

# Concurrency and Computation Practice and Experience

## Concurrency and Computation: Practice and Experience Special Issue on:

### Distributed, Parallel, and GPU-accelerated Approaches to Computational Biology (COMPBIO2013)

#### Call for Papers

Computational Biology is a discipline that performs analyses and simulations of complex biological systems using a computer science approach, which typically means dealing with huge amounts of data.

Although the most powerful computers in the world are heavily involved in computational biology research, the scalability, portability, integration, and usability of bioinformatics software is still an open issue. Nonetheless, *in silico* molecular dynamics simulations, ligand discovery projects, and successes in drug design are examples of the great advantages that high-performance computing can provide to medicine and healthcare.

The challenges brought to information technology by the lightning improvement of novel molecular biology high-throughput technologies, which allow the analysis of inter personal variations in genomics, transcriptomics, proteomics, and metabolomics profiles, clearly call for novel solution in the field of high-performance computing.

The aim of this special issue is to present the latest efforts for bioinformatics applications development that can be exploited in computational biology. We are especially interested in parallel implementations of algorithms and systems, use case descriptions of distributed open access platforms for the bioinformatics community, or successful experiences of large-scale analysis and simulations in the field of computational biology. Topics of interest include, but are not limited to:

- Large scale infrastructures for high-performance bio-computing
- Parallel architectures for bioinformatics applications
- Science gateways for computational biological analyses
- Techniques for biological databases access and integration
- Parallel algorithms for genomics, transcriptomics, and proteomics
- Methods for systems biology network reconstruction, analysis, and simulations
- Algorithms for DNA assembly, sequence clustering, and reads mapping
- Machine learning approaches for SNP analysis and classification
- Gene expression and tissue microarray high-throughput platforms
- Structural approaches for protein modeling and interactions prediction
- Novel approaches to molecular dynamics simulation acceleration
- Large scale *in silico* ligand discovery and drug design projects

The submitted papers must be original, neither published anywhere else nor under any simultaneous consideration in any other venue. Extended contributions with respect to conference proceedings are allowed. In this case they must have at least 30% difference from the original works and a clear identification of the original contributions.

Before submission authors should read the journal's Author Guidelines, which are located at [http://onlinelibrary.wiley.com/journal/10.1002/\(ISSN\)1532-0634/homepage/ForAuthors.html](http://onlinelibrary.wiley.com/journal/10.1002/(ISSN)1532-0634/homepage/ForAuthors.html).

Manuscript must not exceed the maximum of 15 pages and must be submitted online using the journal Manuscript Tracking System at <http://mc.manuscriptcentral.com/cpe> according to the following timetable:

Manuscript Due	February 11, 2013
First Decision Date	March 25, 2013
Revision Due	May 6, 2013
Final Decision Date	June 10, 2013
Final Paper Due	July 15, 2013
Publication Date	3 <sup>rd</sup> Quarter, 2013 (Tentative)

### Guest Editors

**Ivan Merelli**, Bioinformatics Research Unit, Institute for Biomedical Technologies, National Research Council of Italy, Segrate (MI), Italy; [ivan.merelli@itb.cnr.it](mailto:ivan.merelli@itb.cnr.it)

**Daniele D'Agostino**, Advanced Computing Systems and High Performance Computing Group, Institute for Applied Mathematics and Information Technologies, National Research Council of Italy, Genoa, Italy; [dagostino@ge.imati.cnr.it](mailto:dagostino@ge.imati.cnr.it)

**Horacio Perez Sanchez**, Computer Engineering Department, School of Computer Science, University of Murcia, Murcia, Spain; [horacio@um.es](mailto:horacio@um.es)

**Sandra Gesing**, Applied Bioinformatics Group, Center for Bioinformatics & Department of Computer Science, University of Tübingen, Germany; [sandra.gesing@uni-tuebingen.de](mailto:sandra.gesing@uni-tuebingen.de)