

Understanding Biology through Logic

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Abstract

The complexity in biology is staggering. Biological processes involve many components performing complicated interactions. Moreover, they are organized in hierarchies spanning multiple levels going from individual genes and proteins to signalling pathways, through cells and tissues, to organisms and populations. All the levels in this hierarchy are subject to a multitude of interdisciplinary efforts to model, analyse and devise ways to make sense of all this complexity. Mathematical models (and using computers to simulate them) have been used for these purposes for many years. The abilities of modern computers and their increased availability have greatly advanced this kind of modelling. However, in the last decade (or so) computational and logical thinking have started to change the way biological models are constructed and analysed. The work of the logic-in-computer-science research community to formalize and enable analysis of computer systems inspired several pioneers to try and harness these capabilities to the design and analysis of computer models of biological systems. This approach, which we later termed “executable biology”, calls for the construction of a program or another formal model that represents aspects of a biological process. By analysing and reasoning about such artefacts we gain additional insights into the mechanisms of the biological processes under study. Over the years, these efforts have demonstrated successfully how this logical perspective to biology can be beneficial for gaining new biological insights and directing new experimental avenues. In this tutorial, I will give an introduction to this approach. I will survey different modelling paradigms and how they are being used for biological modelling through models of cell fate decision-making, organism development, and molecular mechanisms underlying cancer. I will also highlight verification and the usage of formal methods to gain new biological insights. Time permitting, I will touch upon some of the challenges involved in applying synthesis to the development of models directly from experimental data and the efforts that are required to make the computational tools that we develop widely adopted by experimentalists and clinicians in the biological and medical research community.

Categories and Subject Descriptors I.6.3 [*Simulation and Modeling*]: Applications; J.3 [*Life and Medical Sciences*]: Biology and genetics

General Terms Theory

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