

Nigel Delaney

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🌐 www.evolvedmicrobe.com

🐙 [github://evolvedmicrobe](https://github.com/evolvedmicrobe)

Education

Harvard University

Cambridge, MA

Ph.D. Biology

2012

A.M. Statistics

Committee: Christopher J. Marx (advisor), John Wakeley, Daniel Hartl and Scott Edwards

GPA: 4.0 Biology, 4.0 Statistics

UC San Diego

La Jolla, CA

B.S. Biology

2004

B.A. History

Magna cum laude

GPA: 4.0 Biology, 3.8 Overall

Honors and Awards

Certificate of Distinction in Teaching - Harvard University 2008

NSF Graduate Research Fellowship 2007

James Mills Peirce Fellowship (awarded to top incoming Harvard graduate students) 2006

Top Graduating Senior - UCSD Ecology and Evolution 2004

Research and Work Experience

Massachusetts General Hospital / Broad Institute

Boston, MA

Research Fellow in Computational Biology

Nov. 2012 - Present

- Developed mtDNA sequencing and analysis for Broad CLIA exome sequencing product.
- Analyzed three large-*P*/small-*N* metabolomics studies.

Organismic and Evolutionary Biology, Harvard University

Cambridge, MA

Graduate Researcher, Marx Laboratory

Sep. 2006 - Oct. 2012

- Used automation and response surface methods to create a high-throughput system to evolve and measure bacterial populations.
- Designed experiment and conjugate Gibbs sampling method to estimate evolutionary potential and genetic interactions.

The Scripps Institution of Oceanography

La Jolla, CA

Staff Research Associate, Scripps Photobiology Group

Sep. 2003 - June 2006

- Developed apparatus to measure carbon fixation rates of antarctic phytoplankton under different temperature and light conditions using small experimental volumes.
- Planned and participated in research expeditions, including two to Antarctica.
- Wrote software and web applications to store and analyze oceanographic data.

Publications

H.H. Chou, **N.F. Delaney**, N. Leiby, J.A. Draghi, C.J. Marx (2014) “Mapping the Fitness Landscape of Gene Expression Uncovers the Cause of Antagonism and Sign Epistasis between Adaptive Mutations.” PLoS Genetics: 10(2).

N.F. Delaney, M.E. Kaczmarek, L.M. Ward, P.K. Swanson, M-C Lee, C.J. Marx (2013) “Development of an Optimized Medium, Strain and High-Throughput Culturing Methods for *Methylobacterium extorquens*.” PLoS ONE: 8(4).

W.R. Harcombe, **N.F. Delaney**, N. Leiby, N. Klitgord, C.J. Marx (2013) “The Ability of Flux Balance Analysis to Predict Evolution of Central Metabolism Scales with the Initial Distance to the Optimum.” PLoS Computational Biology: 9(6).

N.F. Delaney, J.R. Echenique, C.J. Marx (2013) “Clarity: an Open-Source Manager for Laboratory Automation.” Journal of Laboratory Automation: 18(2).

L.M. Chubiz, M-C Lee, **N.F. Delaney**, C.J. Marx (2012) “FREQ-Seq: A Rapid, Cost-Effective, Sequencing-Based Method to Determine Allele Frequencies Directly from Mixed Populations.” PLoS ONE: 7(10).

N.F. Delaney, S. Balenger, C. Bonneaud, C.J. Marx, G.E. Hill, N. Ferguson-Noel, P. Tsai, A. Rodrigo, and S. V. Edwards (2011). “Ultrafast evolution and loss of phage defense following host shift in a wildlife pathogen.” PLoS Genetics: 8(2).

H. H. Chou, H. C. Chiu, **N. F. Delaney**, D. Segre and C.J. Marx (2011). “Diminishing returns epistasis among beneficial mutations decelerates adaptation.” Science: 332 (6034).

Weinreich, D. M., **N. F. Delaney**, M. A. DePristo and D. L. Hartl (2006). “Darwinian evolution can follow only very few mutational paths to fitter proteins.” Science: 312(5770).

C. Hewes, **N.F. Delaney**, B. Seegers, B. G. Mitchell, M. Kahru, O. Holm-Hansen, M. V. Ardelan, H. Dulaiova, P. Henderson, M. Charette, J. K. Iriarte and N. Silva. (2006) “Phytoplankton survey of the Northern Antarctic Peninsula.” AMLR 2005/2006 Field Season Report: NMFS-SWFSC-397.

Mentorship and Community Service

Peer-review referee: Nature, PLoS Genetics, PLoS Computational Biology, Journal of Laboratory Automation.

Supervised Trainees: Managed and trained two full-time technicians (funding from an NSF CAREER award I co-wrote). Mentored 2 Harvard undergraduate summer projects.

Open Source Software Contributions:

Clarity: Open source laboratory automation scheduler and device drivers.

Curve Fitter: Visualization and analysis of bacterial growth curves using mixture models to account for systematic biases and enhance replication.

.NET Bio: Project developer. Rewrote and optimized several algorithms and parsing libraries.

Freq-Seq: Estimates allele frequencies in mixed populations using a novel and low-cost method.

Misc: Demonstrated competence in diverse languages with bug fixes and/or unit tests to Biopython, GATK (Java) and F# Charting projects.