

Information, Control and Evolution of Cellular Networks, H. Kim¹, P. Davies¹ and S.I.Walker^{1,2,3}

¹Beyond Center for Fundamental Concepts in Science, Arizona State University, Tempe AZ USA ²School of Earth and Space Exploration, Arizona State University, Tempe AZ USA, ³Blue Marble Space Institute of Science, Seattle WA USA. Email: sara.i.walker@asu.edu

Introduction

Life seems distinctive in its ability for information management, and hence it is often described using analogies from logic modules, information flows and computation [1]. It has therefore been hypothesized that information might play a crucial role in the execution of biological function distinguishing living and non-living physical systems [2]. To test this hypothesis, we quantify characteristics of informational structure of two representative Boolean biological networks by computing information transferred within the networks, and comparing the results with the same analysis performed on ensembles of random networks. We also demonstrate how the distinctive pattern of biological information flow is related to biological functional modules that govern the cellular fate.

Model and Methods

Our study focuses on two model systems: the cell-cycle regulatory network of the fission yeast *Schizosaccharomyces Pombe* [3] and that of the budding yeast *Saccharomyces cerevisiae* [4]. An interesting feature to emerge from previous studies of these two networks is the presence of a small subset of nodes — called the control kernel— that regulates the function of the networks [5]. For both cell-cycle regulatory networks, we investigate the processing of information among nodes by using transfer entropy [6] with particular focus on the control kernel. We compare the results for the biologically functional cell-cycle networks with random Boolean networks constructed to share topological properties with the reference biological networks, including scale-free structure.

Results

Our information theoretic approach reveals that the biological networks in our study process more information than the random networks on average. Also, biological networks also exhibit a scaling relation in information transferred

between nodes that distinguishes them from random, where the biological networks stand out as distinct even when compared with random networks that share important topological properties, such as degree distribution, with the biological network. We show that the most biologically distinct regime of this scaling relation is associated with a subset of control nodes that regulate the dynamics and function of each respective biological network.

Conclusion

Our results suggest that previously unidentified information-based organizational principles that go beyond topological considerations, such as a scale-free structure. Thus, information may be intrinsic to the operation of living systems, where the informational architecture of biologically evolved networks has the potential to distinguish biological networks from other classes of networks. Also, our results imply that the global informational architecture of biological networks may influence the controllability for biological functions of the networks.

References

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