

Nikolai Vetr

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EDUCATION AND TRAINING

Postdoc, Montgomery Lab, Stanford University *Current*
Pathology + Biomedical Data Science

PhD, University of California, Davis *2020*
Dissertation: *Exploring and Extending Multivariate Brownian Diffusion Models of Phenotypic Evolution for Bayesian Phylogenetic Inference*
Committee: Tim Weaver (Chair), Shara Bailey, Peter Wainwright
GPA: 4.0/4.0 — Anthropology + Population Biology + Data Science & Informatics

BA, Vanderbilt University *2013*
GPA: 3.9/4.0 — Earth & Environmental Sciences + Ecology, Evolution & Organismal Biology
Departmental Honors, *summa cum laude*

ADDITIONAL EDUCATION

Discussion Groups *2013 - 2020*
I've served as an active participant in groups on Computational Molecular Evolution, Paleoanthropology, Quantitative Genetics, and Machine Learning. I've been the founder and lead in groups on Python, Applied Linear Algebra, Bayesian Data Analysis, and Deep Learning.

Workshops *2013 - 2020*
I've attended or led multiple workshops ranging in duration from 2h to 9d on Universal Design, Science Communication, Bayesian Phylogenetics, Database Management, Natural Language Processing, Carpentries Instructor Training, and other topics.

LANGUAGES

Programming	Natural
Fluent:	Russian, English
Proficient: R, RevBayes, Stan, BASH	Spanish
Beginner: Python, C++, CSS, HTML, JS	

SERVICE

JOURNAL REVIEW

Evolution (2017), *Science Communications* (2018), *Cell Reports* (2021), *Human Genetics and Genomics Advances* (2022)

GRANT REVIEW

WAI Grants (2021, 2022, 2023)

LEADERSHIP

Founder & Lead, Applied Bayesian Statistics Research Cluster

2019 - 2020

I founded, coordinated, and supervised an interdisciplinary research cluster of 70+ scientists and statisticians across numerous career stages (PhD Student, Postdoc, PI, Industry Researcher), financially and spiritually sponsored by the UC-Davis *Data Science & Informatics Unit*

Director & President, Board of Directors, Wild Animal Initiative

2020-Present

I serve on the Board of Directors at the [Wild Animal Initiative](#), a non-profit dedicated to researching the lives of wild animals. In this role, I help to oversee the organization's activities and policies as described in their mission statement and bylaws, approve financial decisions, decide on board meeting agendas, and engage in related activities. I've also served as chair of both the DEI and Science committees

Director & President, Board of Directors, Rethink Priorities

2023-Present

I serve on the Board of Directors at [Rethink Priorities](#), a non-profit focused on cause prioritization and research in animal welfare, artificial intelligence, climate change, and global health and development. Responsibilities are similar to above. Over several years I have also extensively consulted on or performed statistical model fitting, data visualization, and related activities

PROJECTS

POSTDOCTORAL WORK

My postdoctoral work in the Montgomery Lab focuses on exploring and developing statistical methods to better understand the molecular mechanisms by which genetic and environmental variation structure phenotypic variation, especially insofar as that understanding might have translational applications in contexts such as drug discovery and personalized medicine. Current and recent projects include:

- Integrating GWAS and eQTL mapping results with transcriptomic, proteomic, and ATAC-seq data to help **identify the molecular transducers of physical activity** through the MoTrPAC Consortium [\[LINK\]](#)
- Streamlining the Bayesian workflow by creating text-processing utilities to **deterministically translate Stan code to R** (or other interpreted languages), allowing for dynamic exploration of model structure and easier automated acquisition of posterior predictive probabilities or distributions (for simulation experiments, or to assess observation-specific goodness of fit) [\[LINK\]](#)
- Designing novel probability models to infer differential **allele-specific expression patterns linked to ovarian cancer** throughout the course of tumor development using data from mmPCR-seq [\[LINK\]](#)
- Developing **integrative methods to link multiomic response with trait expression** that appropriately propagate upstream inferential uncertainty [\[LINK\]](#)
- Hierarchically modeling the **temporal dynamics of whole-transcriptome expression data** following environmental perturbation using linear combinations of logistic functions to characterize temporal behavior in expected rates of gamma-poisson distributed read counts [\[LINK\]](#)
- Exploring causal inferential implications of **aging clocks** [\[LINK, example\]](#)
- Developing easy-to-use tools for **frequentist testing** of novel generative immune response models
- Describing **novel informative correlation matrix distributions** for use in multivariate, multilevel diffusion models [\[LINK\]](#)
- Understanding the proteomic signatures of **allogeneic renal transplant rejection** [\[LINK\]](#)
- Exploring sources of linkage disequilibrium unrelated to crossing over (eg assortative mating) in a simulation framework [\[LINK\]](#)

- Collaborating on the description and implementation of **Bayesian differential expression models** [\[LINK\]](#),
- Describing theoretical expectations for **rare-variant effects on outlier detection** [\[LINK, example\]](#)

DISSERTATION WORK

My dissertation work primarily centered on Bayesian computational phylogenetics methods development, specifically extending and exploring multivariate Brownian (mvBM) diffusion models to novel character evolutionary applications and contexts [\[LINK\]](#). Components of this this work included:

- through simulation experiments, **exploring the informativeness and reliability of continuous character alignments** at retrieval of simulating tree topology, with subsequent application to a craniometric dataset
- the **effects of model misspecification** in the above, both with respect to the evolutionary process and with respect to accommodating missing data and measurement error
- developing and implementing novel optimizations to **reduce the time complexity** of likelihood calculation under the phylogenetic mvBM model from $O(n^3)$ to $O(n^2)$, modularizing particular operations to **avoid redundant computation** during Met-Hastings, and inventing substantially **more efficient, tunable proposal distributions** over correlation matrices of arbitrary dimensionality while inherently respecting PSD constraints. In total, **reducing the runtime required** to fit this popular evolutionary model under typical empirical conditions from months to hours
- **comparing model-based phylogenetic methods to more common heuristic (maximum parsimony, distance) methods**, both in simulation and empirically (using ape and old-world monkey datasets), and contrasting their performance to methods that use molecular (e.g. nucleotide sequence) data
- **joint inference of ancestral character states** in a monkey dataset, with additional theory development on imputing unobserved tip characters in a phylogenetically sensible way
- layering a **high-dimensional probit model atop mvBM to accommodate discrete traits** and comparing it with both more traditional and novel CTMC (*Continuous Time Markov Chain*) models of discrete trait substitution, with application to human dental variation

In addition to the above dissertation contents, parallel work involving related skills included:

- **comparison of morphological relaxed clock models** in a species-rich fish dataset whose tree height straddles the K-Pg boundary [\[LINK\]](#)
- **approximating truncated biogeographic diffusions using data augmentation** on phylogenies to sample migration histories while respecting (land, water) barriers to explore latitudinal / climactic drivers of morphological differentiation in modern humans [\[LINK\]](#)
- high-dimensional multilevel generalized linear mixed models (GLMMs; Gamma-Poisson, in this case) in Stan to **heart transplant patient immune response** data both before and after an acute rejection episode [\[LINK\]](#)
- a hierarchical univariate Ornstein-Uhlenbeck model in Stan to the ‘evolution’ of **nitrogen concentrations in manure ponds** across California to predict values after an arbitrary amount of time has passed in an arbitrary pond [\[LINK\]](#)

PERSONAL PROJECTS

I’ve written many dozens of one-off scripts devoted to data visualization, text mining, web scraping, animation, replicating published analyses or algorithms from scratch, generating artwork, solving everyday

difficulties, and exploring off-the-cuff ideas proposed by myself or colleagues. Sometimes these require the flexibility of implementing everything from scratch, sometimes I'm able to make do with glueing a bunch of API calls together.

Recent examples here include but are not limited to:

- Exploring the space of valid crossword puzzles via MCMC to **generate crosswords that adhere to specific shapes determined by a user-specified images** (and hints + answers) [[LINK](#), [example](#)]
- Implementing on AWS a **multimodal, SMS-based chat assistant** for family not quite able to operate browser- or app-based interfaces, but very familiar with sending text messages [[LINK](#)]
- As above, but instead of a chatGPT clone, hooking the API calls to a voice interface to create an admittedly high latency, **LLM-powered voice assistant** (not unlike Amazon Alexa or Google Home) to run on family computers.
- **Generating board (or other) meeting minutes from video recordings**, interleaving image-to-text output at the appropriate timestamps extracted using temporal variance in multivariate picture heterogeneity, also incorporating speaker diarization methods to better identify who motioned this or seconded that [[LINK](#)]
- Leveraging wavelets and other transforms to **compress and vectorize raster images** [[LINK](#), [example](#)], with initial attempts to expand into higher dimensional spaces (eg time or 3D objects) [[LINK](#), [example](#)]
- Automated **infilling and text-wrapping** of arbitrary images with arbitrary text [[LINK](#), [example](#)]
- Automated **processing and overlay of in/outpainted images** [[LINK](#), [example](#)]
- **Generating seating charts** under various (attitudinal, geographic) optimization criteria for an ice-breaker activity, including in the multi-round iterated case where participants move [[LINK](#), [example](#)]
- Making other **small animations** leveraging basic geometric and linear algebraical operations [[LINK](#), [example](#)]
- Fitting multilevel GLMMs in Stan to **consumer dietary and attitudinal response datasets** (zero-inflated Poisson and ordered logit, respectively) measuring the effects of exposure to a relevant advertisement urging dietary change [[LINK](#)]
- Implementing an efficient, conditional multivariate ordinal probit model for **personalized movie rating predictions**, exploiting basic properties of Schur complements [[LINK](#)]
- Writing a **“falling rain” parody generator** for the Matrix 4 release [[LINK](#), [example](#)]

I've also consulted individuals & organizations in a minor role (e.g. over a ~ 1 h meeting) on many additional projects throughout my postdoc and graduate school.

FIELD & LABWORK

Archaeological / Paleontological Excavation

2013

During the Summer 2013 field season I helped in excavation efforts ongoing at La Ferrassie, a Neandertal archaeological and paleontological site in Savignac-de-Miremont, France

Water Quality Analysis

2011

I performed water quality analyses (of salinity, reactive nitrogen concentration, etc.) of a large set of streams distributed across the North Island of New Zealand

Stable Isotope Ecology

2012 - 2013

I examined how environmental and ecological conditions were recorded in enamel stable isotope ratios (carbon and oxygen) and dental microwear textures for several marsupial taxa throughout Australasia

TEACHING

Associate Instructor*, University of California, Davis

2015 - 2020

As instructor-of-record, I've taught three quarters of an upper-division paleoanthropology course, two quarters of an upper-division evolutionary primatology course, and one quarter of an introductory course on human evolution. In these roles, I created or modified all the lab and lecture materials, designed and graded assignments and tests, mentored individual students, delivered lectures, and either supervised teaching assistants or administered and oversaw lab activities

Teaching Assistant*, University of California, Davis & Vanderbilt University

2012 - 2020

I have taught a total of 14 discussion sections for courses on human evolution and paleoanthropology, as well as the lab for an introductory cell biology course at Vanderbilt University. As a TA, I occasionally gave guest lectures on various subjects (mostly statistical phylogenetics)

Outreach Lecturer, University of California, Davis

2013 - 2020

I've given multiple yearly talks on human evolution to elementary and middle school students on location and visiting UC-Davis, as well as during campus-wide events (e.g. *Picnic Day*). I've also assisted in miscellaneous workshops targeted at adults, e.g. on NLP during UC-D Data Science Health Day

Course Coordinator, Workshop in Applied Phylogenetics

2019

I served as a course coordinator for world-renowned, widely-attended, week-long workshop in applied computational Bayesian phylogenetics held in May 2019 at the Bodega Marine Laboratory

Carpentries Instructor

2019

I have completed Instructor Training and Checkout for The Carpentries organization and am fully certified to teach courses in the Data and Software Carpentries

*student evaluations available upon request

RESEARCH OUTPUT

PAPERS

- [1] Abell, N., **Vetr, N.***, Montgomery, S., et al. 2023. *A Survey of High Depth Allele-Specific Expression Across Normal Tissues and Ovarian Cancers*. In Prep.
- [2] **Vetr, N.**, Gay, N., and Montgomery, S. 2023. *The impact of exercise on gene regulation in association with complex trait genetics*. Conditionally accepted to Nature Communications pending Editorial Revisions. [[LINK](#)]
- [3] **MoTrPAC Study Group[†]**. 2022. *Temporal dynamics of the multi-omic response to endurance exercise training across tissues*. Accepted to Nature. [[LINK](#)]
- [4] Carpenter, B., Chen, S., and **Vetr, N.** 2022. *Bayesian Models of Gene Expression and RNA Sequencing*. [[LINK](#)]
- [5] Gates, K., Panicker, A., Biendarra-Tiegs, S., **Vetr, N.**, Higueta, M., Nelson, T., Pereira, N., and Griffiths, L. 2021. *Shotgun Immunoproteomics for Identification of Nonhuman Leukocyte Antigens Associated With Cellular Dysfunction in Heart Transplant Rejection*. Transplantation 106(7). DOI: 10.1097/TP.0000000000004012 [[LINK](#)]
- [6] **Vetr, N.**, Bailey, S., Moore, B., and Weaver, T. 2020. *Human Population History from Discrete Dental Traits Under an Approximate Multivariate Ordinal Probit*. [[LINK](#)]

- [7] **Vetr, N.** and Weaver, T. 2020. *Primate Phylogenetics with Landmark Data: A Model-Based, Multivariate Brownian Approach*. [\[LINK\]](#)
- [8] **Vetr, N.**, May, M., Moore, B., and Weaver, T. 2019. *Bayesian Phylogenetic Inference Under Multivariate Brownian Motion*. [\[LINK\]](#)
- [9] **Vetr, N.**, DeSantis, L., Yann, L., et al. 2013. *Is Rapoport's Rule a Recent Phenomenon? A Deep Time Perspective on Potential Causal Mechanisms*. *Biology Letters* 9(5): 1-5. DOI: 10.1098/rsbl.2013.0398 [\[LINK\]](#)

*dual first authorship

†Author Group: 2 (of 8)

CONFERENCE PRESENTATIONS

- [1] **Vetr, N.**, Gay, N., and S. Montgomery. 2022. *The impact of exercise on gene regulation in association with complex trait genetics*. Poster session presented at the American Society of Human Genetics' annual meeting, 2022.
- [2] **Vetr, N.**, Gay, N., and S. Montgomery. 2022. *Integrating Exercise-Induced Gene Expression and Human Phenotypic Variation*. Poster session presented at NIH-NLM T15 Training Conference 2022.
- [3] **Vetr, N.**, May, M. Moore, B., and T. Weaver. 2018. *Adapting multivariate Brownian diffusion models to Bayesian inference of human population history and phylogeny*. Oral session presented at the 87th Annual Meeting of the American Association of Physical Anthropologists.
- [4] Desantis, L., **Lashinsky, N.**, Romer, J., Greshko, M., and Loffredo, L. 2013. *University Students' Acceptance of Climate Change and Evolution: Are Skeptics just Anti- Science?* Poster presented despite second authorship at the 73rd Annual Meeting of the Society of Vertebrate Paleontology.
- [5] **Lashinsky, N.**, DeSantis, L. Yann, S. Donohue, and R. Haupt. 2013. *Is Rapoport's Rule a Recent Phenomenon? A Deep Time Perspective on Potential Causal Mechanisms*. Oral session presented at the 73rd Annual Meeting of the Society of Vertebrate Paleontology.
- [6] **Lashinsky, N.** and DeSantis, L. 2012. *Assessing how the extant lesser forest-wallaby *Dorcopsulus vanheurni* and Lumholtz's tree kangaroo *Dendrolagus lumholtzi* record their environment: establishing a baseline for studies of extinct marsupials*. Poster presented at the 5th Annual Meeting of the South-eastern Association of Vertebrate Paleontology.

GRANTS & AWARDS

NIH T15	2021
Excellence in Data Science Community Training and Outreach	2019, 2020
Outstanding Graduate Student Teaching Award Nominee	2016, 2019, 2020
Conference Travel Award	2012, 2018
1st Place Picnic Day Exhibit Award in "Secrets of Nature" Category	2017
NSF Graduate Research Fellowship	2015
Summer Research Grant	2014, 2015
Graduate Scholars Fellowship	2013
Departmental Honors in Earth and Environmental Sciences	2013
Eugene H. Vaughan Undergraduate Research Assistantship in Geology	2012

Geology Travel Grant	<i>2012</i>
Vanderbilt Undergraduate Summer Research Grant	<i>2012</i>
Ross Family Scholarship	<i>2012</i>
National Merit Scholarship	<i>2009</i>