



### European Conference on Parallel Computing

#### Topic 17: High-Performance Bioinformatics

##### Description

Genome sequencing projects and their successor projects have produced enormous amounts of biological data including genome sequences, protein structures and gene expression profiles, to name a few. High performance computational biology and bioinformatics are definitely required to extract valuable biological and biomedical knowledge from the ever-increasing biological data. New computational techniques and new theoretical models are required to simulate complex biological behavior of biological systems. This track focuses on high-performance and high-throughput computing necessary for management of biological data, extraction of meaning from biological data and using such data in models of biological systems, and modeling and simulation of biological systems. Applications using parallel programming, grid computing, and/or specialized computational systems are of particular interest – particularly the challenges of scaling to very large scales (100s of TeraFLOPS to PetaFLOPS).

Authors should report relevant experiences, present novel approaches to existing problems and raise important novel issues. Topics of interest include, but are not limited to, those in the following list:

##### Focus

- Computational biology and bioinformatics applications on grid systems
- Petascale computational biology
- Computation pipelines and workflows for computational biology and biological data integration
- Ontologies and semantic web approaches for bioinformatics
- Supervised and unsupervised analysis and categorization of genomic and proteomic data
- Mathematical modeling and simulation systems for systems biology
- Predictive biology: how do we get there?
- High performance architectures and systems for computational biology, systems biology, and bioinformatics

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