

Tyler Hether | Resume

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I'm a well-rounded data scientist whose interests are at the interface of data science, mathematics, and biology. I think my greatest attribute is the ability to quickly pick up new skills.

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, 2006

Employment

- **University of Oregon** Eugene, Oregon
Postdoctoral Associate & Bioinformatics Data Scientist June 2016 – present
To better foster scientific discovery across otherwise disparate research projects within the lab, I created and administer an Apollo (Jbrowse) genome browser on a cloud-based linux web server. I also provide bioinformatic support for lab members that range from designing experiments and providing statistical consultations to generating and implementing programming solutions to employing complete end-to-end data analysis.
- **University of Idaho** Moscow, Idaho
Research Assistant & Graduate Fellow August 2010 – May 2016
My dissertation examined the genomic response to environmental stress by experimentally evolving populations of budding yeast. Meiotic recombination plays a key role this response and we needed a fine-scale landscape of recombination "hotspots" to make sense of the data. As a part of my fellowship, I came up with a cost-effective way to infer genotypes from recombinant lines using sparse data (low-coverage sequence data). I created a Hidden Markov model solution that allowed us to save thousands of dollars in sequencing costs. I generalized my method and built an R package for use in the greater scientific community.
- **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 this package 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 and Scripting Languages.** In descending order of expertise: R, bash/linux, L^AT_EX, C++, Python, MySQL, Markdown, Mathematica, and Perl. Actively learning: JavaScript, Scala, php, Django.
- **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-diagnostic 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) and JavaScript-based applications (e.g., Apollo, anvi'o, Stacks) in my work flow.