

Tyler Duncan Hether

University of Idaho
Bioinformatics & Computational Biology
Life Sciences South 441D
PO Box 443051, Moscow, ID. 83844-3051

Phone: (208) 301-3259
Fax: (208) 885-7905
Email: tyler.hether@gmail.com
Source Code: <https://github.com/tylerhether>

Education

Ph.D. Bioinformatics & Computational Biology, University of Idaho. 2016

Dissertation: "Genetic Networks, Adaptation, & the Evolution of Genomic Islands of Divergence".

M.S. Biology, University of Central Florida. 2010

Thesis: "Using landscape genetics to assess population connectivity in a habitat generalist".

B.S. Biology, University of Central Florida. 2006

Programming & Scripting Languages (in descending order of expertise)

R, bash/linux, \LaTeX , C++, python, mathematica, & perl

Employment

University of Idaho 2010–present.

University of Central Florida 2006–2010.

Grants & Fellowships Awarded

Eugene Magelby Natural Sciences Scholarship, 2015–2016

NSF DDIG "The role of genetic interactions in adaptation", 2014–2016

Bioinformatics & Computational Biology Fellowship "Develop computational tools to analyze recombination rate variation from low-coverage sequence data", 2014–2016

NSF BEACON Graduate Fellowship "The Genetic Architecture of Multi-dimensional Adaptation & Speciation", 2011–2013

Sigma Xi Grants-in-Aid of Research "Evaluating the role of landscape features on gene flow", 2008–2009

Selected Publications*

*for full list, please visit <https://scholar.google.com/citations?user=St7QVnoAAAAJ&hl=en>

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.

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

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.

Selected Talks

Evo-Wibo. Presentation title: "Evolving genomic islands from standing genetic variation: an experimental approach with the budding yeast". Primary author, 2016.

BEACON seminar series. Talk title: "Recombination rate and gene conversion heterogeneity: implications for 'genomic islands' of divergence". Primary author, 2013.

Evolution. *Hamilton Award Nominee*. Presentation Title: "Genetic regulatory motifs constrain adaptation through curvature in the landscape of mutational variation" Primary author, 2013.

IBEST Science Exposition, University of Idaho. Poster Title: "Spatial autocorrelation structure of genomic sequence divergence under neutrality using coalescent simulations" Contributing author, 2012.

Seventh Annual Southeastern Ecology and Evolution Conference (SEEC), Atlanta, Georgia. Presentation Title: "Using landscape genetics to evaluate habitat permeability in an abundant frog" Primary author, 2010.

Evolution. Presentation Title: "Testing for selection along a cline of color change in a polymorphic frog" Contributing author, 2008.

Journal Referee

Biological Journal of the Linnean Society, *Evolution*, & *Molecular Ecology*

Last updated: April 28, 2016

<https://sites.google.com/site/buddingyeastbiologist/>