

# 4<sup>th</sup> International Conference on **Proteomics & Bioinformatics**

August 04-06, 2014 Hilton-Chicago/Northbrook, Chicago, USA

## High performance computing and private clouds for bioinformatics applications

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The explosion of medical and biological data in the last several years has required an associated increase in the scale and sophistication of the automated systems and intelligent tools to enable the researchers to take full advantage of the available databases. The availability of vast amount of biological data continues to represent unlimited opportunities as well as great challenges in biomedical research. Developing innovative data mining techniques and clever parallel computational methods to implement them will surely play an important role in efficiently extracting useful knowledge from the raw data currently available. The proper integration of carefully selected/developed algorithms along with efficient utilization of high performance computing systems (both locally and in the cloud) form the key ingredients in the process of reaching new discoveries from biological data. This talk focuses on addressing several key issues related to the effective utilization of High Performance Computing (HPC) and private/cloud computing in bioinformatics research, in particular, how to efficiently utilize HPC systems and various resources in the clouds in the analysis of massive biological data. A major issue is that regard is how to maintain the necessary level of privacy and security for executing computationally-intensive biomedical applications on private and public clouds. Another key issue is how to develop network filters for massive biological networks that would utilize parallel algorithms to construct networks samplers that would preserve original network structures while uncovering new ones. The integration between biomedical informatics and HPC/cloud computing will undoubtedly be a major driver in the next generation of biomedical research.

### Biography

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 currently serves as the director of the UNO Bioinformatics Core Facility that supports a large number of biomedical research projects in Nebraska. He has published numerous articles in various IT areas including scheduling, distributed systems, VLSI design, 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 currently developing several next generation Bioinformatics tools for integrating, and mining various types of biological data. This includes the development of new graph theoretic models for assembling short reads obtained from high throughput instruments, as well as employing a novel correlation networks approach for integrating and analyzing large heterogeneous biological data associated with various biomedical research areas, particularly projects associated with aging and infectious diseases. 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, particularly to study mobility profiling for aging research.

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