Seth Temple, PhD

Statistician, Geneticist

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https://github.com/sdtemple

Objective: Analytical solutions to scientific problems in simple, creative, & reproducible ways

Specialties: random processes, uncertainty quantification, correlation, evolution, epidemiology

EXPERIENCE

Schmidt AI in Science Fellow, University of Michigan   2024 - 2025

Researcher, University of Washington   2019 - 2024

- Developed methods and theory to study recent genetic evolution
- Conducted enormous, extensive, and runtime efficient simulation studies
- Consulted Alzheimer's research group on experimental designs of association studies
- Taught experimental design, regression, machine learning, and statistical genetics

Researcher, Fred Hutchinson Cancer Research Center   June '23 – Dec '23

- Developed methods for anomaly detection & time series clustering in SARS-COV-2
- Collaborated on models for non-neutral effects of synonymous mutations

Researcher, Los Alamos National Laboratory   June '20 – October '20

- Modeled spatial & temporal effects on mosquito-borne disease w/ missing data
- Applied machine learning to map & visualize geography of mosquitos

Actuary Trainee, Liberty Mutual Insurance   Sum. '17, July 18' – Aug '19

- Automated and documented reserving analyses in SQL, Excel, and SAS
- Modeled pricing in light of environmental catastrophes and spatial adjacency

EDUCATION

PhD, MS, Statistics, University of Washington   2019 - 2024
- NDSEG Fellow, NIH Trainee in Statistical Genetics
- Advisors: Sharon Browning and Elizabeth Thompson

BS, Mathematics, *Summa cum laude,* University of Oregon   2014 - 2018

SKILLS

Soft skills:

- Excellence in research presentation: Z.W. Birnbaum Award + WNAR conference award
- 6+ years teaching and tutoring, including as graduate course lead instructor
- 2+ years consulting for and collaboration with non-statisticians

Technical skills:

- Package development using Python (expert) or R (expert)
- Reproducible bioinformatics pipelines using Snakemake
- Other software/languages: Bash, git, Excel, SQL, C++
- Cluster computing using slurm or qsub

PUBLICATIONS [(Google Scholar)](...)

Temple, S.D., Waples, R.K., & Browing, S.R. Modeling recent positive selection using identity-by-descent segments. *bioRxiv* (2023). https://www.biorxiv.org/content/10.1101/2023.11.13.566947v2. In peer-review.

Temple, S.D., & Thompson, E.A. Identity-by-descent in large samples. *bioRxiv* (2024). https://www.biorxiv.org/content/10.1101/2024.06.05.597656v1. In peer-review.

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.

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

Temple, S.D. Statistical inference using identity-by-descent segments: perspectives on positive selection. University of Washington (2024). Dissertation sent to committee.

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

Horimoto, Andrea R. V. R., Lisa A. Boyken, Elizabeth E. Blue, Kelsey E. Grinde, Rafael A. Nafikov, Harkirat K. Sohi, Alejandro Q. Nato Jr, 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.

SOFTWARE

https://github.com/sdtemple/isweep: extensively documented Python package and bioinformatics pipelines; statistical inference of recent positive selection

https://github.com/sdtemple/flare-pipeline: bioinformatics pipeline for large sample whole genome analyses; haplotype phasing and local ancestry inference

https://github.com/sdtemple/btvoccu: R package for Bayesian logistic regression modeling in epidemiology w/ specific missing data scenario

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