Seth Temple, Ph.D. in Statistics

Modeling in evolution and epidemiology using rigorous statistics

About Me: I have developed several interpretable, computationally efficient, and robust statistical methods for challenging problems in biology. Much of my work involves modeling spatiotemporal processes in limited data scenarios or in the face of complex correlation structures. I am interested in extending my expertise to problems at the intersection of machine learning and health. In internships, collaborations, and consultations, I have quickly learned new application areas to offer valuable statistical insights to research teams. I have been recognized for my ability to communicate complex scientific topics clearly and effectively.

EXPERIENCE

Post-doctoral Fellow, Schmidt AI in Science, **University of Michigan** 2024–2025

- Developing probabilistic deep learning models to simulate publicly available genetic data that is representative of a population sample but protects individual privacy
- Working group on physics-informed neural networks in basic science

Researcher, **University of Washington** 2019–2024

- Proposed multiple-testing corrections in detecting evidence of natural selection and phenotypic case-control associations
- Proved central limit theorems in light of correlations from unobserved genealogies
- Developed a suite of methods to model selection with uncertainty and infer causal alleles
- Developed a linear runtime algorithm versus worse-case quadratic runtime
- Assistantship on Gaussian mixture models for genetic ancestry

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

- Developed a novel method to detect and cluster adaptive SARS-CoV-2 variants based on amino acid mutation counts over time
- Provided feedback on machine learning models for non-neutral synonymous mutations

Researcher, **Los Alamos National Laboratory** 06/30–10/20

- Extended Gibbs sampler for Bayesian spatiotemporal regression in specific missing data mechanism in mosquito-borne epidemiology
- Developed and visualized predictive maps for mosquito prevalence

Actuary Trainee, Liberty Mutual Insurance 06/17–09/17, 07/18–08/19

EDUCATION

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

- NDSEG Fellow, NIH Trainee in Statistical Genetics
- Advisors: Sharon Browning and Elizabeth Thompson

B.S., Mathematics, *Summa cum laude*, **University of Oregon** 2014– 2018

SKILLS

Excellent presentations: Z.W. Birnbaum Award, WNAR conference award, Seattle Science Slam

6+ years teaching/tutoring, including as the lead instructor of a graduate course

Coding: Python + Snakemake and R (expert), C++, SQL, and bash (intermediate)

Computing: slurm and qsub clusters, terabytes of genetic sequence data

SOFTWARE

https://github.com/sdtemple/isweep: extensively documented Python package supporting 5 research articles and containing 4 automated pipelines for large-scale genomic analyses of natural selection.

https://github.com/sdtemple/flare-pipeline: automatic pipeline using Python and R for preliminary analyses in genomic analyses that require Tb's disk memory, 100's Gb RAM, and 10's CPUs on slurm clusters.

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

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

PUBLICATIONS

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). https://doi.org/10.1016/j.ajhg.2024.08.023.

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). https://doi.org/10.1007/s00477-022-02257-4

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

Temple, S.D., & Thompson, E.A. Identity-by-descent in large samples. *bioRxiv* (2024). https://www.biorxiv.org/content/10.1101/2024.06.05.597656v2

Temple, S.D., Browning, S.R., & Thompson, E.A. Fast simulation of identity-by-descent segments. bioRxiv (2024). https://www.biorxiv.org/content/10.1101/2024.12.13.628449v1

Temple, S.D. Statistical Inference using Identity-by-Descent Segments: Perspectives on Recent Positive Selection. PhD thesis. University of Washington (2024). https://www.proquest.com/docview/3105584569

Temple, S.D. The Tweedie Index Parameter and Its Estimator. Bachelor's thesis. University of Oregon (2018). https://scholarsbank.uoregon.edu/xmlui/handle/1794/29040

Writing in progress:

Temple, S.D., Chapman, N., Thornton, T.A., Wijsman, E.M., & Blue, E.E. Multiple-testing corrections in case-control studies using identity-by-descent segments.

Collaborations:

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). https://doi.org/10.1186/s13071-021-05051-3.

Haddox, H.K., Angehrn, G., Sesta, L., Jennings-Shaffer, C., **Temple, S.D.**, Galloway, J.G., DeWitt, W.S., Matsen IV, F.A., & Neher, R.A. SARS-CoV-2's mutation rate is highly variable between sites and is influenced by sequence context, genomic region, and RNA structure. *bioRxiv* (2025). https://www.biorxiv.org/content/10.1101/2025.01.07.631013v1

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.