

---

# Nikolai G. Vetr

---

✉ [nikgvetr@stanford.edu](mailto:nikgvetr@stanford.edu) | ☎ +1 (602) 578-9196 | [in linkedin.com/in/nikolai-vetr](https://www.linkedin.com/in/nikolai-vetr) | [github.com/NikVetr](https://github.com/NikVetr)  
⚙ [vetr.dev](https://vetr.dev) | 🎓 [Nikolai Vetr](#) | 📄 [Full CV](#) | 📍 Redwood City, CA

## Summary

---

Computational biologist and data scientist focused on Bayesian statistics, multi-omic data integration, and machine learning methods development. Extensive experience developing and evaluating novel statistical models, visualizations, and computational tools to address complex biological questions across varied domains.

## Education

---

- PhD University of California, Davis** 2020  
*Anthropology + Population Biology + Data Science & Informatics*  
Dissertation: “Exploring and Extending Multivariate Brownian Diffusion Models of Phenotypic Evolution for Bayesian Phylogenetic Inference”
- BA Vanderbilt University** 2013  
*Earth & Environmental Sciences + Ecology, Evolution & Organismal Biology*  
– Departmental Honors, *summa cum laude*

## Experience

---

- Stanford University** – Postdoctoral Researcher Stanford, CA | 2020 – Present  
*Montgomery & Wheeler Labs (Pathology, Genetics, Biomedical Data Science)*
- Integrated differential expression results with drug, perturbation target, and biobank databases with approx. 1TB of input data to provide causal inferential insights into the results of a large-scale animal experiment (*Nat. Comms.*, 2024).
  - Made key contributions to multi-omic analysis (GWAS, eQTL, transcriptomics, proteomics, ATAC-seq) of exercise response data for the MoTrPAC, identifying molecular transducers of physical activity (*Nature*, 2024).
  - Developed novel Bayesian probability models and analysis pipelines for differential allele-specific expression analysis in ovarian cancer using high-depth mmPCR-seq (*ASHG*, 2024).
  - Derived and implemented powerful and efficient computational methods for Bayesian data analysis, including novel correlation matrix prior and proposal distributions, efficient model reparameterizations, and code translation utilities.
    - Runtime and power improved by multiple orders of magnitude vs. conventional parameterizations on typical datasets (eg 10-50x for multilevel GLMs with K = 3 sets of “random intercepts”, contingency tensors, iterated filtration enrichment estimation).
- Rethink Priorities** – Board President / Director Global | 2023 – Present
- Led Board of Directors for research non-profit focused on cause prioritization, overseeing strategic direction, executive performance, and financial governance, leveraging data modeling skills (eg time series of fundraising performance).
  - Provided statistical consulting on Bayesian modeling, causal inference, and data analysis for projects spanning GenAI, global health, survey response data, and computational biology.
- University of California, Davis** – Instructor / Consultant Davis, CA | 2015 – 2020
- Developed and delivered lectures, labs, and assessments for upper-division courses in Human and Primate Biology.
  - Founded and led interdisciplinary *Applied Bayesian Statistics Research Cluster* (70+ members), providing training and consultation on Bayesian and Deep Learning methods to the academic research community.
  - Led workshops and served as a certified Carpentries instructor, teaching coding and data science skills to researchers.
  - Won multiple awards for biology and data science outreach and teaching activities.

## Technical Skills

---

**Programming:** R, Stan, BASH, Python, C++, JS, Git, AWS, RevBayes

**Statistical / ML Methods:** Bayesian Inference, Monte Carlo Methods, Multilevel Models, GLMs / GLMMs, Time Series Analysis, Causal Inference, Optimization, Computer Vision, NLP, Measurement Error, Sparse Estimation, Outlier Detection, Signal Processing, Spatial Autocorrelation, Missing Data Imputation, ODEs, D/CTMCs

**Bioinformatics:** Multi-omic Data Integration (Genomics, Transcriptomics, Proteomics, Epigenomics), Association Mapping, ASE Analysis, Population and Quantitative Genetics, Interactive / Dynamic Data Visualization, HPC

**Domain Knowledge:** Molecular Biology, Human Genetics, Exercise Physiology, Evolutionary Biology, Human Anatomy

**Languages:** English (Native), Russian (Native), Spanish (Proficient)