

Accelerator Architecture in Computational Biology and Bioinformatics workshop

(AACBB-2018)

In conjunction with 24th IEEE International Symposium on High-Performance Computer Architecture (HPCA-2018)

Vienna, Austria, February 24, 2018

Call for Papers

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 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

Submission Guidelines

Interested authors are encouraged to submit papers (2-5 pages) through EasyChair:

<https://easychair.org/conferences/?conf=aacbb2018>.

The full version should be a PDF file in HPCA24 submission format. For formatting instructions please refer to:

http://hpca2018.ece.ucsb.edu/pages/guidelines_for_submission.html

Authors should submit the paper by **Sunday, November 30, 2017**.

All papers will be evaluated based on their relation to the subject, novelty, fundamental insights, experimental evaluation, and potential for long-term impact.

Author Notification is by **December 20, 2017**.