

An Approach to evolving Cell Signaling Networks in Silico

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Cell Signaling Networks(CSN) are complex bio-chemical networks which, through evolution, have become highly efficient for governing critical control processes such as immunological responses, cell cycle control or homeostasis. From a computational point of view, modeling Artificial Cell Signaling Networks (ACSNs) in silico may provide new ways to design computer systems which may have specialized application areas.

To investigate these new opportunities, we review the key issues of modeling ACSNs identified as follows. We first present an analogy between analog and molecular computation. We discuss the application of evolutionary techniques to evolve biochemical networks for computational purposes. The potential roles of crosstalk in CSNs are then examined. Finally we present how artificial CSNs can be used to build robust real-time control systems.

The research we are currently involved in is part of the multi disciplinary EU funded project, ESIGNET, with the central question of the study of the computational properties of CSNs by evolving them using methods from evolutionary computation, and to re-apply this understanding in developing new ways to model and predict real CSNs. This also complements the present requirements of Computational Systems Biology by providing new insights in micro-biology research.