

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
Daniela Besozzi, University of Milano-Bicocca, Italy
Petros Drineas, Purdue University
Niina S. Haiminen, IBM
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Rob Patro, Stony Brook University
Saumyadipta Pyne, Indian Institute of Public Health, Hyderabad
Sanjay Ranka, University of Florida
Hagit Shatkay, University of Delaware
Alexandros Stamatakis, Heidelberg Institute for Theoretical Studies
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