International Workshop on High Performance Computing for Bioinformatics Applications (HPCBA 2015)

CALL FOR PAPERS

The International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2015)

April 15-17, 2015
Granada, Spain

SCOPE AND OBJECTIVES

Incorporating new advancements of High Performance Computing (HPC) in the domain of Life Sciences and Biomedical Research continues to receive tremendous attention of researchers, biomedical institutions and the rest of the biomedical community. Although medical instruments have benefited a great deal from the technological advances of the couple of decades, the impact of integrating IT advancements in addressing critical problems in biomedical research remains limited and the process of penetrating IT tools in the medical profession continues to be a very challenging problem. Due to the computational intensive problems in life sciences, the marriage between the Bioinformatics domain and high performance computing is critical to the advancement of Biosciences. In addition, the problems in this domain tend to be highly parallelizable and deal with large datasets, hence using HPC is a natural fit. The Bioinformatics domain is rich in applications that require extracting useful information from very large and continuously growing sequence of databases. Most methods used for analyzing DNA/Protein sequences are known to be computationally intensive, providing motivation for the use of powerful computational systems with high throughput characteristics.

Moreover, high-throughput wet lab platforms such as next generation sequencing, microarray and mass spectrometry, are producing a huge amount of experimental "omics" data. The increasing availability of omics data poses new challenges to bioinformatics applications that need to face in a semi-automatic way an overwhelming availability of raw data. Main challenges regard: 1) the efficient storage, retrieval and integration of experimental data; 2) their efficient and high-throughput preprocessing and analysis; 3) the building of reproducible "in silico" experiments; 4) the integration of analysis results with pre-existing knowledge usually stored into ontologies.

As the storage, preprocessing and analysis of raw experimental data is becoming the main bottleneck of the analysis pipeline, parallel computing is playing an important role in all steps of the life sciences research pipeline, from raw data management and processing, to data integration and analysis, and to data exploration and visualization. Moreover, Cloud Computing is becoming the key technology to hide the complexity of computing infrastructures, to reduce the cost of the data analysis task, and especially to change the overall business model of biomedical research and health provision.

The focus of data analysis and data mining tools in biomedical research highlights the current state of research in the key biomedical research areas such as bioinformatics, medical informatics and biomedical imaging. Addressing performance concerns in managing and accessing medical data, while facilitating the ability to integrate and correlate different biomedical databases remains an outstanding problem in biomedical research. The amount of available biomedical data continues to grow in an exponential rate; however, the impact of utilizing such resources remains minimal. The development of innovative tools in HPC environments to integrate, analyze and mine such data sources is a key step towards achieving large impact levels. The workshop focuses on topics related to the utilization of HPC systems and new models

of parallel computations in problems related to Bioinformatics and Biomedical Informatics, along with the use of data integration and data mining tools to support biomedical research and Health Care.

The Workshop topics include (but are not limited to) the following:

- HPC for the Analysis of Biological Data
- Bioinformatics Tools for Health Care
- Parallel Algorithms for Bioinformatics Applications
- Ontologies in biology and medicine
- Integration and analysis of molecular and clinical data
- Parallel bioinformatics algorithms
- Algorithms and Tools for Biomedical Imaging and Medical Signal Processing
- Energy Aware Scheduling Techniques for Large Scale Biomedical Applications
- HPC for analyzing Biological Networks
- Next Generation Sequencing and Advanced Tools for DNA Assembly
- HPC for Gene, Protein/RNA Analysis and Structure Prediction
- Biomedical Visualization Tools
- Efficient Clustering and Classification Algorithms
- Correlation Networks in Biomedical Research
- Data Mining Techniques in Biomedical Applications
- Heterogeneous Data Integration
- HPC systems for Ontology and Database Integration
- Pattern Recognition and Search Tools in Biological and Clinical Databases
- Ubiquitous Medical Knowledge Discovery and Exchange
- HPC for Monitoring and Treatment Facilities
- Computer Assisted Surgery and Medical Procedures
- Remote Patient Monitoring, Homecare Applications
- Mobile and Wireless Healthcare and Biomedical Applications
- Cloud Computing for bioinformatics, medicine, and health systems

PROSPECTIVE PARTICIPANTS OF THE WORKSHOP

The Workshop has a focus on interdisciplinary nature and is designed to attract the participation from several groups including Computational Scientists, Bioscientists and the fast growing group of Bioinformatics researchers. It is primarily intended for computational scientists who are interested in Biomedical Research and the impact of high performance computing in the analysis of biomedical data and in advancing Biomedical Informatics. Bio-scientists with some background in computational concepts represent another group of intended participants. The interdisciplinary group of research groups with interests in Biomedical Informatics in general and Bioinformatics in particular will likely to be the group attracted the most to the workshop.

WORKSHOP COORDINAROTS

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BIOSKETCH: 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, data analytics, 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 data analytics, wireless networks and Bioinformatics. He has been leading a Research Group at UNO that focuses on developing innovative computational approaches to classify biological organisms and analyze big bioinformatics data. The research group is currently developing several next generation data analysis tools for mining various types of large-scale 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 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 and energy-aware wireless infrastructure to address tracking and monitoring problems in medical environments, particularly to study mobility profiling for healthcare research.