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Form, Function, and Evolvability in Biological Networks ANDREW MUGLER, Physics Dept, Columbia University, ETAY ZIV, College of Physicians and Surgeons, Columbia University, ILYA NEMENMAN, CCS-3/CNLS, Los Alamos National Laboratory, CHRIS H. WIGGINS, Dept of Applied Physics & Applied Math/C2B2, Columbia University — A driving problem in systems biology for several years has been exploring the extent to which the topology of a small biological network constrains or guides its function. The absence of such constraint would allow a given network to evolve without rewiring its underlying form. We introduce a quantitative measure of this evolvability that does not rely on pre-defining the preferred function of a given topology. We then study the stochastic description of the experimental setup of Guet [1], treating chemical inducers as functional inputs and the expression of a reporter gene as the functional output. We take an information-theoretic approach, allowing the system to set parameters that optimize signal processing ability, thus enumerating the highest-fidelity functions. We find that, while all networks studied are highly evolvable by our measure–meaning that the function has little dependence on location in parameter space–the evolvability is correlated with individual topological features. Certain topological attributes, then, are shown (with statistical significance) to convey evolvability to biological networks.
[1] C. C. Guet et al., Science **296**, 1466 (2002).

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