

## **Einladung zur Vortragsreihe** *Algorithmische Bioinformatik*

**Herr Dr. Dr. Axel Mosig,**  
**CAS-MPG Partner Institute for Biological Sciences, Shanghai,**

spricht über

### **Pattern Discovery Methods for Comparative Genomics and Bioimaging**

Datum: Dienstag, 6. Januar 2009  
Zeit: 16:00 Uhr s.t.  
Ort: B-IT, Dahlmannstr. 2, Rheinsaal

In recent years, algorithms for discovering patterns in biological data have emerged as important tools for biologists. This talk presents several such algorithms that we developed in the context of sequence analysis and bioimaging, as well as their application in studying biological systems.

The first part of the talk deals with algorithmic approaches for the comparative analysis of biological sequences. We elucidate combinatorial structures that emerge from modeling evolutionary patterns of non-protein-coding sequences, in particular *cis*-regulatory modules and non-coding RNAs. A thorough understanding of these combinatorial structures leads to pattern discovery algorithms for detecting and annotating such functional non-coding nucleotide sequences in genomic sequences. As we demonstrate through detailed and in many cases wet-lab supported studies, our novel algorithms are suitable to identify a number of non-coding RNA genes as well as regulatory elements in promoter regions of certain *Hox*-genes.

In the second part, we introduce algorithms for identifying biologically relevant patterns in image data. Through the rapid technological progress in recent years, bioimaging has become a driving force for understanding biological systems. Yet, turning image data into quantifiable scientific measurements often poses major challenges. In this context, we introduce the concept of topological alignments, and demonstrate how they can be applied to tracking cells in *Live Cell Imaging* data.