ACM is pleased to announce that it has taken over sponsorship of the former International Joint Conference on Bioinformatics, Systems Biology, and Intelligent Computing (IJCBS), and will be holding the newly renamed **International Conference On Bioinformatics and Computational Biology (ACM-BCB)** in August 2010 in Niagara Falls, NY. This conference builds on the success of IJCBS 2009 in Shanghai, and is the start of ACM’s efforts to better support the bioinformatics and computational biology community.

We invite you to submit papers with unpublished, original research describing recent advances on all aspects of Bioinformatics and Computational Biology. All papers will undergo peer review by the conference program committee; accepted papers will be published in the conference proceedings (in CD) and in the ACM Digital Library. Authors of selected papers will be invited to extend their papers for submission to several journals. We also invite you to submit tutorial/workshop proposals focusing on problems and new challenges of Bioinformatics and Computational Biology. Submit your proposal to tutorial/workshop chairs.

Papers should not exceed 10 pages in ACM template on 8.5 x 11 inch paper (see ACM templates at http://www.acm.org/sigs/publications/proceedings-templates). Papers should be submitted via the link (https://cmt.research.microsoft.com/BCB2010/).

### Topics

- Assembly algorithms for the next generation sequencing
- Genome annotations via mass spectrometry
- Gene discovery and protein function prediction
- Functional genomics algorithms for high throughput data generation methods
- DNA and protein motif discovery
- Models of gene expression regulation at RNA level
- Algorithms for comparative and evolutionary genomics
- Molecular evolution and phylogeny reconstruction
- Multiple genome alignment
- Computational genomics for plant and animal genomes
- Engineering of bioinformatic databases
- Models of gene expression networks
- Computational proteomics and metabolomics
- Prediction of protein-protein interactions
- Protein structure prediction and molecular dynamics
- Visualization of biomolecular and cellular structure, dynamics and interactions
- Modeling of metabolic pathways
- Computational epigenomics
- Models of cellular and multicellular systems
- Prediction of cellular network dynamics from incomplete information
- Clinical genomics and proteomics
- Data mining in biomolecular databases
- High performance computing for complex biomolecular and cellular systems

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- Zihua Hu, SUNY at Buffalo
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**Key Dates**

<table>
<thead>
<tr>
<th>Event</th>
<th>Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tutorial/Workshop Proposals</td>
<td>Jan. 1, 2010</td>
</tr>
<tr>
<td>Paper Submission</td>
<td>Feb. 15, 2010</td>
</tr>
<tr>
<td>Notification to Authors</td>
<td>April 15, 2010</td>
</tr>
</tbody>
</table>