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Emergence of sparsity and motifs in gene regulatory networks

We consider a simple model of gene regulatory dynamics derived from the statistical framework describing the binding of transcription factors to DNA. We show that the networks representing essential interactions in gene regulation have a minimal connectivity compatible with a given function. We discuss statistical properties using Monte Carlo sampling. We show that functional networks have a specific motifs statistics. In the case where the regulatory networks are to exhibit multi-stability, we find a high frequency of gene pairs that are mutually inhibitory and self-activating. In contrast, networks having periodic gene expression patterns (mimicking for instance the cell cycle) have a high frequency of bifan-like motifs involving four genes with at least one activating and one inhibitory interaction.