

## **Call for Papers**

IEEE Design & Test Special Issue on  
Hardware Acceleration in Computational Biology  
Publication date: January/February 2014

*Guest Editors:*

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The role of computing in molecular biology research has never been more defining. The synergy has reached a critical juncture where the rate of data generation is rapidly outpacing the rate at which it is processed. Most of the data processing for computational biology applications currently is done in software, which could take very long running times. For example, aligning even hundreds of sequences using progressive alignment tools such as ClustalW requires several hours on state-of-the-art workstations. With sequencing technologies becoming increasingly high-throughput and increasingly commonplace at biologists' research labs, large-scale sequence analysis, often involving millions to even tens of millions of sequences, has become one of the primary bottlenecks in the path to scientific discovery. The computational biology domain also hosts a set of compute-intensive applications wherein the underlying problems are proven to be computationally intractable (e.g. phylogeny reconstruction). These aspects collectively position computational biology as a domain that has the potential to immensely benefit through the incorporation of the latest advancements from the computing community.

*IEEE Design and Test of Computers* seeks original manuscripts for a special issue on "Hardware Acceleration in Computational Biology" scheduled for publication in January/February 2014. The topics of interest include, but are not limited to:

- FPGA, GPU, Multicore-based hardware accelerator platforms targeting different kind of bioinformatics applications including but not limited to: sequence alignment, phylogeny reconstruction, computational biochemistry, molecular dynamics, protein structure prediction, systems biology, synthetic biology, and vaccine and drug discovery.
- Algorithmic optimization and parallelization for computational biology; HPC perspective.
- Acceleration on hybrid architectures – e.g., CPU-GPU platforms.
- Novel data movement and placement strategies for both traditional and hybrid architectures
- Graph-based modeling and analysis of biological data on high performance architectures

### **Submission and review procedures**

Prospective authors should follow the submission guidelines for IEEE Design & Test. All manuscripts must be submitted electronically to the IEEE Manuscript Central Web site at <http://www.manuscriptcentral.com/>. Indicate that you are submitting your article to the special issue on "Hardware Acceleration in Computational Biology". All papers will undergo the standard IEEE Design & Test review process.

### **Schedule**

- Submission deadline: April 15, 2013
- Reviews completed: June 1, 2013
- Article revisions due: July 15, 2013
- Notice of final acceptance: September 15, 2013
- Materials due for edit: October 15, 2013
- Publication date: January/February 2014

**Questions**

Please direct questions regarding the special issue to guest editors Partha Pande (pande@eecs.wsu.edu) and Ananth Kalyanaraman (ananth@eecs.wsu.edu).

