

Aaron Darling

NSF Postdoctoral Fellow – Univ. of Queensland and UC Davis

aaronardling@ucdavis.edu, <http://secretmicrobe.org>**Education:**

University of Wisconsin, Madison, WI	Ph.D.	2001-2006	Computational Biology
University of Wisconsin, Madison, WI	B.Sci.	1998-2000	Computer Science
Simon's Rock College, Great Barrington, MA		1997-1998	Liberal Arts

Relevant Professional Experience:

2006-present	<i>NSF Postdoctoral Fellow</i> – Recombination among populations of bacteria, with Mark A. Ragan (Univ. of Queensland) and Jonathan A. Eisen (Univ. of California – Davis)
2002-2006	<i>Graduate Research Assistant</i> – Parallel bioinformatics applications, under Wu Feng and Carla Kuiken, Los Alamos National Laboratory, Los Alamos, NM
2001-2006	<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:

2006-2009	NSF Award DBI-0630765
2005	NAS Travel Fellowship for the “Tapestry of Life” conference
2005	Orion Multisystems “Personal Supercomputing Contest”
2005	NIGMS Travel Fellowship for the “Evolution of Infectious Disease” conference
2005	Dept. of Energy "2005 Award for Excellence in Technology Transfer"
2004	R&D 100 Award for “mpiBLAST: A high speed software catalyst for genetic research”
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
2002-2006	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

Peer Reviewed Publications:

- Dynamics of genome rearrangement in bacterial populations. Aaron E. Darling, Istvan Miklos, Mark A. Ragan. *PLoS Genetics* 2008. 4(7):e1000128
- Inference of genomic flux in bacteria. Xavier Didelot, Aaron Darling, Daniel Falush. *Genome Research* 2008.
- Gapped extension for local-multiple-alignment of interspersed DNA repeats. Todd J. Treangen, Aaron E. Darling, Mark A. Ragan, Xavier Messeguer. *Lecture Notes in Computer Science*. 2008. 4983:74-86.
- Enteropathogen Resource Integration Center (ERIC): bioinformatics support for research on biodefense-relevant enterobacteria. Jeremy D. Glasner, Guy Plunkett III, Bradley D. Anderson, David J. Baumler, Bryan S. Biehl, Valerie Burland, Eric L. Cabot, Aaron E. Darling, Bob Mau, Eric C. Neeno-Eckwall, David Pot, Yu Qiu, Anna I. Rissman, Sara Worzella, Sam Zaremba, Joel Fedorko, Tom Hampton, Paul Liss, Michael Rusch, Matthew Shaker, Lorie Shaull, Panna Shetty, Silpa Thotakura, Jon Whitmore, Frederick R. Blattner, John M. Greene, and Nicole T. Perna. *Nucleic Acids Research*, 2008. (36):D519.
- Procrastination leads to efficient filtration for local multiple alignment. Aaron E Darling, Todd J Treangen, Louxin Zhang, Carla Kuiken, Xavier Messeguer, Nicole T. Perna. *Lecture Notes in Bioinformatics* 4175:126-137, Springer-Verlag 2006
- Genome-wide detection and analysis of homologous recombination among sequenced strains of *E. coli*. Bob Mau, Jeremy D. Glasner, Aaron E. Darling, Nicole T. Perna. *Genome Biology* 2006. 7(5):R44.
- ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. Glasner JD, Rusch M, Liss P, Plunkett G 3rd, Cabot EL, Darling A, Anderson BD, Infield-Harm P, Gilson MC, Perna NT. *Nucleic Acids Research* 2006 34:D41-5.
- Identifying evolutionarily conserved segments among multiple divergent and rearranged genomes. Bob Mau, Aaron E. Darling, Nicole T. Perna. *Lecture Notes in Bioinformatics* 3388:72-84, Springer-Verlag 2005.
- Mauve: Multiple Alignment of Conserved Genomic Sequence With Rearrangements. Aaron C. E. Darling, Bob Mau, Frederick R. Blattner, Nicole T. Perna. *Genome Research* 2004. 14(7):1394-1403.
- GRIL: Genome Rearrangement and Inversion Locator. Aaron E. Darling, Bob Mau, Frederick R. Blattner, Nicole T. Perna. *Bioinformatics* 2004 Jan;20(1):122-124

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- The design, implementation, and evaluation of mpiBLAST. Aaron Darling, Lucas Carey, Wu-chun 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

Invited Publications:

Take off with mpiBLAST parallel searching. Lucas Carey, Aaron Darling, Wu-chun Feng. *ClusterWorld Magazine* 2(3), March 2004.

Oral Presentations At Scientific Meetings (2007 onwards):

- Efficient sampling of minimal inversion histories
October 2008 – The 6th RECOMB Comparative Genomics meeting (Paris, France)
- Next-Generation Metagenomics
August 2008 – CSIRO Minisymposium on Metagenomics (Brisbane, Australia)
- Genome alignment for population genomics
July 2008 – Workshop on Statistical Metagenomics (Berlin, Germany)
- Bayesian analysis of genome rearrangement in *Yersinia pestis*
March 2008 – 1st Australian phylogenetics workshop (Naracoorte, Australia)
- Population modeling of whole genome evolution?
September 2007 – St. John's Workshop on Advances in Bacterial Genomics (Oxford, UK)
- Bayesian analysis of genome rearrangement in *Yersinia pestis*
September 2007 – The 5th annual RECOMB comparative genomics meeting (San Diego, CA)
August 2007 – Institute for Molecular Bioscience Seminar Series (Brisbane, Australia)
July 2007 – Evolution 2007 conference (Christchurch, New Zealand)
- The Jekyll and Hyde lifestyle of pathogenic bacteria revealed by genome phylogenies
February 2007 – New Zealand Phylogenetics Meeting (Mt. Ruapehu, New Zealand)

Contributed Book Chapters:

- Genome Rearrangement by the Double Cut and Join Operation. Richard Friedburg, Aaron E. Darling, and Sophia Yancopoulos. *Bioinformatics: Data, Sequence Analysis and Evolution*. Vol 452. Chapter 18. pp 385-416. Springer Press 2008.
- Analyzing patterns of microbial evolution using the Mauve genome alignment system. Aaron E. Darling, Todd J. Treangen, Xavier Messegeur, Nicole T. Perna. *Comparative Genomics* (Bergman Eds.), Humana Press, November 2007.
- In-silico Detection of Genes in Bacteriophage Genomic Sequences. Andrew M. Kropinski, Mark Borodovsky, Tim J. Carver, Ana M. Cerdeno-Tarraga, Aaron Darling, Padmanabhan Mahadevan, Paul Stothard, Donald Seto, Gary Van Domselaar, David S. Wishart. *Bacteriophages: Methods and Protocols*, Volume 2. Humana Press. *In Press*.

Reviewer for Journals and Conferences:

- Genome Biology
- BMC Bioinformatics
- FEBS Letters
- Nucleic Acids Research (NAR)
- Bioinformatics
- Molecular Biology and Evolution (MBE)
- European Conference on Computational Biology (ECCB)
- Intelligent Systems for Molecular Biology (ISMB)
- Workshop on Algorithms in Bioinformatics (WABI)
- RECOMB Comparative Genomics
- IEEE Computer Systems Bioinformatics conference (CSB)
- IEEE Transactions on Computational Biology (TCBB)
- International Journal of High-Performance Computing and Networking

In the popular press:

- The Register: "Los Alamos lends open-source hand to life sciences" 06/29/2003
- Genome Technology: "Parallel BLAST: Chopping the database" 01/01/2005
- The Scientist: "Seven Technologies That Are Transforming The Life Sciences: BLAST" 08/29/2005

Published conference abstracts and posters:

- “Aligning genomes with lineage-specific rates of gene flux and rearrangement” Aaron E. Darling, Bob Mau, Nicole T. Perna
 - October 2006 – International *E. coli* Alliance conference (Jeju Island, Korea)
 - September 2006 – 14th conference on Microbial Genomics (Lake Arrowhead, CA)
 - August 2006 – Intelligent Systems for Molecular Biology (Fortaleza, Brazil)
- “Mauve Genome Alignments Reveal Homologous Recombination in Enterobacteria” Aaron E. Darling, Bob Mau, Jeremy Glasner, Nicole T. Perna
 - October 2005 – Computation and Informatics in Biology and Medicine Retreat (Madison, WI)
 - September 2005 – 13th Small Genomes Conference (Madison, WI)
 - June 2005 – Intelligent Systems for Molecular Biology 2005 (Detroit, MI)
- “Multiple Alignment of Rearranged Genomes” Aaron E. Darling, Bob Mau, Mark Craven, Nicole T. Perna
 - November 2004 – ASM Midwest Regional meeting (Madison, WI)
 - October 2004 – RECOMB Comparative Genomics (Bertinoro, Italy)
 - October 2004 – Computation and Informatics in Biology and Medicine Retreat (Madison, WI)
 - August 2004 – IEEE Computational Systems Biology (Palo Alto, CA)
- “Methods for Multiple Genome Comparison” Aaron Darling, Bob Mau, Frederick R. Blattner, Nicole T. Perna
 - October 2003 – Computation and Informatics in Biology and Medicine Retreat (Madison, WI)
 - August 2003 – The 2003 Molecular Genetics of Phage and Bacteria Meeting (Madison, WI)
- “An Open-Source Parallelization of BLAST” Aaron Darling, Adam Englehart, Wu Feng
 - February 2003 – O’Reilly Bioinformatics Technology Conference (San Diego, CA)
- “mpiBLAST: Delivering super-linear speedup with an open-source parallelization of BLAST” Aaron Darling, Lucas Carey, Wu Feng
 - January 2003 – Pacific Symposium on Biocomputing 2003 (Kauai, HI)
- “mpiBLAST: Parallelization of BLAST for computational clusters” Aaron Darling, Wu Feng
 - November 2002 – Supercomputing 2002 (Baltimore, MD)
- “Mauve: Multiple Genome Alignments” Aaron Darling, Bob Mau, Frederick R. Blattner, Nicole T. Perna
 - October 2002 – Computation and Informatics in Biology and Medicine Retreat (Madison, WI)
 - September 2002 – 10th Small Genomes Conference (Lake Arrowhead, CA)
 - August 2002 – Intelligent Systems for Molecular Biology (ISMB) 2002 (Edmonton, Canada)
- “BLASTing away on Green Destiny” Aaron Darling, Wu Feng
 - August 2002 – IEEE Computer Society Bioinformatics (CSB) 2002 (Stanford, CA)

Statement of Research Interests and Experience

My current research investigates the molecular evolution of genomes. The recent availability of genome sequences from numerous closely-related microbes enables the application of population-genetic techniques on the genomic scale. At the genome scale, mutational processes such as recombination, gene gain, loss, and genome rearrangement can be considered in the framework of population genetics.

I am applying modern statistical and computational techniques to investigate historical episodes of gene sharing among microbes, in an effort to characterize why gene sharing works and how barriers to homologous recombination have formed. These evolutionary analyses are facilitated by multiple genome alignment and phylogenetic inference, both of which are computationally intensive. As part of my Ph.D. work, I developed a multiple genome alignment system that can efficiently and accurately align a large number of microbial genome sequences.

At the moment I am focusing on a data set of over 30 enterobacteria. This group of organisms is phenotypically diverse, consisting of innocuous lab strains, and of human, animal and plant pathogens. 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.

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. R. Blattner and N. T. Perna.