

Emily Rocke

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Education

Ph.D., Computer Science and Engineering, University of Washington, 2003.

Dissertation: Gapped Motif Discovery in Biosequences

Advisor: Martin Tompa

M.S., Computer Science and Engineering, University of Washington, 1999.

A.B., Computer Science, Princeton University, 1996.

Research Interests

Computational and experimental genomic analysis:

- Discovering functional motifs in DNA and protein sequence
- Developing computational tools to explore chromatin structure and rearrangement
- Experimental exploration of the relationship between gene regulatory motifs and chromatin
- Computational tools for biosequence comparison and pattern recognition

Professional Experience

Postdoctoral researcher, University of Washington Genome Sciences Dept., Spring 2003–2004.

Discovering gene regulatory elements in *C. elegans*; experimental tests of these sites' functions.

Learning basic laboratory techniques in molecular biology and genetics.

Advisor: Jim Thomas

Research assistant, University of Washington Computer Science and Engineering,

Summer 1997–Autumn 1998; Autumn 1999; Spring 2000–Winter 2003.

Created and implemented an algorithm to find approximate gapped repeats in biosequences.

Discovered an improved method of scoring protein sequence alignments.

Advisor: Martin Tompa

Research intern, Verity, Inc., Sunnyvale, CA, Summer 2000.

Researched methods of classifying and predicting behavior of web users.

Explored the graph structure of the internet.

Advisor: Prabhakar Raghavan

Web developer, Animarc, Inc., New York, NY, February–September 1999.

Wrote perl CGI scripts for web commerce; programmed SQL database.

Supervisor: Marc Hadfield

Research assistant, University of California, Davis, Graduate School of Management,

Summer 1991–1992, Summers 1994, 1996.

Created a statistical software package in C++ and Visual Basic.

Supervisor: David Rocke

Technology intern, Recording for the Blind and Dyslexic, Princeton, NJ, summer 1995.

Worked on the lisp program AsTeR (Audio System for Technical Reading) to generate automatic readings of equations from LaTeX documents.

Teaching Experience

Teaching assistant, University of Washington Computer Science and Engineering.

Computational Biology (graduate course), Winter 2000. Instructor: Martin Tompa.

Introduction to Algorithms, Winter 1997. Duties included guest lectures, assisting design of homework, solution sets. Instructor: Richard Karp.

Computer Programming I, Summer 1997. Duties included teaching two sections, assisting homework design. Lecture section: Brendan Mumey and Joshua Seims.

Program coordinator, tutoring program for women and minorities in CSE, 1996-97

Responsible for matching tutors with students in appropriate areas.

Personally tutored students in courses including introductory data structures, intermediate data structures and algorithms, and introduction to formal models.

Honors

- Awarded UW Genome Training Grant Postdoctoral Fellowship for training in laboratory genetics, 2004-2005.
- Awarded UW Genome Training Grant Predoctoral Fellowship, 2000-2002.
- Awarded CSE department Research Fellowship, 1996-97.
- Member, Sigma Xi.
- Graduation with honors, Princeton University, 1996.
- National Merit Scholar.

Personal

U.S. Citizen

Refereed Publications

Copies of publications are available at <http://www.gs.washington.edu/~ecrocke/>

Author who gave the conference presentation marked with *

A Hybrid Scoring Function for Protein Multiple Alignment. Emily Rocke*. Proceedings of the 2nd Workshop on Algorithms in Bioinformatics (WABI) 2002.

Characterizing History Independent Data Structures. Jason Hartline*, Edwin Hong, Alexander Mohr, William Pentney, and Emily Rocke. International Society for Analysis, its Applications and Computation (ISAAC) 2002. © Springer-Verlag.

Using Suffix Trees for Gapped Motif Discovery. Emily Rocke*. Proceedings of Combinatorial Pattern Matching (CPM) 2000. © Springer-Verlag, LNCS series.

An Algorithm for Finding Novel Gapped Motifs in DNA sequences. Emily Rocke* and Martin Tompa. Proceedings of the Second Annual International Conference on Computational Molecular Biology (RECOMB) 1998.

Abstracts

Possible Effect of Chromatin Structure on nhr family regulation. Emily Rocke*, Marc Van Gilst, and James Thomas. Abstract and talk given at West Coast Worm Meeting, August 2004.

Longer Sequence Surrounding Motif Distinguishes Regulatory Elements from False Positives. Emily Rocke* and James Thomas. Abstract and poster presented at the Eighth Annual International Conference on Computational Molecular Biology (RECOMB) 2004.