

Bridging Spatial and Temporal Scales in Biological Data Visualization

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The study of biological processes carried out in living organisms is among the central foci of modern science. The field is nowadays by large extent computational, there are many kinds of digital models that characterize particular aspects of life. To provide a comprehensive view on biological phenomena, visualization offers itself for integrating multiple models into one visual environment.

One of the interesting challenges, associated with such a visual integration, is to communicate phenomena that are simultaneously described on several spatial and temporal scales. In my talk I will discuss visualization techniques that bridge five orders of magnitude of spatial scale by interactively displaying structural information from a single atom level up to entire bacteria cell size with complete molecular machinery.

When dealing with simulation of molecular interactions in living organisms, agent-based models are used to model long sequences of Brownian motion that randomly carry out several physiologically relevant events. One such event occurs on average every thousandth simulation iteration in the agent based simulation. In order to perceive random motion but also to see relevant events simultaneously, we bridge two temporal scales that are three orders of magnitude apart from each other. The approach is based on a special timelapse approach inspired from scientific animation techniques.

In the last part of my talk I will present a technique for interactive 3D visualization of molecular reaction pathways that is controlled in a top-down manner by quantitative simulation and is simultaneously co-visualized. In such visual environment the viewer can interactively control the visualization as well as simulation parameters.