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Biological clocks and oscillators: Periodic control of large transcriptional programs

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The circadian clock exerts broad effects on organism physiology by controlling phase-specific expression of genes over a 24hr period. Across animals and plants thousands of genes (up to 80% of the genome) are under circadian clock control. Similarly, thousands of genes in eukaryotic organisms are expressed in a phase-specific manner during the cell division cycle, as well as in parasite developmental cycles observed during malaria infection. The underlying clock/oscillator mechanisms driving these large transcriptional programs are thought to be moderately-sized (~ 20–50 nodes) gene regulatory networks, yet the specific players and their regulatory relationships have not been fully elucidated. To understand the function of these networks, our work has aimed to discover network topologies and the associated parameter regimes that govern the dynamic gene expression programs. Although network structure and function has been studied experimentally in model organisms such as budding yeast, experimental resources are not available in important non-model organisms like the malaria parasite, P. falciparum. Thus, our inference methods have relied on the use of time-series transcriptomic studies that describe the complex dynamics of these periodic gene expression programs. Relevant biological problems, data sets, and integrated quantitative/experimental approaches will be discussed.

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