Approaches for Interoperability for Biomodeling – From Genome to Organ Systems

Richard C. Ward
Oak Ridge National Laboratory
Oak Ridge, Tennessee

Bioinformatics and biological modeling are faced with an enormous range in both spatial and temporal scale. From genes, to proteins, to membrane transport, to organ function represents a spatial range from nanometers to meters; time scales can vary from orders of picoseconds for protein folding to years for life span. To evaluate life processes across even a portion of these scales will be an exceptionally difficult computational problem. But modern computer hardware and software has made extraordinary advances as well, making computations envisioned only years ago now possible in reasonable time. Even though hardware becomes faster, few of the problems will be solved by hardware alone. Equally important are software design issues, often referred to as information technology (IT), which will be necessary to take advantage of the new hardware advances. This talk will examine a number of important IT issues centered around interoperability, which we define as the development of common data formats, utilizing Extensible Markup Languages (XML) and Ontologies, separation of front-end (client) and back-end (computation) with a middleware layer to improve flexibility, and creating problem-solving environments that integrate data acquisition (e.g. X-ray CT scans), data analysis (e.g. segmentation), model building (meshing), simulation, and visualization of results. The future of biological research will require continuous improvement in the application of IT to increasingly complex problems.