Tyler Hether | Resume

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A well-rounded, recent graduate in bioinformatics and computational biology whose interests are at the interface of data science, mathematics, and biology. Self-motivated, question-driven and detail-oriented person who enjoys working together with a team to create solutions to a wide-variety of biological and computational challenges.

Education

Ph.D, Bioinformatics & Computational Biology   University of Idaho, 2016
"Genetic Networks, Adaptation, & the Evolution of Genomic Islands of Divergence"

M.S., Biology   University of Central Florida, 2010
"Using landscape genetics to assess population connectivity in a habitat generalist"

B.S., Biology   University of Central Florida, 2010

Employment

University of Oregon   Eugene, Oregon
Postdoctoral Associate & Bioinformatics Data Scientist   June 2016 – present
I contribute to and create bioinformatic workflows and programming solutions for a range of biological questions related to microbial metagenomics, gene regulatory network and expression changes, nematode genetic diversity, and reduced representation DNA sequencing.

University of Idaho   Moscow, Idaho
Research Assistant & Graduate Student   August 2010 – May 2016
I examined the genomic response to environmental stress by experimentally evolving populations of budding yeast, built a statistical toolkit – a Hidden Markov Model-based R package – for analyzing meiotic recombination rates from low-coverage next-generation sequence data, and expanded on classical models of quantitative genetics using a network theory paradigm.

University of Central Florida   Orlando, Florida
Research Assistant & Graduate Student   August 2007 – July 2010
I isolated and characterized microsatellite markers for a range of species and identified landscape correlates to genetic connectivity between frog sub-populations using machine learning algorithms.

Expertise and Interests

Data Science ❖ Genomics ❖ Recombination ❖ Scalability ❖ HMMs ❖ Genotype to Phenotype ❖ Molecular Evolution ❖ Experimental Evolution ❖ RNA sequencing ❖ R ❖ Rcpp ❖ Genetic Architecture ❖ Data Visualization ❖ Quantitative Genetics

Select Software on Github

HMMancestry. *'R package using the Forward-Backward algorithm to infer genotypes, recombination hotspots, and gene conversion tracts from low-coverage next-generation sequence data'*

I created the R package HMMancestry to infer recombination breakpoints, gene conversion tracts, hotspots, and coldspots in high-throughput, next-generation sequence data, even when sequencing coverage is relatively low. This package leverages nearby genetic content to infer local ancestry using a 'Hidden Markov Model'. This package can analyze both haploid and diploid individuals and has built-in simulating and maximum-likelihood estimating functions for added user flexibility.

Flip2BeRAD. *'Python and C++ utilities for flipping RADseq reads'*

I built a utility for flipping the forward and reverse raw reads generated from paired-end sequencing when the sample barcode is found on the reverse (paired-end) read. For some RADseq protocols (e.g., BestRAD), the barcode plus cut site combination can occur on the reverse read. This is problematic when downstream programs (e.g., stacks) require that these be on the forward read. I built two flavors of Flip2BeRAD: a fuller featured Python script and a quicker C++ variant.

- **NetworkEvolution.** *'Evolving networks in a quantitative genetics framework'*

  I created NetworkEvolution, a C++ program used to simulate two quantitative traits for a user-defined number of populations evolving to identical fitness optima under a quantitative genetics framework. A key feature of NetworkEvolution is the ability to simulate two classes of mutations: those in the allelic (coding) alleles and those in the cis-regulatory regions of a two gene genetic network.

Technical & Personal Skills

- **Programming Languages.** In descending order of expertise: R, bash/linux, LaTeX, C++, Python, Mathematica, and Perl. Actively learning: Java and Scala.

- **Other.** Experience with high performance computing in R (via Rcpp) and reproducibility of documents, results, and reports using Sweave. Experience in molecular and microbiology laboratory bench work. Experience presenting and disseminating findings at scientific conferences as well as in smaller groups and one-on-one.

Publications

- **Hether, T.D.** and Hohenlohe P.A. Stochastic adaptation, overdominance, and reproductive isolation emerge from directional selection on simple genetic networks. *In review*

- **Hether, T.D.**, Wiench C.W., and Hohenlohe P.A. Novel molecular and analytical tools for efficient estimation of rates of meiotic crossovers and non-crossover gene conversions. *In review*

- Hand, B.K, **T.D. Hether**, R.P. Kovach, C.C. Muhlfeld, S.J. Amish, M.C. Boyer, S.M. O'Rourke, M.R. Miller, W.H. Lowe, P.A. Hohenlohe, & G. Lukart. 2015. Genomics and introgression: Discover and mapping of thousands of species-diagnoistic SNPs using RAD sequencing. Current Zoology 61 (1): 146-154

- **Hether, T.D.** and P.A. Hohenlohe.2014. Genetic regulatory network motifs constrain adaptation through curvature in the landscape of mutational (co)variance. Evolution (68) 4: 950-964.

- Rosenblum, E.B., B.A. Sarver, J.W. Brown, S. Des Roches, K. M. Hardwick, **T.D. Hether**, J.M. Eastman, M.W. Pennell, and L.J. Harmon. 2011. Goldilocks meets Santa Rosalia: an ephemeral speciation model explains patterns of diversification across time scales. Evolutionary Biology. 39, number 2, 255-261.

- **Hether, T.D.** and E.A. Hoffman. Machine learning identifies specific habitats associated with genetic connectivity in *Hyla squirella*. 2012. J. Evolutionary Biology 25, issue 6, 1039-1052

- Degner, J.F., D.M. Silva, **T.D. Hether**, J.M. Daza, E.A. Hoffman. 2010. Fat frogs, mobile genes: unexpected phylogeographic patterns for the ornate chorus frog (*Pseudacris ornata*). Molecular Ecology 19, issue 12, 2501-2515.

- Jenkins D.G, ..., **T.D. Hether**, et al. 2010. Isolation by distance: 20th century relic or reference standard for 21st century landscape genetics? Ecography 33, issue 2, 315-320.

- **Hether, T. D.** and E. A. Hoffman. Characterization of five dinucleotide and six tetranucleotide polymorphic microsatellite loci for the squirrel treefrog (*Hyla squirella*). Appeared in D. Abdoullaye, I. Acevedo, A.A. Adebayo, et al. 2010. Permanent Genetic Resources added to Molecular Ecology Resources Database 1 August 2009-30 September 2009. Molecular Ecology Resources 10, 232-236.

- Degner, J. F., **T. D. Hether**, and E. A. Hoffman. 2009. Eight novel tetranucleotide and five cross-species dinucleotide microsatellite loci for the ornate chorus frog (*Pseudacris ornata*). Molecular Ecology Resources 9, 622-624.

Other Interests & Extracurricular Activities

- **Big data.** What happens when data gets really large and needs to be summarized in real-time? Recently, I've been learning how to use Apache Kafka and Twitter's streaming API to analyze gigabytes of local or streaming social media data efficiently. While it's a hobby of mine, these skills could have numerous industrial and biomedical applications.

- **Data visualization.** Distilling large amounts of data down to make meaningful inferences is as much an art as it is a science. To this end, I employ a variety of visualization and statistical packages (e.g., ggplot2, dplyr) in my daily work flow.

- **Outdoors.** While technology is great, I also like to get outdoors. Road cycling is one of my favorite activities. My favorite ride is the Trail of the Coeur d'Alene – a pristine 72 mile bike trail that spans Idaho's panhandle from Washington to Montana where moose outnumber people. Hiking is another favorite pastime, both because it immerses one with nature as well as lends itself to great landscape photography opportunities.