13th IEEE International Workshop on High Performance Computational Biology (HiCOMB 2014)

May 19, 2014
Arizona Grand Resort, Phoenix, AZ, USA
in conjunction with the 28th International Parallel & Distributed Processing Symposium

Message from the Workshop Chairs

It is our privilege and honor to welcome you to the 13th IEEE International Workshop on High Performance Computational Biology. In the last years, the interdisciplinary fields of Computational Biology and Bioinformatics have received a lot of attention. Due to astonishing developments in sequencing technology, biological data are being produced in laboratories all over the world in a rate that is much higher than the speed needed to process them. The public repositories for genomic data, such as the one maintained in NCBI (*National Center for Biotechnology Information*), have attained exponential growth rates. In this scenario, successful biology research laboratories will be the ones that are able to analyze this huge amount of data, producing accurate results faster. High Performance Computing is being used to accelerate the production of results, bridging the gap between the generation of biological data and its analysis. Also, with High Performance Computing approaches, more elaborate methods can be executed in reasonable time. The goal of HiCOMB is to provide a forum to discuss the latest research developments in High Performance Computing solutions for Computational Biology and Bioinformatics problems.

The technical program committee of HiCOMB 2014 was organized by Program Chair Alba Cristina Magalhaes Alves de Melo from University of Brasilia along with eighteen members of a prestigious technical program committee. All submissions have received at least 2 reviews while 91.67% received 3 or 4 reviews. Based on the reviews, nine papers were selected for presentation at the workshop and inclusion in the proceedings. Selecting 9 papers was difficult, but in the end we hope you agree we have selected some of the best forays into the cutting edge work in the High Performance Computational Biology field. These papers cover a wide range of Computational Biology topics such as next-generation sequence analysis, phylogenetic search, simulation of biochemical pathways, metagenomics analysis and DNA/transcriptome assembly. They also tackle important topics in High Performance Computing related to accelerators such as GPUs (*Graphics Processing Units*), FPGAs (*Field-Programmable Gate Arrays*) and Intel MIC (*Many-Integrated Core*), as well as cluster and cloud systems. In addition to the regular papers, the program includes two invited talks, from Umit Catalyurek (Ohio State University) and Ananth Kalyanaraman (Washington State University). The keynote presentation was delivered by Stephen Larson, coordinator of the openworm project, which has the ambitious goal of creating the world's first virtual organism in a computer.

Many people contributed to the success of this instance of HiCOMB. We are very grateful to the program committee members for submitting timely and thorough reviews. We also wish to thank all the authors, who worked hard to submit the best results of their research, without which this high quality program would not have been possible. Finally, we want to thank the keynote and invited speakers for their excellent talks. We plan to continue this workshop in the forthcoming years and look forward to your continuing support to this endeavor.

Alba Cristina Magalhaes Alves de Melo, Srinivas Aluru, David Bader

978-1-4799-4116-2/14 $31.00 © 2014 IEEE
DOI 10.1109/IPDPSW.2014.212

Workshop Organizers

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Program Chair:

Alba Cristina Magalhaes Alves de Melo (University of Brasilia, Brazil)

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