The Development of Next Generation Bioinformatics Tools

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Hesham H. Ali is a Professor of Computer Science and the Lee and Wilma Seaman Distinguished Dean of the College of Information Science and Technology (IS&T), at the University of Nebraska at Omaha (UNO). He is also the deputy director for computational sciences of the Nebraska Informatics Center for Life Center (NICLS), and a member of Nebraska Center for Bio-security. He received his Ph.D. from the University of Nebraska-Lincoln in 1988, and his BS and MS from the University of Alexandria, in 1982 and 1985, respectively, all in Computer Science. He has published numerous articles in various IT areas including scheduling, distributed systems, wireless networks, and Bioinformatics. He has also published two books in scheduling and graph algorithms, and several book chapters in Bioinformatics. He is currently serving as the PI or Co-PI of several projects funded by NSF, NIH and Nebraska Research Initiative (NRI) in the areas of wireless networks and Bioinformatics. He has been leading a Bioinformatics Research Group at UNO that focuses on developing innovative computational approaches to identify and classify biological organisms. The research group is developing a new assessment system for evaluating transcription factor binding sites tools, and a stochastic model for predicting biomarkers in cancer. He has also been leading two funded projects for developing secure wireless infrastructure and using wireless technologies to address tracking and monitoring problems in medical environments.

Abstract

The last few years have witnessed significant developments in the area of Bioinformatics. The explosive availability of biological data continues to require an associated increase in the scale and sophistication of the automated systems and tools to enable the researchers to take full advantage of the available databases. However, the majority of the current tools tend to be simplistic, generic, domain independent, purely computational and static data analysis tools. We use the term "First Generation Bioinformatics Tools," to identify such tools that include basic sequence comparison tools, phylogenetic trees building tools and motif profiling tools. Although these first generation tools played an important role in the early stages of Bioinformatics, they fall far short from the tools needed to properly analysis and mine the massive data that expected to become available from the recently developed high throughput sequencing technology. In this talk, we present a new model for the "Next Generation Bioinformatics Tools", which is based on developing highly intelligent and dynamic software systems that incorporates biological knowledge and gains intelligence from the increasing availability of biological data. These tools attempt to gain higher degrees of sophistication through genuine integration of Information Technology algorithms and biological knowledge. We present examples of recently developed intelligent tools and expert systems that produced exciting results, in the areas of aging research and recognition of microorganisms, which could not have been obtained without such innovative integration.

Welcome to the Talk!

Time: 9:00-10:00, Thursday, October 21, 2010

Site: Room 2206, 2nd Teaching Building, Zhangjiang Campus, Fudan University

Host: Research Center for Dataology and Datascience, School of Computer Science, Fudan University