Towards Computational Epidemiology: From Mathematical Models to Computational Tools

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The domains of Computational Biology and Bio-Informatics have harnessed the computational power of high-performance computing to tackle the computational complexity of tasks associated with genomics research. This effort undoubtedly deserves its own field of research; however, there are other domains in which scientists can take advantage of recent advances in Computer Science and Scientific Computing. One such domain is Epidemiology with its multiplicity of sub-domains, including Field Epidemiology, Epidemiological Genomics, Infectious Disease Epidemiology, Social and Behavioral Epidemiology, and Surveillance.

Epidemiologists are often faced with the challenge of dealing with data that are sparse, widely distributed, and incomplete (often due to confidentiality and other constraints). This may result in conflicting information that confound or disguise the evidence leading to wrong conclusions. Today, the role of epidemiologists has become even more pronounced as the significance of Public Health has been recognized. To meet the increasing demands, the field of Epidemiology is in need of specific computational tools that would enable the professionals to respond promptly and accurately in their efforts to control and contain disease outbreaks. Increased globalization, highly mobile populations, and possible exposure to infectious diseases pose new public health threats. It is vital to develop new tools that take advantage of today's communication and computing infrastructures. Computational models for the simulation of global disease dynamics are required to facilitate adequate what-if analyses. This necessitates adapting fundamental Computer Science concepts to the specific problems in Epidemiology.

This talk focuses on the design of a simulation infrastructure that facilitates the study of communicable diseases in different spatial domains. After motivating the need for the field of computational epidemiology, this presentation will highlight various issues that must be considered when developing an experimental simulation environment. Depending on the level of spatial resolution of the model, different computing paradigms may be applicable. Two of these computational paradigms are: Multi-Agent Systems and Stochastic Cellular Automata. Their role in the design of a disease outbreak simulator will be discussed in detail. Recent advances in high-performance computing facilitate the execution of complex simulation models. The availability of data from geographic information systems (GIS), new visualization techniques (i.e. virtual reality) and high-performance computing paradigms, such as cluster and grid computing will greatly contribute to the development of tools that facilitate the work of today's epidemiologists. The talk concludes with the discussion on a proposed design of a simulation environment that can take advantage of cluster and grid computing infrastructures.

Biography: Armin R. Mikler received his Diploma in Informatics from Fachhochschule Darmstadt, Germany in 1988. After spending one year as a Fulbright exchange student at Iowa State University (ISU), he joined ISU as a graduate student and received his MS and Ph.D. in Computer Science in 1990 and 1995 respectively. From 1995 to 1997, he worked as a postdoctoral research associate in the Scalable Computing Laboratory at Ames Laboratory, USDOE. In 1997, Dr. Mikler joined the faculty in Computer Science at the University of North Texas (UNT) where he holds the rank of associate professor in Computer Science with joint appointment in the Department of Biological Sciences. His research interests include: Intelligent Network Management, Distributed Coordination of Intelligent Mobile Agents, Distributed Decision Making, Multi-Agent Simulation and Stochastic Cellular Automate applied to Computational Epidemiology. Dr. Mikler has established and is the director of the Network Research Laboratory (NRL) which provides the necessary computational infrastructure to conduct large scale simulations. As a member of the Institute of Applied Science at UNT, he has been conducting collaborative and interdisciplinary research in computational science, specifically in the areas of quantitative analysis of ecological processes and Biocomplexity. Dr. Mikler is an associate editor of the Telecommunication Systems Journal and a member of the ACM and the IEEE Computer Society.