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Optimizing information flow in small genetic networks ALEKSANDRA M. WALCZAK, Princeton University, GASPER TKACIK, University of Pennsylvania, CURTIS G. CALLAN, WILLIAM BIALEK, Princeton University — Many of the biological networks inside cells can be thought of as transmitting information from the inputs (e.g., the concentrations of transcription factors or other signaling molecules) to their outputs (e.g., the expression levels of various genes). On the molecular level, the relatively small concentrations of the relevant molecules and the intrinsic randomness of chemical reactions provide sources of noise that set physical limits on this information transmission. Given these limits, not all networks perform equally well, and maximizing information transmission provides a candidate design principle from which we might hope to derive the properties of real regulatory networks. As a starting point, I will consider the simple case of one input transcription factor that controls many genes. I will discuss the properties of these specific small networks that can transmit the maximum information. Concretely, I will show how the form of molecular noise drives predictions not just of the qualitative network topology but also the quantitative parameters for the input/output relations at the nodes of the network. In an attempt to link these general theoretical considerations to real biological systems, I will illustrate the predictions on the example of transmission of positional information in the early development of the fly embryo.

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