

A Grand Challenge: Full Reactive Modeling of a Multi-Cellular Animal

(Invited Talk)

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Abstract. Biological systems exhibit the characteristics of reactive systems remarkably, and on many levels; from the molecular, via the cellular, and all the way up to organs, full organisms, and even entire populations. Thus, a different brand of bioinformatics arises, in which, rather than “we” solving “their” computational problems, we use “our” languages, methods and tools to model and analyze “their” complex systems. This talk proposes a grand challenge for computer scientist and biologists: to model a full multi-cellular animal as a reactive system. We would like to construct a full, true-to-all-known-facts 4-dimensional model, that would be animated, flexible and comprehensive, and would enable full and realistic simulation of the animal’s development and behavior over time (the fourth dimension). It should help uncover gaps in our knowledge, correct errors, suggest new experiments and help predict unobserved phenomena. We actually have a particular organism in mind, the *C. elegans* nematode worm, a suggestion that is in line with the extraordinarily insightful proposal of Sydney Brenner, co-recipient of the 2002 Nobel Prize, who chose this organism 30 years ago to challenge biologists with the task of discovering the entire development and neurobiology of a living creature. The talk will argue the (long-term) feasibility of the challenge, by describing two pieces of preliminary modeling work: (i) T-cell behavior in the thymus, using statecharts with Rhapsody, linked with Flash animation, and (ii) parts of the vulval development of *C. elegans*, using LSCs with the Play-Engine.