

# Nikolai Vetr

## Stanford University, California

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## EDUCATION

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**Postdoc**, Montgomery Lab, Stanford University Current

Computational Biology; Depts: Pathology, Genetics, Biomedical Informatics, Computer Science

**PhD** 2020

University of California, Davis

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** 2013

Vanderbilt University

GPA: 3.9/4.0 — Earth & Environmental Sciences; Ecology, Evolution & Organismal Biology

Departmental Honors, *summa cum laude*

## ADDITIONAL EDUCATION

**Discussion Groups** 2013 - 2020

Active participant in groups on Computational Molecular Evolution, Paleoanthropology, Quantitative Genetics, and Machine Learning. Founder and lead in groups on Python, Applied Linear Algebra, Bayesian Data Analysis, and Deep Learning

**Workshops** 2013 - 2020

Have attended 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

**Online Courses** 2013 - 2020

In addition to reading textbooks through discussion groups or on my own, I've worked through several online courses, such as Gilbert Strang's *Linear Algebra* (MIT OpenCourseWare 18.06) or Andrew Ng's *Deep Learning Specialization* (Coursera)

## LANGUAGES

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### Programming

**Fluent:**

**Proficient:** R, RevBayes, Stan, BASH

**Beginner:** Python, C++, CSS, HTML, JS

### Natural

Russian, English

Spanish

## SERVICE

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### JOURNAL REVIEW

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

### GRANT REVIEW

WAI Grants (2021, 2022, 2023)

# PROJECTS

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## 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 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 using a variety of EDA and regression-based tools (e.g. LDSC)
- Hierarchically modeling the **temporal dynamics of whole-transcriptome expression data** following a perturbation using linear combinations of logistic functions to describe how expected rates of gamma-poisson distributed read counts behave across time
- Other current projects involve developing **integrative methods to link multiomic response with trait expression** that appropriately propagate upstream inferential uncertainty, exploring causal inferential implications of **aging clocks**, developing easy-to-use tools for **frequentist testing** of novel generative models, describing **novel informative correlation matrix distributions** (primarily for use in multivariate, multilevel diffusion models), understanding the proteomic signatures of different varieties of both **allogeneic and xenogeneic transplant rejection**, fitting **high-order G x E interaction models**, collaborating on the description and implementation of **Bayesian differential expression models**, describing theoretical expectations for **rare-variant effects on outlier detection**, and identifying variation in **allele-specific expression in the context of ovarian cancer**

## DISSERTATION WORK

My dissertation work primarily centered on Bayesian computational phylogenetics methods development, specifically focused on extending and exploring multivariate Brownian (mvBM) diffusion models to novel applications and contexts. Projects in association with this work have involved:

- through simulation **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. 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
- **comparison of morphological relaxed clock models** in a species-rich fish dataset whose tree height straddles the K-Pg boundary

- **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
- **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

## SIDE PROJECTS

Throughout my PhD, I've undertaken a number of side projects, some of which directly extended my dissertation work to non-evolutionary contexts and some of which used more distantly related methods. These have often been self-motivated, but also sometimes done in collaboration with or response to requests by third parties (e.g. as statistical co-author). These side-projects have included developing, fitting, interpreting, describing, and visualizing results from:

- 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
- 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
- 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
- an efficient, conditional multivariate normal model in R that provides **personalized movie rating predictions** (given ratings for some movies and a large-but-sparse dataset of user reviews, what are the expected ratings and variances of unrated movies?) using probit and logit-normal transforms, exploiting basic properties of Schur complements
- a Bayesian ConvNet fitted to **medical (skin lesion & other) image data**, currently in prep for a workshop I'll be hosting through *Data Science & Informatics*

## MINOR 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.

I've also consulted individuals & organizations in a minor role (e.g. over a  $\sim 1$ 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

As an undergraduate researcher, 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

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**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 the labs

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

2012 - 2020

I have taught a total of 14 discussion sections for the aforementioned human evolution and paleoanthropology courses (see above), 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*

## LEADERSHIP

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**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 these role, I help to oversee the organization's activities and policies as described in their mission statement and bylaws, as well as approve financial decisions. I've also served as chair of both the DEI and Science committees and currently serve as Board President

**Coordinator**, Reading & Discussion Groups

2014 - 2020

I've founded and coordinated reading groups on Python, Applied Linear Algebra, Bayesian Data Analysis, and Deep Learning

# RESEARCH OUTPUT

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## PAPERS

- [1] **Vetr, N.**, Gay, N., and Montgomery, S. 2022. *The impact of exercise on gene regulation in association with complex trait genetics*. In Review by Nature Communications. [\[LINK\]](#)
- [2] MoTrPAC Study Group. 2022. *Temporal dynamics of the multi-omic response to endurance exercise training across tissues*. In revision for Nature. [\[LINK\]](#)
- [3] Carpenter, B., Chen, S., and **Vetr, N.**, 2022. *Bayesian Models of Gene Expression and RNA Sequencing*. [\[LINK\]](#)
- [4] 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 [\[LINK\]](#)
- [5] **Vetr, N.**, Bailey, S., Moore, B., and Weaver, T. 2020. *Human Population History from Discrete Dental Traits Under an Approximate Multivariate Ordinal Probit*. [\[LINK\]](#)
- [6] **Vetr, N.** and Weaver, T. 2020. *Primate Phylogenetics with Landmark Data: A Model-Based, Multivariate Brownian Approach*. [\[LINK\]](#)
- [7] **Vetr, N.**, May, M., Moore, B., and Weaver, T. 2019. *Bayesian Phylogenetic Inference Under Multivariate Brownian Motion*. [\[LINK\]](#)
- [8] **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 [\[LINK\]](#)

## 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

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<b>NIH T15</b>	2021
<b>Excellence in Data Science Community Training and Outreach</b>	2019, 2020
<b>Outstanding Graduate Student Teaching Award Nominee</b>	2016, 2019, 2020
<b>Conference Travel Award</b>	2012, 2018
<b>1st Place Picnic Day Exhibit Award in "Secrets of Nature" Category</b>	2017
<b>NSF Graduate Research Fellowship</b>	2015
<b>Summer Research Grant</b>	2014, 2015
<b>Graduate Scholars Fellowship</b>	2013
<b>Departmental Honors in Earth and Environmental Sciences</b>	2013
<b>Eugene H. Vaughan Undergraduate Research Assistantship in Geology</b>	2012
<b>Geology Travel Grant</b>	2012
<b>Vanderbilt Undergraduate Summer Research Grant</b>	2012
<b>Ross Family Scholarship</b>	2012
<b>National Merit Scholarship</b>	2009

## OTHER

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### Computer Hardware

Familiar with computer assembly and repair. Constructed and networked an 8-node (64C/128T) Ryzen-based Beowulf cluster running macOS for dissertation work, with analyses parallelized using *GNU Parallel*, as well as a portable 5-node Raspberry Pi cluster running Linux. Have designed and assembled similar systems for academic colleagues after consultation on their computational needs

### Outdoors

Avid and experienced outdoorsman, having coordinated and lead many hiking, backpacking, and climbing trips of varying group size over distances typically between 50-150km, but ranging upwards to 1,300km, and have also backpacked and hitchhiked through several countries. Sporadically partake in other adventure sports (snowboarding, kayaking, cycling, etc.)

### Photography

Hobbyist photographer, graphic designer, and illustrator focusing on portrait, landscape, and wildlife photography, with post-processing typically done in Capture One and Adobe Photoshop and recently augmented with more sophisticated computational tools (e.g. ANNs)

Other hobbies include woodworking, strength training, running, yoga, writing poetry and prose, travel, and volunteering.