

Abstract Submitted  
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**Biological Networks: Does Function Follow Form?** ETAY ZIV, College of Physicians & Surgeons, Department of Biomedical Engineering, Columbia University, MANUEL MIDDENDORF, Department of Physics, Columbia University, ILYA NEMENMAN, Center for Computational Biology and Bioinformatics, Columbia University, CHRIS WIGGINS, Applied Physics and Applied Mathematics, Center for Computational Biology and Bioinformatics, Columbia University — Recently, studies of biological networks have focused on various topological measures (primarily degree distributions and subgraphs). Relating such graph-theoretic statistics to function is difficult, since a given topology does not uniquely determine function. In fact, a topology's ability to support multiple functions may itself provide a selective advantage to an organism, since a topology with multiple functions can be adaptable (on the time scale of the individual) or evolvable (on the time scale of the species). Here we present a quantitative measure of circuit function and use this measure to test if circuits with well-defined function or functions are common, and if evolvable topologies exist among them.

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