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### Deadlines:

Submission: **April 15<sup>th</sup>**  
Acceptance: **Mai 1<sup>st</sup>**  
Final version: **May 10<sup>th</sup>**  
Early Registration: **May 10<sup>th</sup>**

### Organizer



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## 1st International ISoLA Workshop on

# Modeling, Analyzing, Discovering Complex Biological Structures

<http://www.cs.uni-potsdam.de/isola-bio-2009>

Modern experimentation and data acquisition techniques allow the study of complex interactions in biological systems. This raises interesting challenges for computer scientists, as the models are complex, the amount of data is huge, some information cannot be observed, and measurements may be noisy.

The *ISoLA/Bio* workshop brings together researchers from the fields of computer science, bioinformatics, and computational biology. Bioinformatics and computational biology should be interpreted in a broad sense: computer science methods, for example algorithms or formal methods, applied to all aspects of biological research.

The main goals are to make the communities understand each other better, and to stimulate the development of new techniques specific for biological applications. The aim is to contribute to the cross-fertilization between the research in methods and algorithms in computer science and their applications to complex biological and medical questions by bringing together method developers and bioinformaticians.

We encourage submissions bringing forward methods for

### *modeling/analyzing/discovering complex biological structures*

A non-exhaustive list of topics suitable for this workshop are:

#### Methods

- Machine Learning and Data Mining
- Formal Methods
- Computational Modeling
- Tool environments and tool architectures
- Knowledge Representation
- Deduction and model-checking
- System construction and transformation techniques
- Compositional and refinement-based methodologies
- Logic and Reasoning

#### Applications

- Rational drug design
- Metabolic pathway modeling
- Gene Expression and post-transcriptional regulation
- Systems biology approaches to biomarker identification
- Protein structure prediction
- Interaction Networks
- Virtual Labs
- Biochemical systems
- Regulatory networks
- Medical Research

We invite both

- **abstracts** and **papers** describing contributions to the field and
- **problem statements**, explaining relevant but not yet adequately solved problems, in terms which are clear for the computer scientist.

Particularly welcome are **Regular contributions, Survey papers, Student Papers** and **Tool demonstrations**.

All accepted papers will be invited for a full-length contribution to the Symposiums' Proceedings (post-conference). Selected papers will appear in **STTT** (Springer Verlag, Heidelberg).