

Curriculum Vitae

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Aaron Darling

Graduate Student

University of Wisconsin-Madison

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University of Wisconsin, Madison, WI	Graduate Student	2001	Computer Science
University of Wisconsin, Madison, WI	BS	1998-2000	Computer Science
Simon's Rock College, Great Barrington, MA		1997-1998	Liberal Arts

Relevant Professional Experience:

2002	<i>Graduate Research Assistant</i> – Parallel bioinformatics applications, under Wuchun Feng, Los Alamos National Laboratory, Los Alamos, NM
2001-present	<i>Research Assistant</i> - Comparative genomics, Genome Evolution Laboratory, under Nicole T. Perna and Mark Craven, UW-Madison
2001	<i>Information Processing Consultant</i> - Nicole T. Perna Laboratory, UW-Madison
2000	<i>Undergraduate Research Employee</i> – Frederick R. Blattner Laboratory, University of Wisconsin

Awards and Fellowships:

2003	ClusterWorld 2003 Conference Best Paper award for the paper "The Design, Implementation, and Evaluation of mpiBLAST"
2002	PSB 2003 Travel Fellowship by the Department of Energy
2002-2005	NLM Graduate Training Fellowship for Computation and Informatics in Biology and Medicine (CIBM)
2002	ISMB 2002 Best Poster Presentation Award
2002	Winner, 2002 PennySort competition

Statement of Research Experience

My current research investigates the molecular evolution of genomes. Past research into rates and patterns of evolution was based primarily on the statistical analysis of small amounts of DNA sequence data collected from a group of related organisms. Rapid advances in sequencing technology are yielding a large amount of data from a large number of organisms.

My research project involves using modern statistical and computational techniques to address long-standing questions about the relationship between molecular evolution and organismal diversity. Evolutionary analyses are facilitated by multiple sequence alignment and phylogenetic inference, both of which are computationally intensive. Our group recently published a paper describing Mauve, a system for rapid multiple genome alignment in the presence of large-scale evolutionary events such as rearrangement and horizontal transfer. My current research involves refining our scalable multiple sequence alignment system through

improved sensitivity, and applying it to seek correlations among changes in phenotype, genome architecture, and genome content.

Initially I am focusing on a data set of over 20 enterobacterial genomes. This group of organisms is phenotypically diverse, consisting of innocuous lab strains, and of human, animal and plant pathogens. My second target data set consists of 50 sequenced poxvirus genomes with a broad host-range, and in humans cause disease ranging from deadly smallpox to benign skin disorders. By examining the rates and patterns of small- and large-scale evolutionary events among closely related organisms, I hope to provide insight into the evolutionary history of molecular pathogenesis among these bacteria and virii.

As an undergraduate, I worked on a project to develop a set of analytical tools for genome-scale DNA sequence manipulation and comparison, in collaboration with B. Mau, F. Blattner and N. T. Perna.

Publications in Peer Reviewed Journals:

Mauve: Multiple Alignment of Conserved Genomic Sequence With Rearrangements. Aaron C. E. Darling, Bob Mau, Frederick R. Blattner, Nicole T. Perna. *Genome Research* 2004. July 1st.

GRIL: Genome Rearrangement and Inversion Locator. Aaron E. Darling, Bob Mau, Frederick R. Blattner, Nicole T. Perna. *Bioinformatics* 2004 Jan;20(1):122-124

The design, implementation, and evaluation of mpiBLAST. Aaron Darling, Lucas Carey, Wuchun Feng. *Proceedings of the 4th International Conference on Linux Clusters and ClusterWorld 2003*. June 23-26 2003, San Jose, CA.

Complete genome sequence and comparative genomics of *Shigella flexneri* serotype 2a strain 2457T. Wei J, Goldberg MB, Burland V, Venkatesan MM, Deng W, Fournier G, Mayhew GF, Plunkett G 3rd, Rose DJ, Darling A, Mau B, Perna NT, Payne SM, Runyen-Janecky LJ, Zhou S, Schwartz DC, Blattner FR. *Infect Immun* 2003 May;71(5):2775-86

ASAP, a systematic annotation package for community analysis of genomes. Jeremy D. Glasner, Paul Liss, Guy Plunkett III, Aaron Darling, Tejasvini Prasad, Michael Rusch, Alexis Byrnes, Michael Gilson, Bryan Biehl, Frederick R. Blattner, and Nicole T. Perna. *Nucl. Acids. Res.* 2003 31: 147-151

Oral Presentations At Scientific Meetings

Designing and evaluating methods for multiple genome comparison
February, 2004 – CIBM Seminar Series (Madison, WI)
June, 2004 – To appear at annual National Library of Medicine meeting (Indianapolis, IN)

The design, implementation, and evaluation of mpiBLAST.
June, 2003 – ClusterWorld 2003 (San Jose, CA)

Mauve: Multiple Genome Alignments
December, 2002 – CIBM Seminar Series (Madison, WI)

Poster Presentations At Scientific Meetings

Methods for multiple genome comparison
August, 2003 – The 2003 Molecular Genetics of Bacteria and Phages Meeting, Madison, WI

mpiBLAST: Delivering super-linear speedup with an open-source parallelization of BLAST

January, 2003 –Pacific Symposium on Biocomputing 2003, Kauai, HI

mpiBLAST: Parallelization of BLAST for computational clusters

November, 2002 –Supercomputing 2002, Baltimore, MD

Mauve: Multiple Genome Alignments

August, 2002 – Intelligent Systems for Molecular Biology (ISMB), Edmonton, Canada

Received one of ten best poster awards

September, 2002 - Lake Arrowhead Small Genomes Conference

BLASTing away on Green Destiny

August, 2002 – IEEE Computer Society Bioinformatics (CSB) conference, Stanford, CA

Relevant Coursework

CS 525 Linear Programming Methods

CS 537 Introduction to Operating Systems

CS 435 Introduction to Cryptography

CS 760 Machine Learning

CS 838 Seminar: Learning and Modeling Biological Networks

CS 787 Advanced Algorithms and Data Structures

CS 736 Advanced Operating Systems

CS 731 Advanced Artificial Intelligence (with biomedical applications)

GEN 466 Introduction to Genetics

GEN 607 Advanced Microbial Genetics

GEN 612 Prokaryotic Molecular Biology

BMI 576 Introduction to Bioinformatics

BMI 776 Advanced Bioinformatics

BOT 468 Introduction to Systems Biology

STAT 571 Introduction to Biostatistics