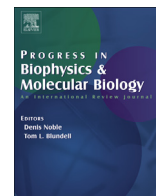




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Biological information systems: Evolution as cognition-based information management

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ABSTRACT

An alternative biological synthesis is presented that conceptualizes evolutionary biology as an epiphenomenon of integrated self-referential information management. Since all biological information has inherent ambiguity, the systematic assessment of information is required by living organisms to maintain self-identity and homeostatic equipoise in confrontation with environmental challenges. Through their self-referential attachment to information space, cells are the cornerstone of biological action. That individualized assessment of information space permits self-referential, self-organizing niche construction. That deployment of information and its subsequent selection enacted the dominant stable unicellular informational architectures whose biological expressions are the prokaryotic, archaeal, and eukaryotic unicellular forms. Multicellularity represents the collective appraisal of equivocal environmental information through a shared information space. This concerted action can be viewed as systematized information management to improve information quality for the maintenance of preferred homeostatic boundaries among the varied participants. When reiterated in successive scales, this same collaborative exchange of information yields macroscopic organisms as obligatory multicellular holobionts. Cognition-Based Evolution (CBE) upholds that assessment of information precedes biological action, and the deployment of information through integrative self-referential niche construction and natural cellular engineering antecedes selection. Therefore, evolutionary biology can be framed as a complex reciprocating interactome that consists of the assessment, communication, deployment and management of information by self-referential organisms at multiple scales in continuous confrontation with environmental stresses.

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Abbreviations: CBE, cognition based evolution; PIF, pervasive information field; HGT, horizontal gene transfer; ERV, endogenous retrovirus; TE, transposable element; miRNA, micro RNA; ncRNA, non-coding RNA; piRNA, piwi-interacting RNA; RNAi, RNA interference; endo-siRNA, endogenous short interfering RNA; *Ei*, effective information; viRNA, virus-derived, small-interfering RNA; mRNA, messenger RNA; HIV, human immunodeficiency virus; *C. elegans*, *Caenorhabditis elegans*; *E. coli*, *Echerichia coli*; LTR, long terminal repeat.

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1. Introduction

Developmental biology can be seen as the study of how information in the genome is translated into adult structure, and evolutionary biology of how the information came to be there in the first place

Maynard Smith

The traditional canonical Neodarwinian evolutionary narrative concentrates on the survival mechanisms of macroscopic organisms through random heritable variations and differential fitness (Bowler, 2003). The sources of those variations have been ascribed to random genetic mutations along fitness landscapes (Poelwijk et al., 2007). As a result, evolution has been typically framed as a direct product of changing gene frequencies (Koonin, 2009). Contemporary research has placed increasing emphasis on the evolutionary role of epigenetics which can further extend genetic expression from a flexible genome (Jablonka and Lamb, 2008; Laland et al., 2015). However, such alterations are typically considered within the framework of an already existing expansive genome upon which smaller modifications might act. An understanding of the mechanisms that permit the erasure of some epigenetic marks and the inheritance of others prior to arbitrating selection is still limited (Feng et al., 2010; Hourri-Zeevi and Rechavi, 2016). The further mechanisms by which genomes accrete their widely variable sizes and ranges of biological expression and still retain effectiveness is not well understood (Eddy, 2012). Surprisingly, the question of why multicellular eukaryotes are obligatory holobionts or how that might affect levels of selection is little considered. (Miller, 2016a; Corning and Szathmáry, 2015; Theis et al., 2016). Most pertinently, although the mystery of cognition has been deeply weighed, there has been little regard for the role of universal basal cognition in biological development and a distinct disinclination to consider its evolutionary implications.

To further evaluate these issues, an exploration of evolutionary development is presented that focuses on the nature of biological information content, and its transfer and management, within the context of cellular faculties and constraints. This perspective is offered as a substantiating complement to previous arguments affirming the central role of self-referential cognition in evolutionary development (Miller, 2016a; Torday and Miller, 2016a, 2016b, 2017a; Miller and Torday, 2017).

2. The origin of biological information

2.1. Self-reference

That aspects of biology such as genes might be considered within an information framework is not new (Dodig-Crnkovic, 2014). Peter Medawar, the eminent British biologist, had addressed the concept decades ago, indicating that, “..... in speaking of genes and chromosomes, the language of information

theory is often extremely apt.” (Kay, 1998). More recently, Griffiths (2017) argued that it is direct common sense to consider the development of evolved characteristics as the expression and transmission of information but laments the difficulty between theory and practice. For Walker and Davies (2013), that linkage is plain, declaring that information became the key to life by achieving “direct and context-dependent causal efficacy over the matter in which it is instantiated.”

It follows that an examination of biology should begin with the recognition that the boundary between the animate and inanimate lies within the capacity of living things to discriminate an individuated status such that physical states become biological information (Miller, 2016a). This can be regarded as a working definition of self-referential cognition in which the living condition is delineated by an awareness of status upon which adjustments might be made. That all living things have this capacity is not conjectural. It is now acknowledged that all living things exhibit basal cognition through such a fundamental awareness of status (Shapiro, 2011; Trewavas and Baluška, 2011; Miller, 2013, 2016a; Baluška and Mancuso, 2009; Dodig-Crnkovic, 2014). This is embodied within cells by negentropic boundary conditions, sustained by chemiosmosis, and maintained by homeostasis (Torday, 2015). The living state therefore extends from the physical environment through Schrödinger's “consumption of negative entropy” within boundary conditions by energy (ATP) transfers in a manner that information-based projections of status can be realized. (Jacob et al., 2006). Thus, intrinsic cellular properties that derive from the physical environment permit the self-referential reactions to environmental stresses that preserve preferred homeostatic flux boundaries. Plainly though, as such actions are achieved through the assessment and use of information and its pragmatic deployment, there is substantial justification for considering biology within an informational construct. (Miller, 2016a; Torday and Miller, 2016a, 2017a; Roederer, 2016; Ball, 2016; Cartwright et al., 2016).

Although the origin of self-reference is unknown, it has been attributed to a derivative of the thermodynamic scale as its own state function as a phase transition (Miller, 2016a; Eigen, 2013). Eigen (2013) considered that phase transition as a complexity threshold that had both entropic and semantic qualities that emerged from the reproduction and transmission of information. Proponents of complexity biology have suggested that this complexity threshold is a matrix of self-organized criticality. These are zones of instabilities that maximize information diversity in which the regulation of information processing might be optimized (Hankey, 2015). It has been proposed that it is within these zones of criticality that coherences can occur that enable the self-observing systems that underlie the integrated feedback loops that enable the living process (Hankey, 2015). Computational research has shown that the most favorable conditions for information storage and transmission can be identified as residing in the vicinity of such phase transition criticalities (Langton, 1990).

Others have considered the emergence of life as a first-order

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