

# Tyler Hether | Resume

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A well-rounded, recent graduate in bioinformatics and computational biology. Interested in combining biology, computer science, and big data to solve complex problems. Self-motivated, detail oriented person who also enjoys working together with a team.

## 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 ❖ Genetic Engineering ❖ 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

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- **Programming Languages.** In descending order of expertise: R, bash/linux,  $\text{\LaTeX}$ , C++, Python, Mathematica, and Perl. Actively learning: Java and Scala.
- **Industry Software Skills.** Most MS Office products including MS Word and MS Excel. Cloud-based word processing (Google Drive suite of tools).
- **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

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J. Degner, T. Hether, and E. Hoffman, "Eight novel tetranucleotide and five cross-species dinucleotide microsatellite loci for the ornate chorus frog (*pseudacris ornata*)," *Molecular Ecology Resources*, vol. 9, no. 2, pp. 622–624, 2009.

E. B. Rosenblum, B. A. Sarver, J. Brown, S. Des Roches, K. Hardwick, T. Hether, J. Eastman, M. Pennell, and L. Harmon, "Goldilocks meets santa rosalia: an ephemeral speciation model explains patterns of diversification across time scales," *Evolutionary biology*, pp. 1–7, 2012.

J. Degner, D. Silva, T. Hether, J. Daza, and E. Hoffman, "Fat frogs, mobile genes: unexpected phylogeographic patterns for the ornate chorus frog (*pseudacris ornata*)," *Molecular Ecology*, vol. 19, no. 12, pp. 2501–2515, 2010.

D. Jenkins, M. Carey, J. Czerniewska, J. Fletcher, T. Hether, A. Jones, S. Knight, J. Knox, T. Long, M. Mannino, *et al.*, "A meta-analysis of isolation by distance: relic or reference standard for landscape genetics?," *Ecography*, vol. 33, no. 2, pp. 315–320, 2010.

D. Abdoullaye, I. Acevedo, A. A. Adebayo, L.-Z. CAO, ..., T. Hether, *et al.*, "Permanent genetic resources added to molecular ecology resources database 1 august 2009–30 september 2009," *Molecular Ecology Resources*, vol. 10, no. 1, pp. 232–236, 2010.

T. Hether and E. Hoffman, "Machine learning identifies specific habitats associated with genetic connectivity in *hyla squirella*," *Journal of evolutionary biology*, vol. 25, no. 6, pp. 1039–1052, 2012.

T. Hether and P. Hohenlohe, "Genetic regulatory network motifs constrain adaptation through curvature in the landscape of mutational (co) variance," *Evolution*, vol. 68, no. 4, pp. 950–964, 2014.

B. Hand, T. Hether, R. Kovach, C. Muhlfeld, S. Amish, M. Boyer, S. O'rourke, M. Miller, W. Lowe, P. Hohenlohe, *et al.*, "Genomics and introgression: Discovery and mapping of thousands of species-diagnostic snps using rad sequencing," *Current Zoology*, vol. 61, no. 1, pp. 146–154, 2015.

## Other Interests & Extracurricular Activities

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- **Data transparency, open source code, and reproducibility.** The expression 'standing on the shoulders of giants' is most applicable in science and coding when you can actually use previous data and analytical tools.
- **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 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.