



SAC 2007

The 22nd ACM Symposium on Applied Computing

March 11 – 15, 2007, Seoul, Korea

Bioinformatics Track

CALL FOR PAPERS

SAC 2007

The ACM Symposium on Applied Computing (SAC) is a primary forum for applied computer scientists and application developers from around the world to interact and present their work. SAC 2007 is sponsored by the ACM Special Interest Group on Applied Computing (SIGAPP) and is presented in cooperation with other ACM Special Interest Groups. For more information on ACM SAC 2007, please visit: <http://www.acm.org/conferences/sac/sac2007/>

Bioinformatics Track

The publishing of the draft of the human genome marked a major step in the advancement of understanding how the human body works at a molecular level by giving biologists the potential genes from which all proteins and molecular interactions can be derived. The genome sequence has ushered in a new era of rapid and exponential growth of data related to how organisms function at a molecular level. DOE's Genomes to Life program for example, will make important contributions in the quest to venture beyond characterizing such individual life components as genes and other DNA sequences toward a more comprehensive, integrated view of biology at a whole-systems level. This track will address research issues related to these challenges.

A large part of the information to support biology research is available on large number of heterogeneous databases in both structured and unstructured formats. The challenge is to obtain information and knowledge from these databases using innovative computational approaches to support and promote biomedical research. One example of such a computational challenge is in identifying biological pathways using data, information, and knowledge scattered over heterogeneous databases. Computational tools using system-theoretic approaches are needed to model metabolic pathways, signal-transduction pathways, genetic regulatory circuits and biological systems. By comparing the genomes and pathways of several species at a high level, we hope to understand how stable biological systems have evolved. Over the last few years, microarray data have provided many insights into the transcriptome and into cellular functions. These data are now increasingly complemented by mass spectrometry data of the proteome, whose analysis poses new computational challenges.

There are no other tracks at SAC that will overlap with this track. This track distinguishes itself from the other major conferences in bioinformatics / computational biology (RECOMB, ISMB, ECCB, WABI) by its focus on data integration and whole-systems bioinformatics. RECOMB and ISMB have their roots in the combinatorics and AI communities and, as does WABI, used to focus, on theoretical research and proof-of-concept implementations. The SAC'07 BIO track, in contrast, provides a forum for integrative work.

Track Topics:

1. Use of natural language processing techniques and/or artificial intelligence techniques to automatically extract multiple biological objects such as gene names, protein names, drugs, organisms, disease, etc., from free-text.
2. Information and knowledge extraction such as object-object interactions (ex: protein interactions, functions, etc.).
3. Software systems to support biological research that integrates multi-format and multi-type data from heterogeneous databases.
4. Information visualization techniques for integrated biological systems.
5. Clustering of very large dimensional data such as microarray and mass-spectrometry data.
6. Clustering algorithms that support biological meaning.
7. Network models and simulations of various pathways.
8. Visualization techniques for network simulations
9. Pathway estimation from genomic data.
10. Computational methods that model cellular mechanisms, the protein machine, and regulatory networks.
11. Algorithms for processing and interpreting large-scale mass-spectrometry data
12. Comparative genomics and genome dynamics (i.e., evolution of whole genomes, e.g., by translocations, reversals, duplications, etc.)

Important Dates

<u>Abstracts/Paper Due:</u>	September 8, 2006 (Firm)
<u>Author notification:</u>	October 16, 2006
<u>Camera-Ready Due:</u>	October 30, 2006

Instructions for Paper Registration and Submission

Authors must register their intent to submit a paper by submitting an electronic abstract of maximum length of 200 words by the due date prior to the actual submission of the paper and obtain a paper identification number. All abstract and paper submission activities will be handled online via: <http://sac.cs.iupui.edu/SAC2007/SubmitAbstract.aspx?TrackID=87>.

Please send any Bioinformatics Track related questions to any of the Track Chairs or to the track email at: bioin@cs.iupui.edu.

Paper Submission Guidelines

Once you have submitted the paper registration form, you will receive a confirmation email. Your paper will be assigned a **paper identification number** and please take note of it. The format of the electronic version of the paper must be PDF. Do not use Word or any other format for the electronic version of your paper. Please use your paper identification number as the file name of your final paper in PDF (ex: nnn.pdf where “nnn” is your paper identification number).

All papers should represent original and previously unpublished works that are currently not under review in any conference or journal. Both basic and applied research papers are welcome.

The paper should not be more than 15 pages long using 11-point font and 1 inch margins on all four sides on letter size paper. Papers that fail to comply with length limitations risk rejection.

The author(s) name(s) and address(s) must NOT appear in the body of the submitted paper, and self-references should be in the third person. This is to facilitate blind review required by ACM. **All submitted papers must include the paper identification number on the front page, above the title of the paper.**

All enquiries and questions should be directed to the Track Chairs. Additional details are available at the track home page at <http://www.cs.iupui.edu/~bioin> and at the conference home page at <http://www.acm.org/conferences/sac/sac2007>.

Paper Publication

All papers will be fully refereed and undergo a blind review process by at least three referees. The conference proceedings will be published by ACM. Hence, all accepted papers should be submitted in ACM 2-column camera-ready format for publication in the symposium proceedings. The final version of the paper should **not** be more than 5 pages long.

Poster Publication of Selected Papers

A set of selected papers will be accepted as poster papers by invitation only and will be published as short papers in the symposium proceedings.

Track Chairs

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