

# Thomas E. Keller

Computational Biologist and Data Scientist

## contact

Atlanta  
30318  
USA

thomas.e.keller  
@gmail.com  
www.linkedin.com/  
in/thomasekeller  
@tek\_keller (Twitter)  
thomas-keller (Github)  
Google Scholar  
thomas-keller.github.io  
(Personal Website)

## programming

Python, R, Spark  
Cython, C,  
Mathematica,  
C++, MATLAB,  
SAS, Perl

## education

2012	<b>Ph.D.</b> Integrative Biology Drs James J. Bull and Claus O. Wilke, advisers	University of Texas at Austin
2005	<b>B.Sc.</b> Zoology, with honors	University of Florida

## professional experience

Sep. 2016-Mar. 2017	<b>Georgia Institute of Technology, Atlanta</b> Developing pipelines and methodology for applying machine-learning techniques to epigenomic datasets to identify candidate biomarkers for schizophrenia. Approaches include clustering and dimension reduction (KNN, PCA), and for downstream analysis logistic regression, random forests, and support vector machines (SVM).	Research Technician IV
2012-2016	<b>Georgia Institute of Technology</b> Responsibilities included writing software to conduct NSF-funded research and mentoring students. Efficiently processing data for these projects required the use of a computer cluster, which meant I learned a bit about distributed systems. Data collection was done primarily with Python. Statistical analyses and figures for analyses for publication were done with R and Bioconductor. Total scientific output will be three first author and two co-author papers.	Postdoctoral Fellow
2006-2012	<b>University of Texas at Austin</b> Responsibilities included supervising undergraduates and working on NIH-funded research and preparing results for publication. In addition I was a teaching assistant for a survey course on biology for non-majors as well as an introduction to computational biology. Simulation code and data collection was primarily in Python or Cython. Statistical analyses and figures for analyses for publication were performed with R and Bioconductor. Total scientific output was three first-author and two co-author publications.	Research and Teaching Assistant
2004-2005	<b>University of Florida, Gainesville</b> Assisted in mutation accumulation experiments with <i>C. elegans</i> and other nematodes that investigated how fitness declines as deleterious mutations accumulate in the absence of negative selection. Research resulted in three co-authored publications.	Lab Technician

## publications

1. L. Hagen, **T. E. Keller**, S. Neely, N. DePaula, C. Cooperman. Crisis Communications in the Age of Social Media: A Network Analysis of Zika-Related Tweets. In Press, *Social Science Computer Review*.
2. I. Mendizabal, J. Zeng, **T. E. Keller**, S. V. Yi. Body-hypomethylated human genes harbor extensive intragenic transcriptional activity and are prone to cancer-associated dysregulation. *Nucleic Acids Research*, doi 10.1093/nar/gkx020 .

3. I. Mendizabal, L. Shi, **T. E. Keller**, G. Konopka, T. M. Preuss, T. Tsieh, E. Hu, Z. Zhang, B. Su, S. V. Yi. Comparative methylome analyses reveal epigenetic loci implicated in transcription regulation of human brains. *Molecular Biology and Evolution*, 33: 2947–2959, 2016.
4. **T. E. Keller**, J. E. Lasky, S. V. Yi. The multivariate association between genome-wide DNA methylation and climate across the range of *Arabidopsis thaliana*. *Molecular Ecology* 25:1823–1837, 2016.
5. **T. E. Keller**, P. Han\*, S. V. Yi. Evolutionary transition of promoter and gene body DNA methylation across invertebrate-vertebrate boundary. *Molecular Biology and Evolution* 33:1019–1028, 2016.
6. I. Mendizabal, **T. E. Keller**, J. Zeng, S. V. Yi. Epigenetics and evolution. *Integrative and Comparative Biology* 54:31–42, 2014.
7. **T. E. Keller**, S. V. Yi. DNA methylation and evolution of duplicate genes. *Proceedings of the National Academy of Sciences* 111:5932–5937, 2014.
8. **T. E. Keller**, C. O. Wilke, J. J. Bull. Interactions between evolutionary processes at high mutation rates. *Evolution* 66:2303–2314, 2012.
9. **T. E. Keller**, S. D. Mis\*, K. E. Jia\*, C. O. Wilke. Reduced mRNA secondary-structure stability near the start codon indicates functional genes in prokaryotes. *Genome Biology and Evolution* 4:80–88, 2012.
10. E. B. O'Dea, **T. E. Keller**, C. O. Wilke. Does mutational robustness inhibit extinction by lethal mutagenesis in viral populations? *PLoS Computational Biology* 6:e1000811, 2010.
11. R. Springman, **T. Keller**, I. Molineux, J. J. Bull. Evolution at a high imposed mutation rate: adaptation obscures the load in Phage T7. *Genetics* 184:221–232, 2010.
12. M. P. Salomon, D. Ostrow, N. Phillips, D. Blanton\*, W. Bour\*, **T. E. Keller\***, L. Levy\*, T. Sylvestre\*, A. Upadhyay\*, C. F. Baer. Comparing mutational and standing genetic variability for fitness and size in *Caenorhabditis briggsae* and *C. elegans*. *Genetics* 183:685–92, 2009.
13. **T. E. Keller**, I. J. Molineux, J. J. Bull. Viral resistance evolution fully escapes a rationally designed lethal inhibitor. *Molecular Biology and Evolution* 26:2041–46, 2009.
14. D. Ostrow, N. Phillips, A. Avalos\*, D. Blanton\*, A. Boggs\*, **T. Keller\***, L. Levy\*, J. Rosenbloom, C. F. Baer. Mutational bias for body size in rhabditid nematodes. *Genetics* 176:1653–61, 2007.
15. C. F. Baer, N. Phillips, D. Ostrow, A. Avalos\*, D. Blanton\*, A. Boggs\*, **T. Keller\***, L. Levy\*, E. Mezerhane\*. Cumulative effects of spontaneous mutations for fitness in *Caenorhabditis*: role of genotype, environment and stress. *Genetics* 174:1387–95, 2006.

\* Undergraduate co-author

## conference presentations

- Multivariate associations between climate and genome-wide methylation in European *Arabidopsis* panels.
  - International Evolution Society Conference, Austin, Tx, 2016.
- Evolution in actin: a protein family drama.
  - International Evolution Society Conference, Norman, OK, 2011.
- Interactions between evolutionary processes at high mutation rates.
  - International Evolution Society Conference, Portland, OR, 2010.
- Quasispecies adapts to overcome mutation load: a problem for lethal mutagenesis?
  - Gordon Conference for Microbial Population Genetics, Andover, NH, 2009.
- Evolution at high mutation rates: not as bad as we think.
  - International Evolution Society Conference, Minneapolis, MN, 2008.

## conference posters

- DNA methylation and the evolutionary divergence of duplicate genes.
  - Society for Molecular Biology and Evolution, San Juan, Puerto Rico, 2014.
- Divergence of methylation maps in humans and higher primates.
  - International Conference on Bioinformatics, Atlanta, GA, 2013.

## mentoring

Supervised four undergraduate students and one high school student, which led to two publications.  
Supervised one Master's student August 2014- August 2015.

## professional activities

- Member, Society for the Study of Evolution, 2008–Present.
- Member Society for Molecular Biology and Evolution 2013–Present.

## professional service

- Reviewer, BMC Evolutionary Biology
- Reviewer, Evolutionary Applications
- Reviewer, Genome Research
- Reviewer, PLoS Computational Biology
- Reviewer, Scientific Reports

## honors, awards, & fellowships

- National Science Foundation Graduate Student Fellowship (Honorable Mention), 2007.
- National Science Foundation Graduate Student Fellowship (Honorable Mention), 2006.
- Houston Rodeo Fellowship, University of Texas at Austin, 2006.