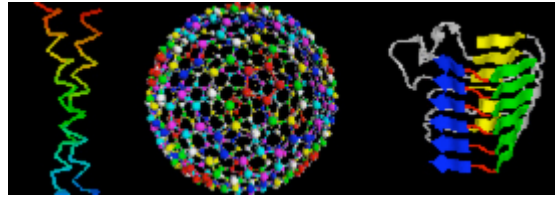


MIT  
Department of Mathematics  
& The Theory of  
Computation Group  
At CSAIL



## Bioinformatics Seminar

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Speaker: Zasha Weinberg, University of Washington

Title: Accurate annotation of non-coding RNAs in practical time

Date: Thursday, 12 May 2005

Time & Location: \*\*\*PLEASE NOTE UNUSUAL DAY & TIME\*\*\*

Refreshments: 3pm in the Star Conference Room at MIT's Building 32, Stata Center Room D-463

Talk: 2:45pm the Star Conference Room at MIT's Building 32, Stata Center Room D-463

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

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Abstract:

The biological significance of non-coding RNAs (ncRNAs) -- functional RNA molecules not coding for proteins -- has only been recognized very recently. This has come with an explosion in the number and variety of known ncRNAs.

The best way to search a genome sequence database for novel ncRNAs that resemble a given family of evolutionarily related ncRNAs seems to be to use statistical models like Covariance Models (CMs). CM searches are highly accurate, but are much too slow to be used in practice (e.g., years of computer time). My work has developed sequence filters to run the CM only on the most promising subsequences. I will describe two techniques. The first technique is a "rigorous filter", i.e., its filtering eliminates only sequences that provably would be rejected by the CM. The second technique is a heuristic, which permits faster searches at a small cost to sensitivity.

These techniques allow an 8-Gbase genome database to be scanned in days or weeks instead of years, and yield new ncRNAs missed by the ad hoc filters that were necessary for practical CM searches until now. I will also discuss my work to apply these techniques to recently discovered ncRNAs. Among other contributions, these homology searches led to the first discovery of a naturally occurring RNA (a glycine-binding riboswitch) that uses cooperative binding.

Joint work with Larry Ruzzo

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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.

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