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Seth Temple, Ph.D. in Statistics

Pioneering machine learning methods for evolution & genetic epidemiology

About Me: I study genetic patterns, their changes, and their disease impact. To address domain challenges where data is large and signals cryptic, I develop <u>interpretable, computationally efficient, and robust statistical methods</u>. As a researcher, I have quickly learned new application areas and offered key insights to multidisciplinary teams. I have been recognized for <u>communicating complex scientific topics clearly and effectively</u>.

EDUCATION

Ph.D., M.S., Statistics, University of Washington   2019 – 2024
- Z.W. Birnbaum Award for the **best Ph.D. candidate exam** in the academic year
- National Defense Science and Engineering Graduate Fellowship (**2% selection rate**, 3-year funding)
- National Institutes of Health Trainee in Statistical Genetics

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

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

SKILLS

Formulating projects, developing methodology, planning and executing analyses, and reporting scientific results

Communication: 6 years teaching/tutoring, including **instructor for graduate statistics course of 30 students**

Coding: Python, Snakemake, R, Unix/bash, git version control, slurm cluster (expert); C++, SQL (intermediate)

ACADEMIC AND INDUSTRY EXPERIENCE

Postdoctoral Researcher, Schmidt AI in Science, University of Michigan   09/24 – Present
- Improving haplotype **phasing—a crucial first step** in genetic analyses—with deep learning
- Planning software and AI models workspace and workshops for postdoctoral researchers
- Proposing and evaluating estimators for infection rates in schools

Graduate Student Researcher, University of Washington   2019 – 2024
- Performed 9 **WGS & SNP array** analyses, including **5 ancestry groups**, ranging from 1k to **500k samples** (e.g., United Kingdom Biobank, TOPMed consortium, and Alzheimer's Disease Sequencing Project)
- Detected **phenotypic case-control associations** and evidence of **natural selection on immune response** while proposing and validating significance levels that protect against false discoveries
- Created a suite of methods to **pinpoint selectively advantageous alleles** and quantify their effect
- Enhanced a genetic admixture method to accommodate more ancestry reference groups
- Proved statistical guarantees that help **calibrate and measure uncertainty in genetic analyses**
- Designed a **fast simulation algorithm** versus alternatives intractable at biobank-scale

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

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

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

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SOFTWARE DEVELOPMENT

https://github.com/sdtemple/isweep: Python package supporting **5 research article**s and containing **5 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 phase and determine ancestry in Alzheimer's Disease Sequencing Project, requiring **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

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
(Under review at *The American Journal of Human Genetics*)

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
(Under review at *Theoretical Population Biology*)

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
(Under review at *Bulletin of Mathematical Biology*)

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).

In preparation:

Temple, S.D., Chapman, N.H., Thornton, T.A., Wijsman, E.M., & Blue, E.E. Multiple-testing corrections in case-control studies using identity-by-descent segments.
(Full manuscript sent to co-authors for submission to *The American Journal of Human Genetics*)

Collaborations:

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. *bioRxiv* (2025). https://www.biorxiv.org/content/10.1101/2025.01.07.631013v1
(Under review at *Nucleic Acids Research*)

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).