Information Encoding and Retrieval Through Biologically Inspired Computing

Crowley, Bill, Otter, Tim*
Crowley Davis Research, Inc., Eagle, ID, USA

As we use the term, "biologically inspired computing" refers to the transfer of knowledge and principles from one domain, biology, into another, math and computer science, with the specific goal of developing more versatile, powerful, and robust rule-based systems. Our mission is to incorporate biological principles into computational models that enable us to *efficiently* solve problems such as encoding and retrieval of complex data sets.

Biologically inspired computing draws upon biology, mathematics, and computer science. In a sense, this is the inverse of conventional modeling, where existing mathematical tools are used to analyze biological processes, simulate them, or predict their outcomes. Instead, we are attempting to derive tools from biology to develop better rule-based grammars and systems that could, in turn, provide greater fidelity in biological modeling allowing, among other features, more effective medical training transfer via simulation.

We have focused upon developmental biology as the main field from which to derive principles to guide the development of rule-based systems, as it relies heavily on chemistry, physics, gene expression, cellular biology, cell signaling, differentiation, morphogenesis and growth.

Desirable features for a computational model are fault-tolerance, robustness, self-correction and built-in feedback mechanisms, among others. In addition the computational model should engender efficient searching for solutions to computational problems.

An example of the power and utility of biologically inspired principles can be seen in the degree of information compression that is achieved by DNA. DNA is the primary information storage medium used by organisms to pass on their traits to their progeny. A single copy of human DNA contains approximately three billion base pairs. While this is an enormous amount, enough DNA to theoretically code for three million genes of average size, there are approximately only 30,000 total genes (or in other words, rules) in the human genome. This is an incredibly small number in relation to the complexity of the human organism. Part of this compression derives from the modular, networked structure of the genome and its resulting combinatorial versatility. The human genome thus represents a significantly compressed information medium.

This research and development project is being conducted by Crowley Davis Research, Inc., under U.S. Army Medical Research Materiel Command Cooperative Agreement DAMD17-02-2-0049. Principal Investigator is Mr. Bill Crowley. Please direct questions to the TATRC Project Officer (Mr. Harvey Magee, 301-619-4002 (magee@tatrc.org) or the Contract Officer's Representative (Dr. Ken Curley, 301-353-9240 (curley@tatrc.org).