Abstract

The research and study on pure *dataflow* (DF) computer architectures has almost reached a dead point since early '90, when several technological issues became insurmountable. Although, the pioneering work of J.B. Dennis at MIT in early seventies, showed to engineers all the potential of the fine grained parallelism, implicit in data flow computing, applied to several prototype machines, still many issues inside architecture model remain partialy unsolved. Because of increasing complexity which grew in solving these issues, the data flow architecture became quickly economically disadvantageous in comparison to von Neumann architecture, so it remained alive only as laboratory project. With the recently works of many computer engineers and biotechnologists, which use biological systems, precisely *gene regulatory networks* (GRNs), to build logic circuits, a new point of view arises concerning this technology and data flow computation. Several properties of GRNs allow to view the memory system and the information processing of dynamic dataflow architecture in entirely different way, so that some constraints may fall. Although these properties may improve solutions to the main data flow architecture issues, several technological (biochemical) problems remain to solve. The work presents a general review of the most studied models of dataflow architectures and their analogies with GRNs. At the end, a few possible implementations of foundamental constructs of dataflow computing using GRNs are presented.

Key words:

Gene regulatory networks, dataflow computing/architecture, parallel computing, stochastic modeling.