sethtem@umich.edu
linkedin.com/sdtemple

Seth Temple, Ph.D. in Statistics

Machine learning methods for biological and environmental data

EDUCATION

Ph.D., M.S., Statistics, University of Washington 2019 – 2024

- Eric and Wendy Schmidt AI in Science Postdoctoral Fellowship
- National Defense Science and Engineering Graduate Fellowship (**2% selection rate**, 3-year funding)
- Z.W. Birnbaum Award for the **best Ph.D. candidate exam** in the academic year
- NIH Trainee award in Statistical Genetics

B.S., Mathematics (summa cum laude), University of Oregon 2014 – 2018

Actuarial Exams: Modern Statistics (9/10), Financial Mathematics (10/10), Probability (8/10)

SKILLS

- Python (torch, keras), git, slurm, Unix, R, Snakemake (expert); SQL, C++ (intermediate)
- Spatial and time series, Bayesian models, Bioinformatics, Networks, Software Dev, Algorithms, NLP
- 6 years teaching, including instructor for statistics course of 30 students + mentoring 4 undergraduates

ACADEMIC AND INDUSTRY EXPERIENCE

Postdoctoral Researcher, University of Michigan 09/24 – Present

- Developing computer vision and state space models for **sparse classification** in bioacoustics
- Building a **software and AI models repository** and workshop for postdoctoral researchers
- Studying statistical estimators in the (separate) domains of genetic relatedness and epidemics

Graduate Student Researcher, University of Washington 2019 – 2024

- Created a **suite of methods** to pinpoint selectively advantageous alleles and quantify their effect
- Designed a **fast simulation algorithm** versus alternatives that are intractable at biobank-scale
- Detected phenotypic **case-control associations** and evidence of natural selection on immune response while proposing and validating significance levels that **protect against false discoveries**
- Performed 9 WGS & SNP array analyses, including 5 ancestry groups, ranging up to 500k samples
- Published **five first-author papers** and one coauthor paper

Graduate Student Researcher, Fred Hutchinson Cancer Research Center 06/23 – 12/23

- Identified and clustered SARS-CoV-2 variants based on **signatures of virus adaptation over time**
- Collaborated on an international project modeling genomic patterns of synonymous mutations

Graduate Student Researcher, Los Alamos National Laboratory 06/20 – 10/20

- Introduced and implemented a **Bayesian spatial model** for mosquito-borne epidemiology
- Developed software to predict and visualize mosquito prevalence in North and South America
- Published **one first-author paper** and one coauthor paper

Actuarial Intern/Assistant, Liberty Mutual Insurance, (18 total months) 2017 – 2019

- Integrated data visualization tools with **ratemaking for weather and climate-based risks**
- Modernized **SQL queries**, modeled surety risks, and automated aspects of quarterly reserving

Natural Language Processing Research Assistant, University of Oregon 01/18 – 06/18

- Built RNNs with keras/tensorflow to predict stop words in processed audio of disabled students

sethtem@umich.edu
linkedin.com/sdtemple

SOFTWARE DEVELOPMENT

https://github.com/sdtemple/isweep: Python package supporting **five research article**s and containing **five automated pipelines** for genomic analyses of natural selection in as many as 500k samples

https://github.com/sdtemple/flare-pipeline: automatic pipeline using Python and R to haplotype phase and determine ancestry in Alzheimer's Disease Sequencing Project (**TBs disk memory, 100s GB RAM, 10s CPUs)**

https://github.com/sdtemple/btvoccu: **R for Bayesian regression** in epidemiology with missing data

https://github.com/sdtemple/pblas: R for simulation and estimation in SIR epidemiology model

PUBLICATIONS

First-author:

1. **Temple, S.D.**, & Thompson, E.A. Identity-by-descent segments in large samples. *Theoretical Population Biology* (2025).
2. **Temple, S.D.**, Browning, S.R., & Thompson E.A. Fast simulation of identity-by-descent segments. *Bulletin of Mathematical Biology* (2025).
3. **Temple, S.D.**, Waples, R.K., & Browning, S.R. Modeling recent positive selection using identity-by-descent segments. *The American Journal of Human Genetics* (2024).
4. **Temple, S.D.**, Manore, C.A. & Kaufeld, K.A. Bayesian time-varying occupancy model for West Nile virus in Ontario, Canada. *Stoch Environ Res Risk Assess* (2022).
5. **Temple, S.D.**, & Browning, S.R. Multiple-testing corrections in selection scans using identity-by-descent segments. *bioRxiv* (2025). https://www.biorxiv.org/content/10.1101/2025.01.29.635528v1
6. **Temple, S.D.**, et. al. Multiple-testing corrections in case-control studies using identity-by-descent segments. *bioRxiv* (2025). https://www.biorxiv.org/content/10.1101/2025.07.03.663057v1
7. **Temple, S.D.** Statistical Inference Using Identity-by-Descent Segments: Perspectives on Recent Positive Selection. *University of Washington* (Ph.D. thesis; 2024).
8. **Temple, S.D.** The Tweedie Index Parameter and Its Estimators: An Introduction with Applications to Actuarial Ratemaking. *University of Oregon* (B.S. Honors thesis; 2018).

Collaborations:

1. Haddox, H.K., Angehrn, G., Sesta, L., Jennings-Shaffer, C., **Temple, S.D.**, et. al. SARS-CoV-2's mutation rate is highly variable between sites and is influenced by sequence context, genomic region, and RNA structure. *Nucleic Acids Research* (2025)
2. Gorris, M.E., Bartlow, A.W., **Temple, S.D.**, et al. Updated distribution maps of predominant Culex mosquitoes across the Americas. *Parasites & Vectors* 14, 547 (2021).
3. Horimoto, A.R.V.R., Boyken, L.A., Blue, E.E., **et al.** Admixture mapping implicates 13q33.3 as ancestry-of-origin locus for Alzheimer disease in Hispanic and Latino populations. *HGG Advances* 4 (3) (2023): 100207.