Hierarchically Evolvable Components for Complex Systems: Biologically Inspired Algorithmic Design

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Biological reaction networks form efficient computational devices capable of controlling information processing in living organisms [2]. Questions about programming techniques for biohardware are of particular interest to explore and substantiate biologically inspired computing paradigms. Research projects within our group investigate different approaches for modelling, simulation, construction, and validation of biohardware components at specific levels of abstraction. We consider two aspects: Firstly, identification of the function of networks found in pro- or eukaryotic cells providing templates for algorithmic elements. Secondly, development of network engineering techniques can adopt and amalgamate those templates in order to achieve and optimise more complex algorithms. Based on findings and implementations of biological systems, dedicated wetlab experimental data embody a first behavioural description [3]. Here, the huge amount of low structured data reflects its inherent stochasticity as well as redundancy [1]. The next level of abstraction is reached by representations of reaction systems on a submodular level. Consequently, cell signalling and gene regulatory networks provide predefined functional units of high reliability. Balanced inhibiting and activating effects lead to system descriptions at a modular level [4]. Finally, data condensation affords chemical organisations [5]. We exemplify interconnections between these levels as well as their application for algorithmic design by RS flip-flops. Beyond engineering methods for biohardware programming, heuristics like evolutionary network reconstruction tools are incorporated [6].

References

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