

# MSIS-Kadelka: Canalization reduces the nonlinearity of regulation in biological networks

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Biological networks such as gene regulatory networks possess desirable properties. They are more robust and controllable than random networks. This motivates the search for structural and dynamical features that evolution has incorporated in biological networks. A meta-analysis of published, expert-curated Boolean biological network models has revealed several such features. Among others, the biological networks are enriched for certain recurring network motifs, the dynamic update rules are more redundant and more canalizing than expected, and the dynamics of biological networks are better approximable by linear and lower-order approximations than those of comparable random networks. Since most of these features are interrelated, it is paramount to disentangle cause and effect. In other words, we aim to understand which features evolution actively selects for. Here, we show that approximability is primarily a function of output bias and effective in-degree and that increased canalization in biological networks can almost completely explain their higher approximability.