

# Tyler Hether | Resume

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🌐 <https://github.com/tylerhether>

Recent graduate in Bioinformatics and Computational Biology. Interested in the interface between biology, computer science, and math to solve real-world biological problems. Self-motivated person who also enjoys working together as a team.

## Previous Employment

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- **The University of Idaho** **Moscow, Idaho**  
*Research Assistant & Graduate Student* *August 2010–May 2016*  
I was a graduate student in the Bioinformatics & Computational Biology program under the tutelage of Paul Hohenlohe. I examined the genomic response to local adaptation by experimentally evolving populations of budding yeast (*Saccharomyces cerevisiae*), built a statistical toolkit (i.e., R package) for analyzing recombination rates in low-coverage sequence data, and expanded on classical models of quantitative genetics using a network theory paradigm.
- **The University of Central Florida** **Orlando, Florida**  
*Research Assistant & Graduate Student* *August 2007–July 2010*  
I primarily worked on using molecular techniques to isolate and characterize molecular markers (microsatellites) from a range of species. I also used machine learning techniques to identify likely habitats associated with genetic connectivity in frogs.

## Education

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### Academic Qualifications.....

- **Ph.D. | University of Idaho** **Moscow**  
*Bioinformatics & Computational Biology, Eugene Magelby Natural Sciences Scholar* *2010–2016*  
*Dissertation: "Genetic Networks, Adaptation, & the Evolution of Genomic Islands of Divergence"*
- **M.S. | University of Central Florida** **Orlando**  
*Biology* *2007–2010*  
*Thesis: "Using landscape genetics to assess population connectivity in a habitat generalist"*
- **B.S. | University of Central Florida** **Orlando**  
*Biology* *2004–2006*

### Notable Github Repositories.....

- **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 and Personal skills

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- **Programming Languages:** in descending order of expertise, R, bash/linux,  $\LaTeX$ , C++, Python, Mathematica, & Perl
- **Industry Software Skills:** Most MS Office products including MS Word and MS Excel. Cloud-based word processing (Google Drive suite of tools).
- **General Business Skills:** Good presentation skills, Works well in MS Powerpoint,  $\LaTeX$ 's Beamer class, and others.
- **Other:** Advanced R plotting skills using the ggplot2 library. 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.

## Interests and extra-curricular activity

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

## References

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- Up to 4 references available on request

## Scientific Publications

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- Summary: # of Citations = 157 | h-index = 5 | i10-index = 4
- For a list of publications, please visit <https://scholar.google.com/citations?user=St7QVnoAAAAJ&hl=en>