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Towards a predictive theory for genetic regulatory networks

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When cells respond to changes in the environment by regulating the expression levels of their genes, we often draw parallels between these biological processes and engineered information processing systems. One can go beyond this qualitative analogy, however, by analyzing information transmission in biochemical “hardware” using Shannon’s information theory. Here, gene regulation is viewed as a transmission channel operating under restrictive constraints set by the resource costs and intracellular noise. We present a series of results demonstrating that a theory of information transmission in genetic regulatory circuits feasibly yields non-trivial, testable predictions. These predictions concern strategies by which individual gene regulatory elements, e.g., promoters or enhancers, read out their signals; as well as strategies by which small networks of genes, independently or in spatially coupled settings, respond to their inputs. These predictions can be quantitatively compared to the known regulatory networks and their function, and can elucidate how reproducible biological processes, such as embryonic development, can be orchestrated by networks built out of noisy components. Preliminary successes in the gap gene network of the fruit fly *Drosophila* indicate that a full ab initio theoretical prediction of a regulatory network is possible, a feat that has not yet been achieved for any real regulatory network. We end by describing open challenges on the path towards such a prediction.