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Poster presentation

Modelling the evolution of transcriptional control networks using stochastic simulations and evolutionary computational methods

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Organisms live in a constantly varying environment with limited resources. In order to thrive, organisms need to be able to respond to environmental changes, to make best use of the available resources, or to protect themselves from potentially harmful agents. One way to achieve this is to regulate how the DNA is transcribed and then subsequently translated. The complex patterns of genes regulating other genes form transcription networks which have evolved over millions of years to achieve the complexity we see in organisms today. Whilst it is possible to disassemble the complex network into smaller functional modules or motifs using various lab-based techniques, these techniques do not allow us to examine the evolution of the motifs and networks, because it is not possible to run laboratory experiments lasting millions of years. One potential solution to this problem is to use computational techniques and perform the evolution *in silico*.

We have developed a model that abstractly incorporates all important transcriptional processes found within prokaryotic organisms. The model is able to evolve an arbitrary level of complexity, and it provides a platform for examining evolution and adaptation to varying environmental conditions. Unlike other mathematical and computational models of prokaryotic cells, protein function is not predetermined in the model. Instead the efficiency of a specific protein to perform a given function is based on the binding affinity of the protein to other molecules (such as food for metabolism). This allows 'jack-of-all-trade' proteins to evolve which can perform many functions, albeit not that well, and very specific proteins which perform a single function extremely well. It also allows for the evolution of very complex transcription networks.

The model is simulated using stochastic processes in order to capture the inherent randomness within cells, and provides an *in silico* evolution platform using mutation and gene duplication/loss operators.

Preliminary results have indicated that the model can survive in a simplistic environment consisting of a single non-varying food source using realistic parameter ranges, and has displayed a realistic cell-cycle time as an emergent property of the model. Current work is studying evolution and adaptation to more complex and varying environments.