NETWORKS IN BIOLOGY AND PERSONALIZED MEDICINE

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Biomedical research is at an exciting time in which vast amounts of data can be collected about cells and patients, but methods to integrate and analyze these data are still in their infancy. The sheer number and variety of measurements is staggering. For instance, investigators are now able to sequence the complete genome of a patient, obtain corresponding profiles of mRNA, protein, and metabolite levels, and systematically map all of the physical interactions that occur among these molecules. This enormous collection of measurements brings about the need for advanced computational tools to integrate and interpret the raw data, to assemble these data into models of biological networks, and – ultimately – to develop executable simulations of the cell which enable personalized patient diagnostics and drugs. In this session, a panel of leading researchers in computational biology will describe the enormous flood of new data and how it is being used to assemble models of molecular networks which inform human health.