
Nikolai G. Vetr

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⚙ 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)

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Nikolai Vetr

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(last update: January 16, 2026)

EDUCATION AND TRAINING

Postdoc, Montgomery & Wheeler Labs, Stanford University Current

Pathology + Biomedical Data Science

PhD, University of California, Davis 2021

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

Workshops 2013 - Present

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

Discussion Groups 2013 - Present

I've actively participated in groups on Computational Molecular Evolution, Paleoanthropology, Quantitative Genetics, Bio-AI Integration, and Machine Learning. I've founded and lead groups on Python, Applied Linear Algebra, Bayesian Data Analysis, and Deep Learning

LANGUAGES

Programming

Fluent:

Proficient: R, RevBayes, Stan, BASH

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

Natural

Russian, English

Spanish

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

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 artificial intelligence, climate change, animal welfare, 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

Director, Secretary, & 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 contribute to the organization's governance according to its mission statement and bylaws, approve and advise financial decisions, set agendas for and chair board meetings, and engage in related activities such as budget forecasting. I've also served as chair of both the DEI and Science committees, and currently serve on the Finance Committee

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

PROJECTS

POSTDOCTORAL WORK

My postdoctoral work in the Montgomery and Wheeler Labs focuses on exploring and developing statistical methods to better understand the molecular mechanisms by which genetic and environmental variation structure phenotypic variation, with an eye to translational applications in contexts such as drug discovery and personalized medicine. I've lately endeavored to port some of these scientific research and publication utilities to static web formats to improve their accessibility and value to the scientific public (eg [1](#), [2](#)). Current and recent projects include:

- Developing a flexible **sum-to-zero tensor (S2Z) parameterization with elliptical family marginals** for broad and varied applications, including sparsity models of contingency tensors but extending to fully general multilevel models. Deriving and implementing forward and back-transforms for the multilevel models allows us to exactly recover "population" model parameters at substantially reduced (in some cases, multiple orders of magnitude) computational cost [[LINK](#)]
- Performing **multi-tissue, multi-omic, analysis and integration of acute exercise response** across multiple exercise modalities and training states, as co-lead of the "highly-active" multiomic landscape paper through the MoTrPAC Consortium, as well as other papers in that package [WiP]
- 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**, allowing for interactive exploration of model structure and streamlined acquisition of posterior predictive probabilities or distributions (for simulation experiments, or to assess observation-specific goodness of fit) [[LINK](#)]
- Developing 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 appro-

- priately propagate upstream inferential uncertainty [[LINK](#)]
- Fitting tractable **high-D interaction models involving multiple filtration steps** for false-negative aware tests of intersectionality [[LINK](#), [slides](#)]
- Propagating inferential uncertainty to **mitigate 0-biasing effects of differential power** on estimates of interdependence [[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 a flexible **NHST testing pipeline** for novel generative immune response models
- Benchmarking inferential performance of **sparse feature selection** methods under conditions of strong input interdependence [[LINK](#)]
- Describing **novel informative correlation matrix distributions** for use in multivariate, multilevel diffusion models, as well as related distributions (e.g. a monotonic dirichlet) [[1](#), [2](#), [3](#)]
- 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](#)], and extending “outlier calling” pipelines to incorporate **tractable scale mixtures** [[LINK](#)]

DISSERTATION WORK

My dissertation work 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 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. Some have required flexible from-scratch implementation, others lean heavily on API calls to existing software and services.

Recent examples 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](#)]
- **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](#)]
- **Generating walking directions** using graph operations on OpenStreetMap data to prioritize other weighted criteria besides time to destination (eg regularly spaced amenities, density of PoI, beauty as proxied by Flickr geolocated metadata, etc.) [WiP]
- **Generating laser cutter input files** for parallel tag / fob creation (to tag deboxed boardgames, provide custom swag, create 3D engravings by discretizing depth maps, etc.) [WiP, [LINK](#)]
- 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 for individuals & organizations in a minor role 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 targetted 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] **Vetr, N.***, Pinkney, S., Montgomery, S., et al. 2026. *Population Effect Estimation in Bayesian Hierarchical Models using Sum-to-Zero Constraints*. In Prep. [[LINK](#)]
- [2] **MoTrPAC Study Group**. 2026. *Multi-Omic, Multi-Tissue Responses to Acute Exercise in Sedentary Adults: Findings from the Molecular Transducers of Physical Activity Consortium (MoTrPAC)*. In review at Cell.
- [3] **Vetr, N.***, Abell, N., Montgomery, S., et al. 2026. *A Survey of High Depth Allele-Specific Expression Across Normal Tissues and Ovarian Cancers*. In Prep. [[LINK](#)]
- [4] Ungar, R., Li, T., **Vetr, N.***, Ersaro, N., Battle, A., Montgomery, S. 2025. *Functional impact of rare variants and sex across the X-chromosome and autosomes*. Accepted to Human Genetics and Genomics Advances. [[LINK](#)]
- [5] **Vetr, N.**, Gay, N., and Montgomery, S. 2024. *The impact of exercise on gene regulation in association with complex trait genetics*. Nature Communications 15(3346): 1-14. DOI: 10.1038/s41467-024-45966-w. [[LINK](#)]
- [6] **MoTrPAC Study Group**[†]. 2024. *Temporal dynamics of the multi-omic response to endurance exercise training across tissues*. Nature 629(8010): 174-183. DOI: 10.1038/s41586-023-06877-w. [[LINK](#)]
- [7] Carpenter, B., Chen, S., and **Vetr, N.** 2022. *Bayesian Models of Gene Expression and RNA Sequencing*. [[LINK](#)]
- [8] Gates, K., Panicker, A., Biendarra-Tiegs, S., **Vetr, N.**, Higuaita, 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](#)]
- [9] **Vetr, N.**, Bailey, S., Moore, B., and Weaver, T. 2020. *Human Population History from Discrete Dental Traits Under an Approximate Multivariate Ordinal Probit*. [[LINK](#)]
- [10] **Vetr, N.** and Weaver, T. 2020. *Primate Phylogenetics with Landmark Data: A Model-Based, Multivariate Brownian Approach*. [[LINK](#)]
- [11] **Vetr, N.**, May, M., Moore, B., and Weaver, T. 2019. *Bayesian Phylogenetic Inference Under Multivariate Brownian Motion*. [[LINK](#)]
- [12] **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.G.**, Montalvo S., et al. 2026. *Prediction of Cardiorespiratory Fitness from Multi-Omic Profiles*. Submitted to ACSM 2026.
- [2] **Vetr, N.G.**, Abell, N.S., Tsang, E., Cheng, N., Linder, S., Smith, K.S., Uzunovi, J., Lamaze, F., Ardlie, K., Awadalla, P., Li, J.B., and S.B. Montgomery. 2024. *High Depth Allele-Specific Expression Across Healthy Tissues and Ovarian Cancer*. Presented at the American Society of Human Genetics annual meeting, Denver CO. [[LINK](#)]
- [3] Katz, D.H., Jin, C.A., ..., G., **Vetr, N.G.**, ..., Snyder, M., Montgomery, S., Ashley, E.A., Wheeler, M.T., for the MoTrPAC Study Group. 2024. *The Multi-omic, Multi-tissue Response to Acute Endurance and Resistance Exercise: Results from the Molecular Transducers of Physical Activity Consortium*. Presented at the American Heart Association Scientific Session, Chicago, IL. (to be presented by D. H. Katz, authors omitted for brevity)
- [4] **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, Los Angeles, CA.
- [5] **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, Buffalo, NY.
- [6] Ungar, R., Li, T., Ersaro, N., **Vetr, N.G.**, Battle, A., and S. Montgomery. 2022. *Functional impact of rare variants and sex across the X chromosome and autosomes*. Poster session presented at the American Society of Human Genetics' annual meeting, Los Angeles, CA. (Presented by R. Ungar)
- [7] Panicker, A.J., Gates, K.V., Biendarra-Tiegs, S.M., **Vetr, N.G.**, Lopera Higuaita, M., Nelson, T.J., Pereira, N.L., and L.G. Griffiths. 2021. *Identification of Non-Human Leukocyte Antigens Associated with Cellular Dysfunction in Heart Transplant Rejection*. Poster session presented at the American Heart Association's annual Scientific Sessions, Nov. 13-15, Boston, MA, and virtual. (Presented by A.J. Panicker)
- [8] **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, Austin, TX.
- [9] **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, Raleigh, NC.
- [10] Desantis, L., **Vetr, 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, Raleigh, NC. (Presented by N. Vetr)
- [11] **Vetr, 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 Southeastern Association of Vertebrate Paleontology, Asheville, NC.

*previously published under the name Lashinsky, N.

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	2012
Vanderbilt Undergraduate Summer Research Grant	2012
Ross Family Scholarship	2012
National Merit Scholarship	2009