

## Seth Temple, Ph.D. in Statistics

Modeling in evolution and epidemiology using rigorous statistics

**About Me:** I develop interpretable, computationally efficient, and robust machine learning methods to address challenging problems in biology. My research involves modeling spatiotemporal or genetic processes in limited data scenarios or in the face of complex correlation structures. In internships and collaborations, I have quickly learned new application areas to offer statistical insights to research teams. I have been recognized for communicating complex scientific topics clearly and effectively.

### PROFESSIONAL EXPERIENCE

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Postdoctoral Fellow, Schmidt AI in Science, University of Michigan 2024 – 2025

- Improving haplotype phasing and genealogy inference with deep learning
- Propose and evaluate estimators for infection rates in school and island populations
- Working group on theoretically-informed neural networks in basic science

Graduate Student Researcher, University of Washington 2019 – 2024

- Proposed **multiple-testing** corrections in detecting evidence of natural selection and phenotypic case-control associations
- Created new statistical methods to model selection with uncertainty and infer causal alleles
- Proved **central limit theorems** in light of correlations from unobserved genealogies
- Designed a **linear runtime algorithm** versus worse-case quadratic runtime
- Improved flexibility of a genetic ancestry method with Gaussian mixture modeling

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

- Pioneered a novel method to **detect and cluster** adaptive SARS-CoV-2 variants based on amino acid mutation **counts over time**
- Provided statistical expertise to collaboration modeling SARS-CoV-2 evolution

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

- Introduced and implemented a fast sampling routine for **Bayesian spatial regression** given a **missing data** mechanism in mosquito-borne epidemiology
- Developed software to predict and visualize mosquito prevalence in North America

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

### EDUCATION

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

- NDSEG Fellow, Z.W. Birnbaum Award, NIH Trainee in Statistical Genetics
- Advisors: Sharon Browning and Elizabeth Thompson

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

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

### SKILLS

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Communication: 6 years teaching, including **lead instructor for graduate course of 30 students**

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

## SOFTWARE DEVELOPMENT

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

<https://github.com/sdtemple/flare-pipeline>: automatic pipeline using Python and R for analyses in genomic analyses that require **TB's disk memory, 100's GB RAM, and 10's 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

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**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).

**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 segments 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.**, Manore, C.A. & Kaufeld, K.A. Bayesian time-varying occupancy model for West Nile virus in Ontario, Canada. *Stoch Environ Res Risk Assess* (2022).

**Temple, S.D.** Statistical Inference Using Identity-by-Descent Segments: Perspectives on Recent Positive Selection. *University of Washington* (Ph.D. thesis; 2024).

**Temple, S.D.** The Tweedie Index Parameter and Its Estimators: An Introduction with Applications to Actuarial Ratemaking. *University of Oregon* (B.S. Honors thesis; 2024).

### 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. (*In preparation for The American Journal of Human Genetics*)

### Collaborations:

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.

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).

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