16th July 2012

Isaac Newton Institute 20th Anniversary Lecture:

Biological Switching Algorithms
by Luca Cardelli, Assistant Director, Microsoft Research, Cambridge

The Isaac Newton Institute (INI) for Mathematical Sciences, associated with Churchill College at Cambridge University, has an international reputation for its advanced research programmes. As part of the INI's 20th Anniversary celebrations, it has sponsored lectures around the UK given by participants who are visiting the Institute.

Dr. Cardelli gave an excellent and well attended lecture with a strong multidisciplinary flavour. He explained how chemical processes involved in the cell cycle can be formalised in terms of process algebra, enabling us to understand the coupled feedback loops that control this central mechanism for sustaining life. Starting with a hypothesis about double switching networks and taking account of the chemical constraints required for a biological implementation in living cells, he neatly derived the coupled structure of double negative and double positive feedback loops that is observed in cell biology. He explained how the dynamic behaviour of interacting populations may be simplified by adding a carefully crafted element of complexity, in the form of an intermediate state, to achieve bi-stability with fast responsiveness to control actions and robustness against external disturbances.

Double switching networks were illustrated with mechanical examples including the use of trammels to design ellipses, as old as Aristotle, and the shishi-odoshi (scare-deer) devices commonly used in rural Japan. However, the main principles in the talk apply more generally to populations of interacting agents, be they software, sensors, cells or people.

The talk was followed by a celebratory dinner also sponsored by the Isaac Newton Institute.

Abstract:

“Biological systems have been traditionally, and quite successfully, studied as 'dynamical systems', that is, as continuous systems defined by differential equation and investigated by sophisticated analysis of their continuous state space. More recently, in order to cope with the combinatorial complexity of some of these systems, they have been modeled as 'reactive systems', that is, as discrete systems defined by their patterns of interactions and investigated by techniques that come from software and hardware analysis.

There are growing formal connections being developed between those approaches, and tools and techniques that span both. Beyond those, the two approaches can be usefully combined to bring new insights to specific examples. In one direction we can ask 'what algorithm does a dynamical system implement' and in the opposite direction we can ask 'what is the dynamics of a reactive system as a whole'. Answers to these questions can establish links between the structure of a system, which is dictated by the algorithm it implements, and the function of the system, which is represented by its dynamic behavior. Since there is depth on both sides, in the intricacies of the algorithms, and in the complexity of the dynamics, a better understanding can emerge of whole systems.

I will focus in particular on a connection between a clever and well-studied distributed computing algorithm, and a simple chemical system (4 reactions). That leads to a connection between that algorithm and a well-known biological switch that is universally found as part of cell cycle oscillators. I will also discuss a general network structure for oscillators, based on the above switches, and how they are implemented 'in practice' in natural systems. These connections are examples of 'network transformations' that preserve some desirable functionality while relaxing constraints (e.g. chemical constraints) on the system.”

Professors Diana Meehan, Madjid Merabti and Paulo Lisboa with Dr Luca Cardelli, alongside Dr Wael El-Deredy (Manchester University) and Dr Nelson Trujillo Barreto (Cuban Neuroscience Centre).