will leverage on the advancements in machine learning models, big data management and analysis as well as large scale modeling and simulations. This topic article endeavors to provide key areas of modeling and methodologies–highlighting new directions and developments, to enable computational systems biology to address the new challenges in biology and medicine.

It is a highly evolved symbolic system of chemical self-description. Although molecular biological coding is generally portrayed in terms of classical bit-transfer events, various biochemical events explicitly require quantum coherence for their occurrence. Whether the implicit transfer of quantum information, qbits, is indicative of wide-ranging quantum computation in living systems is currently the subject of extensive investigation and speculation in the field of quantum biology.

Quantum Biology

Biological entities are involved in intricate and complex interactions, in which uncovering the biological information from the network concepts are of great significance. Benefiting from the advances of network science and high-throughput biomedical technologies, studying the biological systems from network biology has attracted much attention in recent years, and networks have long been central to our understanding of biological systems, in the form of linkage maps among genotypes, phenotypes, and the corresponding environmental factors. In this review, we summarize the recent developments of computational network biology, first introducing various types of biological networks and network structural properties. We then review the network-based approaches, ranging from some network metrics to the complicated machine-learning methods, and emphasize how to use these algorithms to gain new biological insights. Furthermore, we highlight the application in neuroscience, human disease, and drug developments from the perspectives of network science, and we discuss some major challenges and future directions. We hope that this review will draw increasing interdisciplinary attention from physicists, computer scientists, and biologists.

Fork head box family transcription factors play essential roles in development, tissue homeostasis, and disease. Although the biology of several FOX proteins has been studied in depth, it is unclear to what extent these findings

apply to even closely related family members, which frequently exert overlapping but non-redundant functions. To help address this question, we have generated a uniform, ready-to-use expression library of all 44 human FOX transcription factors with a convenient peptide tag for parallel screening assays. In addition, we have generated multiple universal fork head box reporter plasmids, which can be used to monitor the transcriptional activity of most FOX proteins with high fidelity. As a proof-of-principle, we use our plasmid library to identify the DNA repair protein XRCC6/Ku70 as a selective FOX interaction partner and regulator of FOX transcriptional activity. We believe that these tools, which we make available via the Addgene plasmid repository, will considerably expedite the investigation of FOX protein biology. Osteoporosis, a disease characterized by reduced bone mass, is a major health concern in the aging population that can lead to debilitating bone fractures and a reduced quality of life. Although present in both sexes, osteoporosis is more prevalent in females due to estrogen deficiency that occurs following menopause. This relationship between estrogen and bone has been known for over 70 years since the work of Fuller Albright, and although enormous progress in elucidating its effects in bone has contributed to a greater understanding of the underlying biology and clinical significance, major unresolved questions still exist. In this chapter, we will review the general biology of estrogen action in bone and its potential clinical significance in the understanding of osteoporosis. Metabolic engineering allows development of microbial strains efficiently producing chemicals and materials, but it requires much time, effort, and cost to make the strains industrially competitive. Systems metabolic engineering, which integrates tools and strategies of systems biology, synthetic biology, and evolutionary engineering with traditional metabolic engineering, has recently been used to facilitate development of high-performance strains. The past decade has witnessed this interdisciplinary strategy continuously being improved toward the development of industrially competitive overproducer strains. In this article, current trends in systems metabolic engineering including tools and strategies are reviewed.