



Application

Name: Tyler Shimko

Student Data

First name	Middle name	Last name
Tyler	Carter	Shimko
Previous names (ex: maiden name)		
E-mail		

Citizenship

Country of Birth:	United States
U.S. Citizen:	Yes
If no,	
• Country of Citizenship:	
• Permanent Resident Alien:	----
If yes,	
• PRA Number:	
• Port of Entry:	

Name: Tyler Shimko

Current Mailing Address

Street address 1

 [REDACTED]

Street address 2

City

 [REDACTED] [REDACTED]

State

Zip code

Home phone

Cell phone

Work phone

Address effective through (m/d/y): **05/01/2014**

After this date, all correspondence will be sent to the permanent address listed below unless otherwise requested.

Notify the Krell Institute if your address changes after the application has been submitted.

Permanent Address

Street address

 [REDACTED]

City

 [REDACTED] [REDACTED]

State

Zip code

Phone

 [REDACTED] [REDACTED]

Name: Tyler Shimko

Graduate Record Examination

Verification of these scores is required. (Note: Official Graduate Record Examination (GRE) Scores must be sent directly by the Educational Testing Service to the Krell Institute/DOE Computational Science Graduate Fellowship program. The Krell Institute's Institution Code is **6343** and the department code is **5199**)

Your name as it appears on your GRE record: **Tyler Shimko**

Date test taken/to be taken: **06/24/2014**

GRE Test Results

		Reported from ETS	
	<i>Examination</i>	<i>Score</i>	<i>Percentile(%)</i>
Verbal		163	92
Quantitative		161	80
Analytical or Analytical Writing		5.0	93

References

List at least three persons familiar with your academic preparation and your technical abilities. Please have these individuals mail the reference forms directly to Krell Institute.

	<i>Title</i>	<i>First name</i>	<i>Last name</i>	<i>Institution</i>	<i>E-mail</i>	<i>Status</i>
1.	Dr.	Erik	Andersen	Northwestern University		Submitted
2.	Dr.	Gillian	Stanfield	University of Utah		Submitted
3.	Dr.	Leonid	Kruglyak	University of California, Los Angeles		Submitted
4.	Dr.	Erik	Jorgensen	University of Utah		Submitted

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Academic Status

Current Academic Status: **Undergraduate Student**

Have you completed any academic credit towards your computational science/engineering doctoral degree? **No**

If yes, how many terms have you completed? (exclude summer) ----

Official transcripts from every listed institution are a required component of the application including your Fall 2014 transcript, if applicable. Please see the instructions for more information on where to send the transcripts.

Doctoral Institution (Institution where you plan on completing your computational science and engineering doctorate or first choice doctoral university):

Institution	Start Date	Expected End Date	Department	Academic Discipline	GPA	Degree
Stanford University	09/2015	09/2020	Genetics	Genetics		PhD

Department Chair at Doctoral Institution:

First Name	Last Name	Email
Michael	Snyder	[REDACTED]

Other Doctoral Institution Choices (Answer only if not currently at doctoral institution)

			Department Chair Information		
Institution	Department	Academic Discipline	First Name	Last Name	Email
University of Washington	Genome Sciences	Genetics	Robert	Waterston	[REDACTED]
University of California, San Francisco	Bioinformatics	Bioinformatics	Patricia	Babbitt	[REDACTED]

Higher Educational History (All university/colleges attended and degrees obtained with the exception of the doctoral degree listed above):

<i>Institution</i>	<i>Start Date</i>	<i>End Date Expected or Actual</i>	<i>Department</i>	<i>Academic Discipline</i>	<i>Degree</i>	<i>GPA</i>
University of Utah	08/2011	05/2015	Biology	Biology	Bachelors	3.907
					None	
					None	
					None	
					None	

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Graduate Advisor

The graduate advisor is the person from the preferred institution **who views and approves the Program of Study.**

First Name

Lars

Last Name

Steinmetz

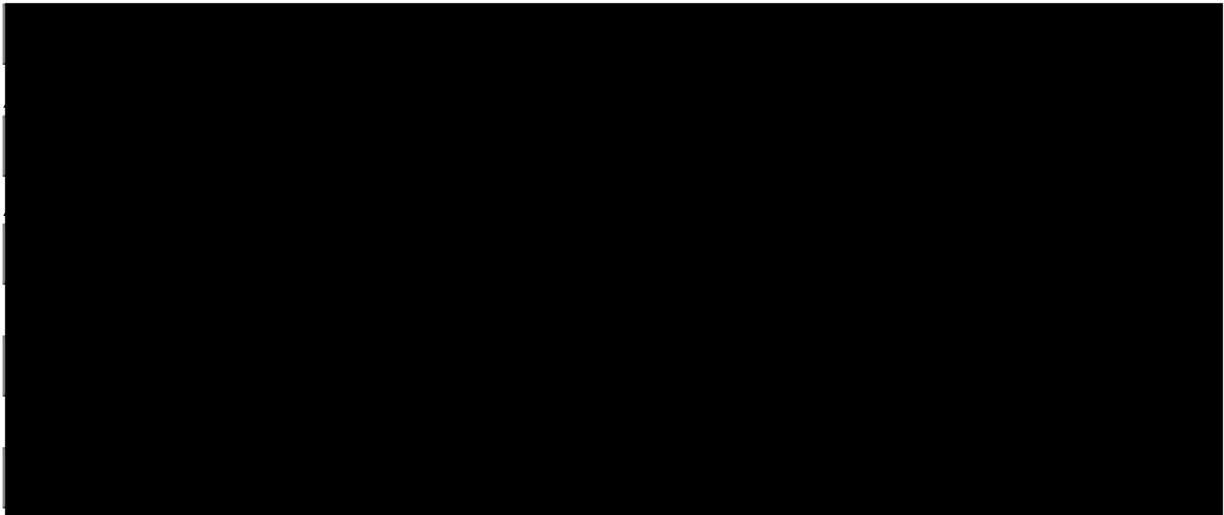
Institution

Stanford University

Title (Dr., Ms., Professor, ...)

Professor

E-mail



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Program of Study

Listed are the courses in science and engineering, applied mathematics, and computer science that you agreed to take on your proposed Program of Study.

University: Stanford University

Course number	Course Title	Credit hours	Term and Year	Grade	Academic Level
Science/Engineering					
GENE 205	Advanced Genetics	3Q	Winter 2016		G
GENE 210	Genomics and Personalized Medicine	3Q	Spring 2016		G
GENE 244	Introduction to Statistical Genetics	3Q	Spring 2016		G
Mathematics and Statistics					
STATS 141	Biostatistics	3Q	Fall 2016		B
STATS 202	Data Mining and Analysis	3Q	Fall 2016		G
STATS 208	Introduction to the Bootstrap	3Q	Fall 2017		G
Computer Science					
CS 145	Introduction to Databases	3Q	Fall 2016		B
CS 149	Parallel Computing	3Q	Winter 2017		B
CS 229	Machine Learning	3Q	Fall 2017		G

I have read this program of study and affirm that, in my opinion, it satisfies the fellowship program requirements. This POS has been approved by my advisor, **Lars Steinmetz**, and I understand that, if offered a fellowship, my advisor and I are required to sign this page and send it to the Krell Institute.

Student's signature _____ Date _____

Graduate Advisor: **Lars Steinmetz**

Graduate Advisor's Institute: **Stanford University**

Graduate Advisor signature _____ Date _____

Krell Institute (Office use only) _____

Krell Institute, Attn: DOE CSGF Coordinator

1609 Golden Aspen Drive, Suite 101, Ames, IA 50010

Phone: 515-956-3696, Fax: 515-956-3699, csgf@krellinst.org

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Course Description

GENE 205: Advanced Genetics

For PhD students in any of the Biosciences Departments and Programs at Stanford University. Emphasis on developing the ability to solve problems using genetic ideas and methods, to understand the nature and reliability of genetic inference, and to apply genetic reasoning to biological research. Weekly paper discussions based on original research papers that define or illustrate the ideas and techniques covered in the lecture.

GENE 210: Genomics and Personalized Medicine

Principles of genetics underlying associations between genetic variants and disease susceptibility and drug response. Topics include: genetic and environmental risk factors for complex genetic disorders; design and interpretation of genome-wide association studies; pharmacogenetics; full genome sequencing for disease gene discovery; population structure and genetic ancestry; use of personal genetic information in clinical medicine; ethical, legal, and social issues with personal genetic testing. Hands-on workshop making use of personal or publicly available genetic data.

GENE 244: Introduction to Statistical Genetics

Statistical methods for analyzing human genetics studies of Mendelian disorders and common complex traits. Probable topics include: principles of population genetics; epidemiologic designs; familial aggregation; segregation analysis; linkage analysis; linkage-disequilibrium-based association mapping approaches; and genome-wide analysis based on high-throughput genotyping platforms.

STATS 141: Biostatistics

Introductory statistical methods for biological data: describing data (numerical and graphical summaries); introduction to probability; and statistical inference (hypothesis tests and confidence intervals). Intermediate statistical methods: comparing groups (analysis of variance); analyzing associations (linear and logistic regression); and methods for categorical data (contingency tables and odds ratio). Course content integrated with statistical computing in R.

STATS 202: Data Mining and Analysis

Data mining is used to discover patterns and relationships in data. Emphasis is on large complex data sets such as those in very large databases or through web mining. Topics: decision trees, association rules, clustering, case based methods, and data visualization.

STATS 208: Introduction to the Bootstrap

The bootstrap is a computer-based method for assigning measures of accuracy to statistical estimates. By substituting computation in place of mathematical formulas, it permits the statistical analysis of complicated estimators. Topics: nonparametric assessment of standard errors, biases, and confidence intervals; related resampling methods including the jackknife, cross-validation, and permutation tests. Theory and applications.

CS 145: Introduction to Databases

The course covers database design and the use of database management systems for applications. It includes extensive coverage of the relational model, relational algebra, and SQL. It also covers XML data including DTDs and XML Schema for validation, and the query and transformation languages XPath, XQuery, and XSLT. The course includes database design in UML, and relational design principles based on dependencies and normal forms. Many additional key database topics from the design and application-building perspective are also covered: indexes, views, transactions, authorization, integrity constraints, triggers, on-line analytical processing (OLAP), JSON, and emerging NoSQL systems.

CS 149: Parallel Computing

This course is an introduction to parallelism and parallel programming. Most new computer architectures are parallel; programming these machines requires knowledge of the basic issues of and techniques for writing parallel software. Topics: varieties of parallelism in current hardware (e.g., fast networks, multicore, accelerators such as GPUs, vector instruction sets), importance of locality, implicit vs. explicit parallelism, shared vs. non-shared memory, synchronization mechanisms (locking, atomicity, transactions, barriers), and parallel programming models (threads, data parallel/streaming, futures, SPMD, message passing, SIMD, transactions, and nested parallelism). Significant parallel programming assignments will be given as homework.

CS 229: Machine Learning

Topics: statistical pattern recognition, linear and non-linear regression, non-parametric methods, exponential family, GLMs, support vector machines, kernel methods, model/feature selection, learning theory, VC dimension, clustering, density estimation, EM, dimensionality reduction, ICA, PCA, reinforcement learning and adaptive control, Markov decision processes, approximate dynamic programming, and policy search.

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Research Statements

This information is vital to the overall evaluation of your application.

Program of Study

Please describe how you expect that the courses listed in your planned program of study will contribute to your own research and will promote the development of a strong interdisciplinary background in computational science. Discuss why you chose these courses.

To contribute the field of quantitative genetics (QG), I must have a strong background in biology, statistics, and computation. I have designed my Program of Study (POS) to include classes covering both the fundamentals of each field and more recent developments.

It will be critical for me to first cultivate an understanding of the current state of QG. Consequently, I have elected to take courses in genetics throughout the first year of the POS. In Advanced Genetics, I will improve my ability to solve problems precisely and accurately using genetic techniques. In Genomics and Personalized Medicine, I will learn the medical implications of QG and will guide my research toward applications in human health. I will then take Introduction to Statistical Genetics, which will strengthen my understanding of the biological and statistical theories underlying QG and alert me to unanswered questions in the field.

The field of QG inherently relies on analyses of large, high-dimensional datasets. In my POS, I have selected three statistics classes that will collectively allow me to glean the maximal amount of information from these data. I will take Biostatistics to solidify my understanding of basic probability and the statistical tests widely used in QG. I will also take Data Mining and Analysis, where I will learn to elucidate relationships from large, complex datasets. I will conclude my study in statistics with Introduction to the Bootstrap. The bootstrap is a widely used statistical procedure to determine error rates in QG studies.

Because of the immense size of the datasets necessarily used in QG studies, it will be critical that I develop an understanding of high performance computing technologies. I will begin this process with Introduction to Databases to learn how to efficiently store and quickly retrieve data. I will then take Parallel Computing to learn how to divide up the computationally intensive task of mapping across multiple processors, ultimately allowing the process to become time efficient. I will complete my series of computer science courses with Machine Learning, where I will learn the computational algorithms that I hope to one day use to predict phenotypes from genome sequence data.

Research Using High-Performance Computing and/or Large Data Analysis

In your area of interest, what new science or engineering could be catalyzed by high performance computing and the new methodologies it enables (e.g., large data analysis and management, massive multiphysics simulation, agent-based models, etc.)? Why do you think this is the case?

What are the HPC challenges that need to be addressed to make this advancement?

The field of quantitative genetics has existed for over a century. However, it is only recently, with advancements in sensing, sequencing, and computing technologies, that quantitative geneticists have been able to connect phenotypic variation to specific genetic variants.

Through a simple statistical calculation, geneticists can determine how much of the variation in a trait is due to genetic factors and how much is due to environmental factors. However, the datasets and analysis techniques currently used to map phenotypes to genetic variants fail to identify all of the genetic loci necessary to explain the genetic component of the phenotypic variance. This "missing" heritability problem is where high performance computing (HPC) could have the largest impact on the field of quantitative genetics.

Until recently, the genetic and phenotypic datasets utilized in genetic mapping studies have been too small to provide the statistical power necessary to detect these small effect genetic variants. With the advent of high-throughput phenotyping and fast, cheap genome sequencing, these datasets are rapidly approaching the size necessary to tackle this problem.

These large datasets shift the bottleneck from data collection to the storage, management, and computational analyses of the these raw data. HPC will help alleviate the problems at this stage in two main ways. First, genetic mappings rely on extremely accurate reference genomes assembled from DNA sequenced at great depth, which presents two challenges that can be solved by HPC: data storage and rapid data analysis. New data compression algorithms and database technologies are shrinking the file size of both the raw sequence reads and the assembled genomic sequence. Additionally, genome assembly and variant calling programs are being built to utilize the parallel processing capabilities of modern computing clusters. Second, HPC will expedite the mapping of phenotypes to genotypes through parallel computing and linear algebra-based mapping techniques. Genetic mapping via matrix math has already cut processing time by several orders of magnitude. Further optimization for parallel processing will speed the mapping steps to scale with the massive influx of data.

Field of Interest and the Role of Computational Science

Please discuss the experiences that have motivated you to pursue both computational science and your field of interest.

In my high school biology classes, I developed an appreciation for the field of genetics and its ability predict the phenotype of an individual. During my freshman year at the University of Utah, I began work in Dr. Erik Jorgensen's lab, utilizing principles of genetics and molecular biology to answer questions in neurobiology. In Dr. Jorgensen's lab, I learned to apply the principles of genetics to the model nematode *Caenorhabditis elegans* and glean important information about the connection between genotype and phenotype.

from crosses between strains.

During the summer following my freshman year, I was able to obtain an internship at Princeton University in Dr. Leonid Kruglyak's lab. While working with Dr. Erik Andersen, a post-doc in the Kruglyak lab, I learned the basics of quantitative genetics and the importance of computation in modern biology. I learned how to uncover genetic variants associated with quantitative phenotypes, traits that vary continuously, such as length or optical density, in our model nematodes. Dr. Andersen introduced me to the statistical computing language R and the packages available to manage and analyze our data. At the end of that summer, I agreed to join Dr. Andersen in his new lab at Northwestern University for the following summers.

While working in Dr. Andersen's lab, I began to grasp the relationship between the data that we collected and the computational analysis of that data. I constructed an R package, COPASutils, to help manage the phenotype data that we collected and prepare it for mapping to genomic intervals. While the *C. elegans* genome is small in comparison to that of humans, the mapping step of our analysis proved to be quite computationally intensive, with some analyses needing to be moved to a computing cluster in order to be completed on a reasonable time scale. These issues in data analysis, along with my experiences building scientific software, have inspired me understand high performance computing so that the methods we have used with small *C. elegans* datasets can be scaled to vastly larger human studies. I seek to develop expertise in parallel computing, data mining, and machine learning to significantly advance the science of quantitative genetics.

List of publications

Please include a list of publications authored or co-authored by the applicant.

Tyler C. Shimko and Erik C. Andersen. (2014) "COPASutils: An R Package for Reading, Processing, and Visualizing Data from COPAS Large-Particle Flow Cytometers." PLOS ONE. DOI: 10.1371/journal.pone.0111090

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Other Planned Courses

Listed are the other courses you plan to take that you believe are particularly pertinent to your proposed or current research in the areas of Mathematics, Science and Engineering, and Computer Science.

Course number	Course Title	Credit hours	Term and Year	Grade	Academic Level
<i>Science/Engineering</i>					
BIOS 200	Foundations in Experimental Biology	6Q	Fall 2015		G
GENE 200	Training Camp	1Q	Fall 2015		G
GENE 211	Genomics	3Q	Winter 2016		G
GENE 215	Frontiers in Biological Research	1Q	Fall 2015		G

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Course Description

BIOS 200: Foundations in Experimental Biology

This course is divided into three 3-week cycles and is focused on the broad themes of Evolution, Energy and Information. During each cycle, students work in small teams and will be coached by faculty to develop an original research project and compose a brief written proposal explaining the research. Skills emphasized include: 1) reading for breadth and depth; 2) developing compelling, creative arguments; 3) communicating with the spoken and written word; 4) working in teams. Peer assessment and workshops; substantial face-to-face discussion with faculty drawn from across the Biosciences programs.

GENE 200: Training Camp

Introduction to basic manipulations, both experimental and conceptual, in genetics and developmental biology.

GENE 211: Genomics

The goal of this course is to explore how different experimental strategies are applied to a variety of biological questions. By experimental strategy, we refer to both the general method and the logic with which the method is applied. An underlying theme of the course is that each strategy we discuss can be applied to problems that cut across different disciplines, for example immunology, cancer biology, or embryology. Genome evolution, organization, and function; technical, computational, and experimental approaches; hands-on experience with representative computational tools used in genome science; and a work knowledge of the scripting language Python.

GENE 215: Frontiers in Biological Research

Literature discussion in conjunction with the Frontiers in Biological Research seminar series in which investigators present current work. Students and faculty meet beforehand to discuss papers from the speaker's primary research literature. Students meet with the speaker after the seminar to discuss their research and future directions, commonly used techniques to study problems in biology, and comparison between the genetic and biochemical approaches in biological research.

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Completed Courses

Please list up to six courses you have completed that are particularly pertinent to your proposed or current research in the areas of Mathematics, Science and Engineering, and Computer Science. Please do not list entry level science/engineering or mathematics courses like Calculus I.

Course number	Course Title	Credit hours	Term and Year	Grade	Academic Level
BIOL5110	Molecular Biology and Genetic Engineering	3S	Fall 2012	A-	B
BIOL5140	Genome Biology	3S	Spring 2014	A	B
BIOL5221	Human Evolutionary Genetics	4S	Fall 2014	A	B
MATH3070	Applied Statistics I	4S	Fall 2013	A	U
MATH3080	Applied Statistics II	3S	Spring 2014	A-	U

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Course Description

BIOL5110: Molecular Biology and Genetic Engineering

Recombinant-DNA principles and techniques; background biology. Basic enzymology of DNA (restriction and modification, sealing, reverse transcription, nick translation, end labeling, etc.), cloning plasmids and their replication, bacteriophage, and basic methodologies.

BIOL5140: Genome Biology

The sequence of the human genome, and that of other animals and plants, highlights the rapid progress in genomics, the study of the DNA sequence and genes of an organism. This course will examine recent findings in the field, with an emphasis on how advances in genomics are revolutionizing the ways by which we assign functions to sequence and genes. While human genomics will feature prominently, examples will be selected from diverse organisms to illustrate basic principle.

BIOL5221: Human Evolutionary Genetics

Theories and methods of molecular population genetics, with emphasis on human examples. How DNA sequence variation is analyzed to infer population history and to identify genes recently subject to selection. Laboratory exercises develop elementary programming skills and show how computation is used to connect models and data.

MATH3070: Applied Statistics I

An introduction to basic probability theory, sampling from normal populations, large-sample problems, sampling from one or two populations, estimation, and testing. R is used to perform statistical analyses. There are three lectures and one 1 1/2 hour lab per week.

MATH3080: Applied Statistics II

Introduction to analysis of variance, regression analysis, correlation analysis, and nonparametric techniques. Continued use of R programming language. There are two lectures and one 1 1/2 hour lab per week.

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Laboratory and Research Experience/Other Employment

Begin with current or most recent employment. Please include employer, dates employment started and ended, position, and nature of work.

08/2014 to Present - Undergraduate Researcher (Stanfield lab, University of Utah, 20-25 hrs/week) - Analyzed genomic sequence data and identified genetic variants implicated in abnormal sperm activation phenotypes in *C. elegans*. To be presented at the University of Utah's 2015 Undergraduate Research Symposium and published as my Honors Thesis.

05/2014 to 08/2014 - Undergraduate Researcher (Andersen lab, Northwestern University, 40-50 hrs/week) - Designed and built software to process data from COPAS large-particle flow cytometers and investigated the genetics of complex traits through the analysis of genetic linkage mapping data from previous summer. Published in Shimko and Andersen, 2014 (PLOS ONE) and presented to the Northwestern University Worm Club on July 30th, 2014.

08/2013 to 05/2014 - Undergraduate Researcher (Stanfield lab, University of Utah, 20-25 hrs/week) - Genetically mapped mutations affecting sperm activation in *C. elegans*.

05/2013 to 08/2013 - Undergraduate Researcher (Andersen lab, Northwestern University, 40-50 hrs/week) - Constructed high-throughput phenotyping pipeline for use in genetic linkage mapping studies with *C. elegans*. Built python program to identify restriction fragment length polymorphism sites closest to a user defined marker in the *C. elegans* genome. To be published in a paper that is currently in preparation.

01/2013 to 05/2013 - Undergraduate Research Advisor (Office of Undergraduate Research, University of Utah, 5-10 hrs/week) - Helped fellow undergraduates find research opportunities on campus and begin involvement in research projects. Collected information about research in progress from faculty members to update program's website.

08/2012 to 05/2013 - Undergraduate Researcher (Jorgensen lab, University of Utah, 10-20 hrs/week) - Investigated protein involved in synaptic vesicle recycling in *C. elegans*. Conducted suppressor screen to identify mutants of interest.

05/2012 to 08/2012 - Undergraduate Researcher (Kruglyak lab, Princeton University, 40-50 hrs/week) - Constructed *C. elegans* strains used to investigate the roles of genomic regions on phenotypes in response to the herbicide paraquat. Presented by Dr. Erik Andersen at the 2013 International *C. elegans* Meeting and the 2013 Society for Molecular Biology and Evolution Meeting. Presented by myself at the 2013 Utah Conference on Undergraduate Research and the 2013 National Conference on Undergraduate Research. To be published in a paper that is currently in preparation.

09/2011 to 05/2012 - Undergraduate Researcher (Jorgensen lab, University of Utah, 10-20 hrs/week) - Constructed universal transgene landing sites in the genome of *C. elegans*. Presented at the University of Utah's 2012 Undergraduate Research Symposium and 2012 Bioscience Symposium for Undergraduate Researchers.

Programming Languages and Models

List (four at most) the programming languages and programming models with which you have experience.

R - I have used the R programming language extensively throughout both my coursework and research. Several of my classes at the University of Utah have included computer labs that have taught the R language. These courses include Calculus for Biologists I and II and Applied Statistics I and II. I began utilizing the R language in the summer of 2012 while working on a research project in Dr. Leonid Kruglyak's lab at Princeton University. Since that time, I have used R in every subsequent research project to varying extents. This past summer, I constructed a new package for the R language, COPASutils, for the reading, processing, and visualization of data from COPAS large particle flow cytometers. I have also used the R language mutant phenotype analysis and genetic mapping.

Python - I have used python in both my coursework and my research. In the class Human Evolutionary Genetics, the Python language was taught in a computer lab for the analysis of genomic data. Additionally, I have used the python language in my research to create a program for the identification of genomic sites useful in restriction fragment length polymorphism analyses. I have also used the python language to tie together R scripts of various function in my genomic mapping experiments.

Java - I have used Java primarily in my coursework. Specifically, my course Introduction to Object Oriented Programming utilized the Java language extensively.

Academic Awards and Honors

Include undergraduate and graduate honors (if applicable).

Myriad Academic Excellence Award (University of Utah College of Science) - Fall 2014 to Spring 2015 - One of 6 awards given to top rising seniors in the College of Science with an interest in studying genetics, cell, or molecular biology, based on academic merit

University of Utah College of Science Dean's Scholarship (University of Utah College of Science) - Fall 2013 to Spring 2014 - One of several awards given to top students in the College of Science based on academic merit

Barry Goldwater Scholarship (Barry Goldwater Scholarship and Excellence in Education Foundation) - Fall 2013 to Spring 2015 - Nationally competitive scholarship given based on merit of prior research experiences and written research proposal. Awarded in sophomore year.

Theodore Verender Hanks Scholarship (University of Utah College of Science) - Fall 2013 to Spring 2014 - Awarded to top applicant in the College of Science who is not a Utah resident based on academic merit

Full Resident/Half Non-Resident Partial Tuition Waiver Scholarship (University of Utah) - Fall 2012 to Spring 2015 - Awarded based on academic merit

Undergraduate Research Opportunities Program Assistantship (University of Utah) - Spring 2012 - Provided funding for one semester to conduct independent research in a university laboratory, awarded based on written research proposal

Dean's List - Fall 2011 to Present

Full Resident Partial Tuition Waiver Scholarship (University of Utah) - Fall 2011 to Spring 2012 - Awarded based on academic merit

Extracurricular Activities

Include technical societies and service organizations.

Biology Student Advisory Committee Member (BioSAC) - Fall 2014 to Present - As a BioSAC member, I was, in part, responsible for the review of University of Utah faculty members for promotion, retention, and/or tenure. The committee also reviewed applications for the reimbursement of travel expenses for undergraduate students to attend special events and present their work at research conferences.

Intramural Football Player - Fall 2014

Undergraduate Research Opportunities Program (UROP) Research Ambassador - Fall 2012 to Fall 2014 - As a UROP Research Ambassador, I presented on my experience in undergraduate research to underclassmen at the University of Utah. I also helped to recruit entering freshmen and high school students into research positions at the university and mentored underclassmen on finding and becoming involved in research experiences.

Fossil Free U - Fall 2012 to Fall 2013 - Fossil Free U was a student organization that I helped co-found to raise awareness and confront the issue of climate change by pushing for the divestment of the University of Utah's endowment from the stocks of the top 200 fossil fuel companies. In Fossil Free U, I was responsible for the collection and presentation of all pertinent statistical data including reviewing academic literature on the effects of climate change and designing a survey to gauge the opinion of the student body on the issue of divestment.

Intramural Football Team Captain - Fall 2011 to Fall 2013

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Additional Comments

Because both of my parents are teachers, I have always been encouraged to learn all I can from those around me and to share my own expertise. I believe that the research process is more efficient when these sharing guidelines are followed. Whether or not I am awarded this fellowship, I eagerly await the opportunity to share all that I learn with others both inside and outside the quantitative genetics community. This fellowship would afford me the freedom to expand my knowledge base and share more expertise in statistics and computer science with those around me.

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DOE CSGF and Other Fellowships

The information that you provide will allow us to target our advertising more effectively. This information is confidential and is not used in review of the fellowship application.

1. Have you applied to other fellowship programs?

- DOE NNSA SSGF
- NSF
- DOD
- University-sponsored Names of fellowships:
- Other Names of fellowships: **Hertz Fellowship**

2. How did you find out about the program?

- DOE CSGF poster
- DEIXIS, DOE CSGF annual publication
- Attended DOE CSGF talk
- Advertisement Name the source:
- Word of mouth from
 - faculty
 - student
 - administrator
- Laboratory staff
- Institutional announcement
- Conference or meeting Name:
- World Wide Web List URL: <http://blog.olgabotvinnik.com/blog/2013/04/28/2013>
- Other Explain:

Applicant Demographics

Applicant data is important in assessing the effectiveness of our efforts to solicit applications from a diverse population. Providing the information on this form is voluntary; omission of information will not affect any decision about your application. We appreciate your cooperation.

Race: Caucasian

Gender: Male

Physical/mental
disability: No