

Abstract Submitted
for the 4CF15 Meeting of
The American Physical Society

New Scaling Relation for Information Transfer in Biological Networks HJUNJU KIM, APS — Life seems distinctive in its ability to process information. However, precisely what distinguishes information handling in living systems from that of their non-living counterparts remains to be rigorously quantified. While useful tools for quantifying information transfer and causal structure exist in complex systems research, they have been little applied to distributed information processing in biological networks, particularly at the most fundamental level of biological organization - biochemistry. Here, we provide a rigorous case study of the informational architecture of two representative biological networks, Boolean models for the cell-cycle regulatory network of the fission yeast (*S. Pombe*) and that of the budding yeast (*S. cerevisiae*). We calculate the information transferred between pairs of nodes within each network in the execution of function and contrast the results with the same analysis performed on ensembles of random networks of two different classes: Random and Scale-Free. We show that both biological networks share features in common that are not shared by either ensemble. In particular, the biological networks in our study, on average, process more information than both classes of random networks. They also exhibit a scaling relation in information transfer between nodes that distinguishes them from either ensemble – even for Scale-Free networks that share important topological properties, such as power-law degree distribution. We show that the most biologically distinct regime of this scaling relation is associated with the dynamics and function of the biological networks. Therefore, our results suggest that previously unidentified information-based organizational principles that go beyond topological considerations, such as a scale-free structure, which may be critical to biological function. 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 network architecture that do not exhibit these informational properties.

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Date submitted: 12 Oct 2015

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