Modularity and Impedance in Trancription Networks

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Synthetic biology, the biological analog to electronics, is a bottom-up engineering discipline: modules are systematically designed with predefined behavior and then combined to build up larger biological circuits carrying out specific complex tasks. A wide range of prototype systems have already been implemented such as oscillators, toggle switches and logic gates, however, these small modules produce the desired behavior only in isolation. When connected, they fail to operate properly due to retroactivity, an effect which extends the notion of impedance to biological systems.

Consequently, this paper primarily focuses on understanding and mathematically characterizing retroactivity in transcription networks. Exploiting the fact that binding and unbinding reactions occur on a much faster timescale than protein production and degradation, the dimension of the ODE model describing the system can be reduced from exponential to polynomial complexity in the number of transcription factors by applying singular perturbation. It is also possible to identify a well-defined and easily computable quantity associated with each gene that can be seen as impedance. By appropriately combining these quantites based on the network structure, one can calculate the internal and input/output impedance of a module, thus providing an analog of Thevenin's theorem regarding transcription networks. Therefore, the behavior of larger systems consisting of interconnected modules become predicable.