Tyler Hether | Resume

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I'm a well-rounded data scientist with interests in problem solving, reproducibility, tool development, data analysis, and visualization. My background is in population genomics so I'm comfortable gaining insights from messy, high-dimensional and large datasets. I think my greatest attributes are the ability to quickly pick up new skills/languages and applying old skills to novel problems. I have three years of industry experience working in a fast-paced startup environment. I'm a self-motivated, question driven and detail oriented person who enjoys working together with a team to create solutions to a wide-variety of data science 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, 2006

Employment

- **Adaptive Biotechnologies Corp.** — Seattle, Washington
  Computational Biologist — March 2017 – present
  To expedite quicker turnaround times of new assay development, I create cloud-based computational tools for R&D. In addition, I design algorithms to better understand the complex profile of V(D)J recombination seen in B- and T-cell receptors. I also had a external-facing role where I analyzed data from ongoing clinical trials and presented these findings to our Pharmaceutical clients.
- **University of Oregon** — Eugene, Oregon
  Postdoctoral Associate — June 2016 – March 2017
  To better foster scientific discovery, I administered an Apollo (Jbrowse) genome browser on a cloud-based linux web server. I also solved bioinformatic challenges for lab members by designing experiments and providing statistical consultations, creating programming solutions, and employing complete end-to-end data analysis.
- **University of Idaho** — Moscow, Idaho
  Research Assistant & Graduate Fellow — August 2010 – May 2016
  I slashed the molecular biology budget by creating an R package for imputing missing genotypes from genetic recombinants using Hidden Markov models on low-coverage next-generation sequencing.
- **University of Central Florida** — Orlando, Florida
  Research Assistant & Graduate Student — August 2007 – July 2010
  I elucidated geospatial correlates to population genetic connectivity using machine learning algorithms.

Expertise and Interests

Data Science ❖ Reproducibility ❖ Immunology ❖ B-cell & T-cell sequencing ❖ Recombination ❖ Docker and Containerization ❖ HMMs ❖ Genotype to Phenotype ❖ Rcpp ❖ Genetic Architecture ❖ Data Visualization ❖ Quantitative Genetics

Public Repositories 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, Python, bash/linux, LaTeX, C++, Markdown, Rmarkdown, jupyter notebooks, SQL, and a working understanding of Perl.
- **Other.** Experience with high performance computing on clusters, Rcpp, and reproducibility of documents. Experience creating pipelines and workflows to automate tasks. Experience presenting and disseminating findings at scientific conferences as well as in smaller groups and one-on-one. Experience with explaining complex processes to both technical and non-technical audiences.

Select Publications

- Thompson, P.A., Srivastava J., Peterson C., Strati P., Jorgensen J.L., **Hether, T.**, Keating M.J., O'Brien S.M., Ferrajoli A., Burger J.A., Estrov Z., Jain N., Wierda W.G. Minimal residual disease undetectable by next-generation sequencing predicts improved outcome in CLL after chemoimmunotherapy. Blood 134 (22): 1951-1959
- DiPaolo R.J., **Hether, T.**, Gilchuk P., Kumar A., Rajeh A., Schiebout C., Maybruck J., Buller R.M., Ahn T.H., Joyce S. Identifying and tracking low-frequency virus-specific TCR clonotypes using high-throughput sequencing. Cell Reports 25 (9): 2269-2378
- 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.