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Model gene regulatory networks under mutation-selection balance

Gene regulatory networks typically have low in-degrees, whereby any given gene is regulated by few of the genes in the network. They also tend to have broad distributions for the out-degree. What mechanisms might be responsible for these degree distributions? Starting with an accepted framework of the binding of transcription factors to DNA, we consider a simple model of gene regulatory dynamics. There, we show that selection for a target expression pattern leads to the emergence of minimum connectivities compatible with the selective constraint. As a consequence, these gene networks have low in-degree, and "functionality" is parsimonious, *i.e.*, is concentrated on a sparse number of interactions as measured for instance by their essentiality. Furthermore, we find that mutations of the transcription factors drive the networks to have broad out-degrees. Finally, these classes of models are evolvable, *i.e.*, significantly different genotypes can emerge gradually under mutation-selection balance.