16th IEEE International Workshop on High Performance Computational Biology (HiCOMB 2017)

Workshop Theme
The size and complexity of genome- and proteome-scale data sets in bioinformatics continues to grow at a furious pace, and the analysis of these complex, noisy, data sets demands efficient algorithms and high performance computer architectures. Hence high-performance computing has become an integral part of research and development in bioinformatics, computational biology, and medical and health informatics. The goal of this workshop is to provide a forum for discussion of latest research in developing high-performance computing solutions to data- and compute-intensive problems arising from all areas of computational life sciences. We are especially interested in parallel and distributed algorithms, memory-efficient algorithms, large scale data mining techniques including approaches for big data and cloud computing, algorithms on multicores, many-cores and GPUs, and design of high-performance software and hardware for biological applications.

Workshop Organizers
Alex Pothen, Purdue University
Ananth Grama, Purdue University

Program Committee
Ariful Azad, Lawrence Berkeley Lab
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Sharma Thankachan, Georgia Tech
Jaroslaw Zola, University at Buffalo, SUNY

Steering Committee Members
David A. Bader, Georgia Institute of Technology
Srinivas Aluru, Georgia Institute of Technology

HiCOMB 2017 Invited Talks

Algorithmic Advances in Transcript Quantification
Rob Patro, Stony Brook University

Big Data Challenges in Personalized Medicine for Cancer
Jason McDermott, Pacific Northwest National Lab