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.

Employment

University of Oregon   **Eugene, Oregon**
Postdoctoral Associate   *June 2016 – present*

I contribute to and create bioinformatic workflows and programming solutions for a range of population genomics problems including nematode genetic diversity and microbial metagenomics.

University of Idaho   **Moscow, Idaho**
Research Assistant & Graduate Student   *August 2010 – May 2016*

I examined the genomic response to local adaptation by experimentally evolving populations of budding yeast (*Saccharomyces cerevisiae*), 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 used molecular techniques to isolate and characterize molecular markers (microsatellites) from a range of species. I also used machine learning algorithms to identify likely habitats associated with genetic connectivity in frogs under a landscape genetics framework.

Education

Ph.D. | University of Idaho   **Moscow**
Bioinformatics & Computational Biology, Eugene Magelby Natural Sciences Scholar   *2016*
Dissertation: "Genetic Networks, Adaptation, & the Evolution of Genomic Islands of Divergence"

M.S. | University of Central Florida   **Orlando**
Biology   *2010*
Thesis: "Using landscape genetics to assess population connectivity in a habitat generalist"

B.S. | University of Central Florida   **Orlando**
Biology   *2006*

Products

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.

○ **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 and LaTeX's Beamer class.

○ **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.

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 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.

Scientific Publications

○ **Summary.** # first authored = 4 | # co-authored = 5 | # citations = 175 | h-index = 6

○ **Details.** Please click or visit *https://scholar.google.com/citations?user=St7QVnoAAAAJ&hl=en*