

Image-Based Computational Biology : Toward a Virtual Embryo

Ivo F. Sbalzarini

Chair of Scientific Computing for Systems Biology,
Faculty of Computer Science, TU Dresden, Germany

Development and morphogenesis of tissues, organs, and embryos emerges from the collective self-organization of cells that communicate through chemical and mechanical signals. Decisions about growth, division, and migration are taken locally by each cell based on the collective information. In this sense, a developing tissue is akin to a massively parallel computer system, where each cell or processor computes robust local decisions, integrating communication with other cells/processors. Mechanistically understanding and reprogramming this system is a grand challenge. Our vision is to develop a virtual computer model of a developing embryo, incorporating the known biochemistry and biophysics into a computational model in 3D-space and time, in order to understand the information-processing aspects of development on an algorithmic basis. While the “hardware” (proteins, lipids, etc.) and the “source code” (genome) are increasingly known, we know virtually nothing about the algorithms that this code implements on this hardware. Using examples from our work, I outline our roadmap toward a virtual embryo, and highlight challenges along the way. These range from globally optimal approaches to image analysis, to novel languages for parallel high-performance computing, to virtual reality and real-time graphics for 3D microscopy and numerical simulations of biochemical and biomechanical models. This cooperative interdisciplinary effort contributes to all involved disciplines.