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STATISTICAL PROPERTIES OF EVOLVED GENE REGULATORY NETWORKS- FEED FORWARD LOOPS IN *ESCHERICHIA COLI*

Max B. Cooper [1], John F. Brookfield [2], Matthew Loose [3]

[1]*University College London, COMPLEX, London, United Kingdom*
[2]*University of Nottingham, Institute of Genetics, School of Biology, Nottingham, United Kingdom*
[3]*University of Nottingham, Institute of Genetics, Nottingham, United Kingdom*

john.brookfield@nottingham.ac.uk

We present an approach to modelling the evolution of small gene regulation networks. When there is a need to convert an input gene expression pattern to an output gene expression pattern, populations can evolve many qualitatively different ways (different network architectures) to solve the same underlying problem. The relative frequencies with which these different network architectures are used constitute testable evolutionary predictions. This principle is illustrated through examination of Feed Forward Loops (FFLs) which are simple three-gene regulatory network motifs. They exist in different types, defined by the signs of the effects of genes in the motif on one another. We examine 36 feed forward loops in *Escherichia coli*, using evolutionary simulations to predict the forms of FFL expected to evolve to generate the pattern of expression of the output gene. These predictions are tested using likelihood ratios, comparing likelihoods of the observed FFL structures with their likelihoods under null models. The very high likelihood ratios generated, of over 10^{11}, suggest that evolutionary simulation is a valuable component in the explanation of FFL structure.