

Third IAPR International Conference on Pattern Recognition in Bioinformatics

15 -17 October 2008, Melbourne

Special Session: SS3 High Performance Computing in Bioinformatics

High-throughput techniques for bioinformatics have led to exponential growth in the amount of publicly available genomic data, e.g. GenBank has nearly doubled in size each year for the past decade. The large size of biological data sets, inherent complexity of biological problems and the ability to deal with error-prone data all result in large run-time and memory requirements. The goal of this session is to provide a forum for discussion of latest research in developing high-performance computing solutions to problems arising from bioinformatics.

Topics include, but are not limited to:

We are especially interested in using modern parallel and distributed architectures, such as Reconfigurable architectures (FPGAs), Streaming architectures (GPUs), Multimedia architectures (CellBE), Multi-core architectures, PC Clusters or Grids for compute-intensive Bioinformatics applications such as

- Biological sequence analysis
- Gene expression analysis and microarrays
- Protein folding and threading
- Protein-ligand docking
- Phylogenetic tree reconstruction
- Biological database scanning (e.g. Blast, HMMer)
- DNA sequence assembly
- Systems Biology

Important dates:

- Paper Submission: 15 April 2008
- Decision Notification: 15 May 2008
- Camera-Ready Submission: 15 June 2008

Paper Submission:

Manuscript must be submitted electronically via the “Paper Submission System” at <http://callforpapers.com.au/prib2008/SubmitPaper.php>. Instructions to authors are available at <http://www.infotech.monash.edu.au/about/news/conferences/prib08/>. All papers will undergo the same review process as all other PRIB 2008 papers and the accepted papers will be published as a volume of *Lecture Notes in Bioinformatics* or Supplementary Proceedings edited by conference chairs.

Special Session Organizers:

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