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

Advance Program

8:25-8:30   Welcome and Introductory Remarks

Section I – Parallel Algorithms for Biological Sequence Analysis
Chair: Michela Taufer, University of Delaware

8:30-9:00   Constructing Similarity Graphs from Large-scale Biological Sequence Collections
Jaroslaw Zola

9:00-9:30   Removing Sequential Bottlenecks in Analysis of Next-Generation Sequencing Data
Yi Wang, Gagan Agrawal, Gulcin Ozer and Kun Huang

09:30-10:00 **Coffee Break**

Section II - Parallel/Distributed Architectures for Biological Applications
Chair: Ananth Kalyanaraman, Washington State University

10:00-10:30 Efficient Computation of the Phylogenetic Likelihood Function on the Intel MIC Architecture
Alexey M Kozlov, Christian Goll and Alexandros Stamatakis

10:30-11:00 Process Simulation of Complex Biochemical Pathways in Explicit 3D Space Enabled by Heterogeneous Computing Platform
Jie Li, Amin Salighehdar and Narayan Ganesan

11:00-11:30 Exploring Large Scale Receptor-Ligand Pairs in Molecular Docking Workflows in HPC Clouds
Kary Ocana, Silvia Benza, Daniel de Oliveira, Jonas Dias and Marta Mattoso

11:30-12:00 A Comparison of a Campus Cluster and Open Science Grid Platforms for Protein-Guided Assembly using Pegasus Workflow Management System
Natasha Pavlovikj, Kevin Begcy, Sairam Behera, Malachy Cambell, Harkamal Walia and Jitender Singh Deogun

12:00-13:30 Lunch

Section III – Keynote and Invited Talks
Chair: Srinivas Aluru, Georgia Institute of Technology

13:30-14:30 Keynote Talk: OpenWorm: Open source biological computing focused on a
model organism
Stephen Larson, OpenWorm, USA

14:30-15:00 Invited Talk: Searching Genomes in GPUs
Umit Catalyurek, Ohio State University, USA

15:00-15:30 Invited Talk: Graph algorithms for computational metagenomics
Ananth Kalyanaraman, Washington State University, USA

15:30-16:00 **Coffee Break**

Section IV – Metagenomics and Assembly
Chair: Jaroslaw Zola, Rutgers University

16:00-16:30 Design and Optimization of a Metagenomics Analysis Workflow for NVRAM
Sasha Ames, Jonathan Allen, David Hysom, Scott Lloyd and Maya Gokhale

16:30-17:00 Parallelization of the Trinity pipeline for de novo transcriptome assembly
Vipin Sachdeva, Chang-Sik Kim, Kirk Jordan and Martyn D Winn

17:00-17:30 HiPGA: A High Performance Genome Assembler for Short Read Sequence
Data
Xiaohui Duan, Kun Zhao and Weiguo Liu