

Introduction

Craig A. Stewart

Workshop Chair

Multiple plans to create petascale computing environments have been announced. This workshop addressed what bioinformatics or computational biology applications can or should accomplish with such facilities, and what obstacles must be overcome in order to implement and use effective and important problems in the life sciences (biology, biochemistry, environmental sciences, etc.).

Five papers were presented at this workshop:

Progress Towards Petascale Applications in Biology: Status in 2006 by Craig A. Stewart, Matthias Mueller, and Malinda Lingwall examines current trends in computing power and explains the need for petascale computing in the life sciences.

Progress in Scaling Biomolecular Simulations to Petaflop Scale Platforms by Blake G. Fitch, Aleksandr Rayshubskiy, Maria Eleftheriou, T.J. Christopher Ward, Mark Giampapa, Michael C. Pitman, and Robert S. Germain describes some issues involved with scaling biomolecular simulations onto massively parallel machines, and examines what it will take to overcome the challenges of petascale computing.

Toward a Solution of the Reverse Engineering Problem Using FPGAs by Edgar Ferrer, Dorothy Bollman, and Oscar Moreno looks at the reverse engineering problem for genetic networks and proposes an efficient approach to finding a solution.

Two Challenges in Genomics That Can Benefit from Petascale Platforms by Catherine Putonti, Meizhuo Zhang, Lennart Johnsson, and Yuriy Fofanov addresses the computational challenges necessary to successfully examine the ever-increasing amount of biological data available, including the number of genomic sequences made publicly available.

High-Throughput Image Analysis on Petaflop Systems by Robert Henschel, Yannis Kalaizidis, and Matthias Mueller describes software developed to assist biologists with image analysis work, integrating high-performance computing systems into their workflow.