Nathaniel Bernard Edelman, PhD

Hutchinson Postdoctoral Fellow
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Summary

Experienced bioinformatician with 6+ years of experience in analysis of genomic data. Leader of international teams of researchers, resulting in 10+ peer-reviewed publications, 10+ presentations at major scientific conferences, and ongoing productive collaborations. Skilled wet lab biologist, with capabilities in DNA and RNA extraction, microscopy, PCR, and qPCR. Creative thinker, problem-solver, and eager collaborator.

Education/Fellowships

Hutchinson Postdoctoral Fellow, Yale Institute for Biospheric Studies 2020-Present

Ph.D. Harvard University, Department of Organismic and Evolutionary Biology 2014-2020
Dissertation Title: *Evolutionary Effect of Hybridization* Cambridge, MA

B.A. Cornell University, Biology, *cum laude* 2007-2011
Concentration: Genetics and Development Ithaca, NY

Relevant Skills

Bioinformatics:

- Fluent in Python, Unix, R
- Pipeline generation and optimization, including processing of common data formats such as BAM, SAM, VCF, BED, FASTA, and FASTQ.
- Analysis of RNA-seq, RAD-seq, whole genome resequencing
- Genome assembly
- Population genetic analyses including population structure, demography, phylogeny, and GWAS
- Simulation in SLiM and msprime.

Wet Lab:

- DNA extraction and sequencing
- RNA extraction and sequencing
- PCR, qPCR
- Dissection, histology, electron microscopy, confocal microscopy

Administrative:

- Project development
- Mentoring, collaboration
- Grant writing, manuscript writing, presentation of research

Scientific Accomplishments

Hutchinson Postdoctoral Fellow, Yale University 2020-Present

- Developed and led a project using a novel linked-read sequencing strategy to identify haplotypes subject to local selection in a wood frog (*Rana sylvatica*) metapopulation
- Assembled the first *de novo* reference genome for *Rana sylvatica*
- Collected, maintained, phenotyped, and extracted DNA from 720 *Rana sylvatica* tadpoles
- Developed statistics and analyses for population-level linked read sequence data

PhD Researcher, Harvard University 2014-2020

- Led an international team of researchers to identify genomic hybridization in the deep history of the *Heliconius* butterfly radiation
- Partnered in the development of a novel genomic method to detect introgression between species
- Fund-raised, organized, and carried out field work in Peru and Bolivia
- Dissected, imaged with bifocal microscopy, and extracted RNA from hundreds of *Heliconius* butterfly ovaries

- Characterized hybrid sterility phenotype between subspecies of *Heliconius* morphologically, genetically, and transcriptionally

Research Technician, Institute of Molecular Pathology, Vienna, AT 2011-2013
Supervisor: Dr. David Keays

- Designed a novel method for single cell transmission electron microscopy
- Identified and characterized magnetic cells in the pigeon *Columba livia*
- Performed single cell qPCR and tissue RNA-sequencing to annotate the *Columba livia* genome

Grants and Honors

AGA President's symposium travel award 2021
American Genetics Association; $400
Hutchinson Postdoctroal Fellowship 2020
Yale University; $134,000.00
Robert G Goelet Research Grant 2015, 2016, 2019
Harvard University; $5,778.00, $1,646.00, $240.00
Putnam Expedition Grant 2017
Harvard University, $3,880.00

Selected Publications

1. **Edelman NB** and Mallet J. 2021. The prevalence and adaptive impact of introgression in animals. Annual Reviews Genetics. 55(1)

2. Rosser N*, **Edelman NB*** *et al.* 2021. Complex basis of hybrid female sterility and Haldane's rule in Heliconius butterflies: Z-linkage and epistasis. Molecular Ecology. *In press*
*Authors contributed equally

3. **Edelman NB** *et al*. 2019. Genomic architecture and introgression shape a butterfly radiation. Science. 366(6465)594-599.

Selected Presentations

AGA President's Symposium 2021: Conservation Genomics, October 11-13, Snowbird, UT
Selected Talk: Edelman NB *et al*: Haplotype-resolved local adaptation with migration in a wood frog metapopulation

Yale Institute for Biospheric Studies, 2020, September 11, New Haven, CT (Virtual)
Invited Departmental Seminar: **Edelman NB**: The evolutionary impact of hybridization in *Heliconius* butterflies

Gordon Research Conference on Ecological and Evolutionary Genomics, 2019, July 13-18, Manchester, NH
Invited Talk: **Edelman NB** *et al*: Genome Architecture and Introgression in *Heliconius* butterflies

II Joint Congress on Evolutionary Biology, 2018, August 18-22, Montpellier, France
Talk: Edelman NB *et al*: Whole genome assembly of 21 Heliconiinae assemblies identifies introgression throughout radiation

References

Dr. James Mallet
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Dr. Paul Frandsen
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