

**The First International Workshop on
Accelerator Architecture in Computational Biology and Bioinformatics
(AACBB-2018)**

Vienna Austria February 24, 2018

In conjunction with 24th IEEE International Symposium on High-Performance Computer Architecture

Abstract:

Over the last decade, the advent of high-throughput sequencing techniques brought an exponential growth in biosequence database sizes. With increased throughput demand and popularity of computational biology tools, reducing time-to-solution during computational analysis has become a significant challenge in the path to scientific discovery.

Conventional computer architecture is proven to be inefficient for computational biology and bioinformatics tasks. For example, aligning even several hundred DNA or protein sequences using progressive multiple alignment tools consumes several CPU hours on high performance computer. Hence, computational biology and bioinformatics rely on hardware accelerators to allow processing to keep up with the increasing amount of data generated from biology applications.

In a typical application, dominant portion of the runtime is spent in a small number of computational kernels, making it an excellent target for hardware acceleration. The combination of increasingly large datasets and high performance computing requirements make computational biology prime candidate to benefit from accelerator architecture research. Potential directions include 3D integration, near-data processing, automata processing, associative processing and reconfigurable architectures.

This workshop will focus on architecture and design of hardware accelerators for computational biology and bioinformatics problems. We plan to present and discuss a variety of acceleration techniques, accelerator architectures and their implications on the development of computational biology. Topics of interest include, but are not limited to:

- Impact of bioinformatics and biology applications on computer architecture research
- Bioinformatics and computational biology accelerator architecture and design
- 3D memory-logic stack based accelerators
- Automata processing in bioinformatics and computational biology applications
- Associative processing in bioinformatics and computational biology applications
- Near-data (in-memory) acceleration of bioinformatics and computational biology applications
- Emerging memory technologies and their impact on bioinformatics and computational biology
- Embedded and reconfigurable architectures
- Field programmable logic based accelerators
- Bioinformatics and computational biology-inspired hardware/software trade-offs

Organizers and co-chairs

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Program Committee

- Ananth Kalyanaraman, WSU
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- Can Alkan, Bilkent University
- Engin Ipek, University of Rochester
- Jason Cong, UCLA
- Mattan Erez, UT Austin
- Mircea Stan, UVA
- Onur Mutlu, ETH/CMU
- Ran Ginosar, Technion
- Srinivas Aluru, GT
- Yuan Xie, UCSB

Event Format

8:45- 9:00	Opening remarks
9:00-10:00	Keynote 1 - Onur Mutlu: “Accelerating Genome Analysis: A Primer on an Ongoing Journey”
10:00-10:30	Invited Talk - Bertil Schmidt: “Next Generation Sequencing: Big Data meets High Performance Computing Architectures”
10:30-11:00	Break
11:00-12:00	Paper session 1 (3 papers)
12:00-13:30	Lunch
13:30-14:30	Keynote 2 - Srinivas Aluru: “Automata Processor and its Applications in Bioinformatics”
14:30-15:00	Invited Talk - Ananth Kalyanaraman
15:00-15:30	Break
15:30-16:10	Paper session 2 (2 papers)
16:10-17:10	Invited Talk - Can Alkan: “Addressing computational burden to realize precision medicine”
17:10-17:20	Closing remarks