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The Informational Architecture of Biological Networks

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An important goal in biology is identifying what features of biological organization may be universal to life and potentially distinguish living systems from other classes of physical system. For example, information is increasingly cited as an important property of biological systems, but it is unclear in what sense information can uniquely characterize life. To address this problem, we use as a case study a Boolean network model for the cell cycle regulation of the single-celled fission yeast (Schizosaccharomyces Pombe) and compare its informational properties to two classes of null model that share commonalities in their causal structure. We report patterns in *local* information processing and storage that distinguish biological from random. Conversely, we find that “emergent” information processing, which we quantify using integrated information theory, does not differ from random for the case presented. We discuss implications for our understanding of the informational architecture of the fission yeast cell cycle network and for illuminating any distinctive physics operative in life.