Finding and Exploiting Hidden Symmetry and Hierarchical Structure in Complex Adaptive Systems

The tutorial introduces examples and ongoing progress in developing "the right stuff", the mathematical and computational intelligence tools for life-like systems, complex adaptive systems, and systems biology -- from those whose structure is stable over some time horizon to those that dynamically grow and change. We present discrete computational intelligence methods for finding and exploiting hidden symmetry and hierarchical structure in complex adaptive systems and in systems biology. A range of topics is covered from *discrete dynamical systems* and *their analysis via algebraic computational tools* to *interaction machines* that grow and change their own structure.

Algebraic structure implicit in discrete dynamical systems, including natural subsystems of hidden symmetries and hierarchical coarse-graining of the dynamics is revealed using methods of Krohn-Rhodes theory (algebraic automata theory). Examples using recently available software tools (SgpDec) that find global hierarchical coordinate systems on discrete dynamical systems with multiple possible inputs/events will be illustrated. We will identify natural subsystems and their hierarchical dependencies. Implications for the evolution of complexity, and state-of-the-art extensions to dynamical systems and software that grow and change will be covered.

Outline: We first introduce automata models of complex adaptive systems, and biological and biochemical networks, such as gene regulatory networks and metabolic networks, and how to carry out their mathematical analysis using general global methods applicable to finite discrete dynamical systems with inputs. These methods generalize well beyond traditional discrete dynamical models such as cellular automata or dynamical systems where a 'clock-tick' is the only input. These more powerful models are prevalent in Systems Biology and Complex Adaptive Systems, in their use of finite automata networks, Boolean Networks, Petri nets, reaction networks, or artificial genetic regulatory networks.

We show how mathematical analyses of such examples supported by open-source computer algebra systems (SgpDec in GAP) that implement cascade decompositions reveal natural subsystems and hidden algebraic structure, such as hierarchies of "weak control" by permutation groups found, e.g., in models of the lac operon for facultative metabolism of lactose in *E. coli* bacteria, and discover finite simple non-abelian groups (SNAGs) -- finitary computationally universal elements -- that we find for example in analysing the p53-mdm2 gene regulatory network employed in cellular responses to damage and cancer. These hierarchies yield global coarse- to fine-graining of the underlying dynamical systems helpful in understanding their structure. (In fact, we've shown that 'most' biological reaction networks give rise to models whose complexity -- the minimal number of hierarchical levels for their synthesis -- can be computed efficiently and they are in principle capable of finitary universal computation.)

Building on the understanding of such finite discrete dynamical systems models, we introduce *interaction machines,* which grow and change their structure dynamically in response to internal and external interactions as natural extensions of standard systems biology models. Cells grow and divide in a manner controlled by the cell cycle, but this results in an increase in the number of components and dimensions, and changes in topology. These features are not well handled by traditional modelling methods (e.g. differential equations models where the number of dimensions, chemical species and mechanisms are fixed at the outset and unchanging), but are needed for adequate models of the differentiated multicellularity in developing organisms.

This extension naturally lets us model biological systems, and computationally processes, whose number and topology of cells, and internal structures, change during development as resources are recruited and reabsorbed or released. Interaction machines also as serve as a novel model for computational processes that grow and dynamically adapt their structure based on interaction, computational loads and resource availability. While many examples will be motivated by biological modelling, the ideas and methods are more general and applicable to software and discrete dynamics systems models in numerous computational intelligence domains.

Useful References:

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A. Egri-Nagy, J. D. Mitchell, C. L. Nehaniv, "SgpDec: Cascade (De)Compositions of Finite Transformation Semigroups and Permutation Groups", *Mathematical Software - ICMS 2014, Lecture Notes in Computer Science* Volume 8592, pp 75-82, Springer Verlag, 2014.

Software: The SgpDec Package for GAP http://gap-packages.github.io/sgpdec/

Chrystopher L. Nehaniv is a mathematician and computer scientist. He received the B.Sc. degree (with honors) from the University of Michigan, Ann Arbor, in 1987, where he studied mathematics, biology, linguistics, and cognitive science, and the Ph.D. degree from the University of California at Berkeley in 1992. He has held academic and research positions at the University of California at Berkeley, in Japan (professorship at University of Aizu, 1993-1998), and Hungary. Since 2001, he has been Research Professor of Mathematical and Evolutionary Computer Science at the University of Hertfordshire, U.K., where he plays leading roles in the Algorithms, Biocomputation, and Adaptive Systems Research Groups. He is the author of over 200 publications and has edited 30 volumes in computer science, mathematics, interactive systems, artificial intelligence, and systems biology. He is also the coauthor of a monograph on algebraic theory of automata networks, and a PI or coPI of numerous European Commission-funded and other funded projects in areas of Computational Intelligence (including Cogniron, RobotCub, ITALK, BIOMICS, StructNet, INTERLACE, etc). His main research interests encompass the notions of dynamics, development, temporally extended experience, cognition and interaction in biological and artificial systems, as complemented by mathematical, information-theoretic, and computer algebraic foundations and methods for designing and understanding complex adaptive systems. He is Associate Editor of the journals *Interaction Studies*, *BioSystems*, *IEEE Transactions on Cognitive and Developmental Systems*, and is Topic Editor-in-Chief of *Intl. J. Adv. Robotic Systems* for the topics Artificial Intelligence in Robotics, and for Human-Robot Interaction. Prof. Nehaniv is Chair of the IEEE CIS Task Force in Artificial Life and Complex Adaptive Systems, and a founding member of the Task Force on Ethical and Social Implications of Computational Intelligence.