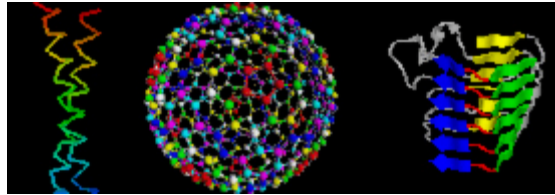


MIT  
Department of Mathematics  
& The Theory of  
Computation Group  
At CSAIL



## Bioinformatics Seminar

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Speaker: Temple F. Smith, PhD, Director Bioinformatics Graduate Studies, Boston University

Title: "The tale of two protein domain problems,

- 1) Novel HMM dissection,
- 2) Very early evolution."

Date: Monday, 12 April 2004

Time & Location:

Refreshments: 11 am in the Applied Mathematics Common Room at MIT's Building 2, Room 349

Talk: 11:30 am to 1 pm in the Applied Mathematics Conference Room Building 2, Room 338

URL: <http://www-math.mit.edu/compbiosem/>

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Abstract:

The first tale is of a modified form of 'designed' Hidden Markov Models for multi-domain proteins to identify the domain fold classes and their probable boundaries. While the second tale is of a combination of multi-alignment, profile and statistical approaches to identify 'signature' protein domains or blocks that suggest a major evolutionary event nearly 2.2 Gyrs ago.

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The seminar is co-hosted by Professor Peter Clote of Boston College's Biology and Computer Science Departments and MIT Professor of Applied Math Bonnie Berger. Professor Berger is also affiliated with CSAIL & HST.

Massachusetts Institute  
of Technology  
77 Massachusetts Avenue  
Cambridge, MA 02139

*For General Questions, please contact [kvdickey@mit.edu](mailto:kvdickey@mit.edu)*