STANFORD UNIVERSITY - APPLICATION FOR GRADUATE ADMISSION App # 58672488

Name: Tyler Carter Shimko
Program: Genetics PHD
Specialization:
Interest 1:
Interest 2:
Interest 3:
Fellowship/Assistantship Interest: No

Term: Autumn 2015-2016
Degree: PHD

Mailing Address, Phone (Valid Until 05-01-2015)

[redacted]

Home Address, Phone

[redacted]

Institution(s) Previously Attended

UNIVERSITY OF UTAH
SALT LAKE CITY, UT
Degree: Bachelor of Science
Attendance: 08-2011 to 05-2015
Country: United States
Field: Biology
GPA: 3.89
Degree Date: 05-2015
Orig. GPA Scale:
Orig. GPA:
Country:
Field:
GPA:

Degree:
Attendance: to
Degree Date:
Orig. GPA Scale:
Orig. GPA:
Country:
Field:
GPA:

Degree:
Attendance: to
Degree Date:
Orig. GPA Scale:
Orig. GPA:

Test Scores

GRE General Test: GRE General Test changed on August 1, 2011. GRE scaled scoring system has changed. ETS will convert scores for tests taken prior to August 1, 2011 so they can be compared directly to scaled scores for the revised GRE.

_____ Reporting on the 200-800 scale __X__ Reporting on the 130-170 scale

_____ Reporting on both the 200-800 and the Estimated Current Score scale (130-170)

Verbal Reasoning			Quantitative Reasoning			Analytical Writing			
Former Verbal Score	Current Verbal Scaled Score	Verbal %	Former Quant Score	Current Quant Scale Score	Quant %	AnWr Score	AnWr %		
	163	92		161	80	5	93	Taken: 06-2014	Future:

GRE Subject:

Score:	%	Taken:	Future:

TOEFL:

Type:	Total:	Taken:	Future:	
Listening:	Reading:	Writing :	Speaking:	Taken:

Citizenship Country/Status: United States / U.S. citizen

Birth Date: 01-26-1993 Birth Country: United States Visa Type:

Registered Perm. Res Number: Number

Ethnicity/Race: **Gender:** Male

Hispanic or Latino (y/n): N

Ethnicity 1:	**Ethnicity 2:**
Ethnicity 3:	**Ethnicity 4:** White - White [European]
Ethnicity 5:	**Ethnicity 6:**

References (three required)

Name: Erik Andersen at Northwestern University

[redacted]

Name: Gillian Stanfield at University of Utah

[redacted]

Name: Leonid Kruglyak at UCLA

[redacted]

Name: Erik Jorgensen at University of Utah

[redacted]

Name: at

Email

Name: at

Email

Stanford History

Prev. Applied Prog.: Academic Year:

Prev. Enrolled Prog.:

Last Enrolled Date: Stanford ID:

Changes to Academic Qualifications Since Last Application

Language Background

First Language: English

Other Languages	Reading	Writing	Speaking

Stanford Faculty Consulted Regarding Application	Date
Stephen Montgomery	10-22-2014
Lars Steinmetz	10-23-2014
Atul Butte	10-23-2014

Also Applying to These Graduate Schools

University of Washington; University of California, Los Angeles; University of California, San Diego; University of California, San Francisco; Northwestern University; University of Cambridge

Non-Stanford Financial Aid, Fellowships, Scholarships

Scholarship/Fellowship Title	Awarded	Awarded for Graduate Study
NSF-GRFP		
Hertz Fellowship		
DOE-CSGF		

Application Options

PhD Applicant consider for Masters? No OK to refer to another department? Yes

HCP? HCP Sponsor Company:

Employment or Professional Activity	From	To

Employer: Northwestern University 05-2014 08-2014
Position/Title: Research / Undergraduate Researcher

Employer: University of Utah 08-2013 05-2014
Position/Title: Research / Undergraduate Researcher

Employer: Northwestern University 05-2013 08-2013
Position/Title: Research / Undergraduate Researcher

Other Name

First Name

Middle Name

Last Name:

Additional Test Scores

Additional Academic Interests

Quantitative Genetics
Bioinformatics

Additional Educational History

Honors, Fellowships, Non-Academic Distinctions, Publications

Myriad Academic Excellence Award; Barry Goldwater Scholarship; Theodore Verender Hanks Scholarship; University of Utah College of Science Dean's Scholarship; Undergraduate Research Opportunities Program Assistantship; Full Resident Partial Tuition Waiver Scholarship; Dean's List

Contributing Factors to Stanford Community

Since both of my parents are teachers, I was raised in an environment in which a strong emphasis was placed on education and on sharing that education with others. Throughout my academic career, I have sought opportunities to share my knowledge and expertise with others, serving as an ambassador and adviser for the University's Undergraduate Research Opportunities Program. Additionally, I have participated in many supplementary academic activities, such as seminars and talks. At Stanford, I will bring with me an insatiable thirst for knowledge, which I intend to share with my fellow students through

Parent or Guardian Occupation and Level of Education

Occupation: Speech Therapist
Secondary School Teacher

Job Title: Speech Therapist
Woodshop Teacher

College Name: The College of New Jersey
The College of New Jersey

Employer: Bridgewater-Raritan Schools
Dunellen High School

Attended College: Yes
Yes

Highest Degree Obtained: Masters
BS

Unites States Military or Veteran Status

Probation, suspension, expulsion by Post-secondary school or program

Prior Convictions No

Application Submission

I hereby apply for admission to graduate study at Stanford University and certify that the information I have provided in my application (including my statement of purpose) is complete, accurate and my own work. I have submitted only one application for admission to graduate study at Stanford for the requested academic year indicated on this application.

I further acknowledge that if I am offered admission, Stanford reserves the right to withdraw that offer of admission if: (1) there is a significant drop in my academic performance or failure to graduate; (2) there is a misrepresentation in the application process; or (3) the University learns that I have engaged in behavior prior to matriculation that indicates a serious lack of judgment or integrity.

I authorize the educational testing service (ETS) to share individual information with Stanford concerning any examination relating to this application. And I agree that Stanford has the right to require me to provide additional information (and/or authorization for the release of information) about any matter relating to my application.

Date Application Submitted Online: 11-28-2014

58672488

Biosciences Ph.D. Admissions Supplemental Form

Name: Shimko (Last) Tyler (First) Carter (Middle) Email: tshimko126@gmail.com

Home Program Selections:

1. Genetics PHD 2. _____ 3. _____

Biochemistry: Computation and Systems Biochemistry:

Biology: Biology Ph.D. Interest: _____

Cancer Biology: Cancer Systems Biology Track Interest: _____

Immunology: Computational and Systems Immunology Track Interest: _____

Neurosciences: Neurosciences Interest/Experience: _____

Faculty of Interest:

Steinmetz, Lars; Montgomery, Stephen; Pritchard, Jonathan; Bustamante, Carlos; Tang, Hua; Butte, Atul; Bhatt, Ami; Fire, Andrew

Significant Research Project:

My most significant research project has taken place over the past two summers in the lab of Dr. Erik Andersen at Northwestern University. In this project, I utilized a large-particle flow cytometer to collect C. elegans phenotype data from a panel of recombinant inbred strains. I then utilized these data, along with existing genotype data, to map physiological responses to different chemical environmental perturbations to specific genomic intervals. These intervals are now in the process of being narrowed to specific causative genes. I also produced, released, and published the COPASutils R package for managing phenotype data from the flow cytometer as a result of this project.

Describe an Interesting Biological or Biomedical Problem:

I am interested in the way that an organism's genetic background and its environment interact to govern its susceptibility to disease. While the pure genetic underpinnings of some diseases, such as sickle cell anemia, are well understood, we know relatively little about how an organism's genotype at specific loci combine with environmental cues to affect that organism's ability to fend off disease. The study of this topic requires expertise in many areas of study. Primarily, the methods of quantitative genetics must be applied in order to uncover causative genomic regions that underlie the phenotype of interest. These methods often require a strong foundation in statistics and computer science, as the necessary data sets are often very large. Then, a knowledge of classical genetic techniques often must be utilized to narrow the identified genomic region to a specific gene. Once a gene is identified, expertise in biochemistry and structural biology must be employed to uncover the molecular mechanism through which an environmental factor, such as chemical presence or concentration, can interact with a specific gene product to influence susceptibility to a particular disease. An understanding of these gene-environment interactions will be necessary for genetic sequence information to become widely used in medical diagnostics or treatments. This problem is interesting to me because of its interdisciplinary nature and potential applications relevant to human health.

Tyler Carter Shimko
58672488

Training Goals:

Through the training that I will receive in a PhD program, I hope to increase my proficiency in the collection and analysis of genomic data, especially with respect to the computational tools currently being used in the field. I also hope to expand my knowledge of the theory underlying the fields of modern quantitative genetics and bioinformatics so that I can make significant contributions to elucidating the genetic-environmental interactive effects that govern disease susceptibility. Additionally, I hope to receive instruction on the proper dissemination of scientific findings so that my research will have the greatest impact possible on the solution of scientific challenges. The Genetics Home Program is very well-equipped to help me achieve my training goals. Through the laboratory rotations in my first year, I plan to gain diverse experience in the sub-fields of genetics. I will then utilize this experience in my later thesis project to further my research and approach it from a fresh perspective. In addition to the expertise that I will gain from my research, I will also have instruction on the theory of computational genetics through the curriculum of the program. Finally, I will gain experience in disseminating scientific information through the various seminars and journal clubs offered by the program. In these settings I will be able to hone my presentation skills as well as learn from successes of my fellow scientists.

Foundations of Graduate Study:

Experience as acquired through coursework, research, or other projects, or plans to obtain or expand such experience before starting Ph.D. Responses in Part Two are only expected for those applying to Biomedical Informatics and the Computational/Systems Tracks of Biochemistry, Cancer Biology, and Immunology, but others are encouraged to respond.

Part One

The experimental analysis of biological or biomedical systems:

I have extensive coursework in the theory of biological systems, especially regarding genetics and genomics. Among the upper-division biology courses that I have taken are Biological Chemistry I and II, which focused on the chemistry of cellular metabolism and the cellular management of DNA [replication, repair, etc.], Molecular Biology and Genetic Engineering, which focused on the theory and practice of the techniques associated with molecular biology, and Cell Lab, which offered practical experience with the most commonly used molecular and cell biology techniques. Additionally, I have taken Genome Biology and Human Evolutionary Genetics, both of which instructed me on the basics of genomic data analysis. In both of these classes, I was exposed to examples of biological experimentation in the primary literature. In addition to classroom instruction, I have been involved in research continuously since my freshman year of college. I have learned neuro- and molecular biology techniques in Dr. Erik Jorgensen's lab at the University of Utah, quantitative genetics techniques in the labs of Drs. Leonid Kruglyak and Erik Andersen at Princeton University and Northwestern University, respectively, and classical genetics techniques in Dr. Gillian Stanfield's lab at the University of Utah. In the aforementioned labs, I have worked on projects that were purely bench work, purely computational, and a mixture of both.

Part Two

Multivariate mathematics (including calculus and linear algebra):

I have taken Calculus for Biologists I and II at the University of Utah. This class set included roughly three quarters traditional calculus in addition to roughly one quarter probability and statistics. Additionally, this course covered the analysis of discrete-time dynamical systems. I have also utilized linear algebra in my research to perform meta-analyses of quantitative trait loci. Consequently, I have pursued self-study of linear algebra in order to validate my methods.

Probability and statistics:

At the University of Utah, I have taken Applied Statistics I and II. In this course set, I covered the basics of probability theory, parametric, and nonparametric statistical tests. I have also taken four semesters of computer labs in the R statistical programming language as part of my Calculus and Statistics course sets. I am currently enrolled in Human Evolutionary Genetics, a course that focuses on the statistical analysis of population genetic data. Additionally, my research projects in quantitative genetics have utilized statistical methods in great depth. I have explored the differences in mapping phenotypes to genotypes using both parametric and nonparametric mapping methods and used to statistical tests to validate my data.

Computation, including fundamentals of computer science and software engineering:

At the University of Utah, I have taken Object Oriented Programming to improve my skills as a programmer. This class utilized the Java programming language. I have also taken four semesters of computer labs in the R statistical programming language for my Calculus and Statistics classes and one semester in the Python programming language for my Human Evolutionary Genetics class. My research has relied heavily on computation as well. I have produced programs to identify restriction fragment length polymorphism sites [https://github.com/TShimko126/Andersen-Lab-Code/tree/master/snipSNPer] and to clean and analyze genome-wide association and linkage mapping data [COPASutils, http://cran.r-project.org/web/packages/COPASutils/index.html].

Honors, Awards, Posters, Presentations, and Publications:

Honors and Awards:

Dean's List - All semesters; Myriad Academic Excellence Award - Spring 2014; Barry Goldwater Scholarship [Nationally competitive, research-based, awarded as a sophomore] - Spring 2013; Theodore Verender Hanks Scholarship - Spring 2013; University of Utah College of Science Dean's Scholarship - Spring 2013; Full Resident/Half Non-Resident Partial Tuition Waiver Scholarship [Merit-based] - Fall 2012-Spring 2014; Undergraduate Research Opportunities Program Assistantship - Spring 2012; Full Resident Partial Tuition Waiver Scholarship [Merit-based] - Fall 2011-Spring 2012

Posters:

Tyler C. Shimko, Erik C. Andersen, and Leonid Kruglyak. Identifying the genes that control paraquat resistance in the roundworm C. elegans. National Conference on Undergraduate Research. April 2013.; Tyler C. Shimko, Erik C. Andersen, and Leonid Kruglyak. Identifying the genes that control paraquat resistance in the roundworm C. elegans. Utah Conference on Undergraduate Research. February 2013.; Tyler C. Shimko, Christian Frokjaer-Jensen, and Erik M. Jorgensen. Universal Transgene Insertion in C. elegans. University of Utah Bioscience Symposium for Undergraduate Researchers. April 2012.; Tyler C. Shimko, Christian Frokjaer-Jensen, and Erik M. Jorgensen. Universal Transgene Insertion in C. elegans. University of Utah Undergraduate Research Symposium. March 2012.

Presentations:

[* indicates presenter] Tyler C. Shimko, Robyn E. Tanny, and Erik C. Andersen*. Using high-throughput fitness assays to decipher the genetic causes of C. elegans drug sensitivities. Society for Molecular Biology and Evolution Meeting. July 2013.; Tyler C. Shimko and Erik C. Andersen*. Using natural variation to decipher the complex genetic cause of C. elegans drug sensitivities. 19th International C. elegans Meeting. June 2013.

Publications:

Tyler C. Shimko and Erik C. Andersen. COPASutils: An R Package for Reading, Processing, and Visualizing Data from COPAS Large-Particle Flow Cytometers. PLOS ONE. [2014, Published]

NIH: Family's annual income below established low-income thresholds? _____

Tyler Shimko
Statement of Purpose (Genetics Home Program)

I first came to appreciate the power of biological research in my high school biology class. In this class, I recognized that genomic research had the power to make predictions about and alter the traits of living creatures. Upon graduating from high school, I chose to attend the University of Utah, where, with the help of the school's Office of Undergraduate Research, I had an immediate opportunity to become deeply involved in research and pursue my interests to the fullest. I have since been fortunate to take part in research at three universities and participate in projects ranging from molecular biology to neurobiology to quantitative genetics. Through these experiences my appetite for discovery has only grown. I now seek to undertake the next step in my scientific education, the pursuit of a PhD, to prepare myself for a career in research.

During my freshman year at the University of Utah, I joined the laboratory of Dr. Erik Jorgensen to assist in the construction of universal transgene insertion sites within the genome of *C. elegans*. My project eventually resulted in the creation of three distinct transgene landing sites. It was exhilarating to discover, create, and share knowledge with others. However, my exposure to the broader research community, through presentations at university-level events, alerted me that there were other opportunities to learn new skills and make significant contributions. To expand my research skill set, I sought summer internships in laboratories focused on computational methods in addition to molecular biology. I obtained an offer from Dr. Leonid Kruglyak, of Princeton University at that time.

In Dr. Kruglyak's lab I worked with Dr. Erik Andersen, a post-doctoral fellow. Dr. Andersen had previously completed a genomic mapping experiment wherein he had determined a region of the *C. elegans* genome that conferred resistance to the herbicide paraquat and he enlisted my help to construct strains in an attempt to identify the causal genomic variations in that region. I explored different techniques, using both molecular biology and genetic crosses, to construct strains with which we could test the hypothesis that we had successfully identified causal genetic variants. Throughout the course of the summer, I supplemented my hands-on laboratory experience with instruction and practice with the computational methods that Dr. Andersen had employed in his mapping experiments. This basic training in computer science and statistics eventually led me to take formal classes in these subjects at the University of Utah. These courses greatly expanded my research potential and prepared me to take on large projects with significant computational components. Dr. Andersen and I continued our collaboration in his new laboratory at Northwestern University in the following summers.

In the fall of 2012, I began a new project in the Jorgensen lab to identify suppressors of the phenotype associated with a mutant protein involved in synaptic vesicle endocytosis. I learned new techniques for the design and implementation of genetic screens and applied my new computational skills whenever possible. However, by the end of the academic year, it became apparent that the phenotype of interest was too weak for our suppressor screens to yield any useful information. While I was originally upset that our project was unsuccessful, I quickly realized that failure is more of the rule than the exception in biological research. To continue toward a career in research, I would need to learn from failure and to fail gracefully. In fact, I learned that failure gives us many answers as well. In this respect, the year had not been wasted.

During my past two summers in Dr. Erik Andersen's lab, I have had the opportunity to explore how genetic variation dictates the way in which organisms respond to their environment. I sought to determine the ways in which the genetic variation present in the worldwide population of the model nematode *C. elegans* affects responses to different chemicals including herbicides, pesticides, chemotherapeutic agents, and anthelmintics (compounds used to treat infections of

parasitic nematodes). I helped to construct and optimize a high-throughput screening technique that allows us to measure the effects of the aforementioned compounds on nematodes in a multitude of ways. This pipeline has allowed us to conduct genome-wide association and linkage mapping studies. Over the past summer, I designed and built software to clean and process the data from our screening experiments and run statistical tests to map phenotypic differences to genetic variants. This software, *COPASutils*, has been published in the journal *PLoS ONE* and made freely available on the Comprehensive R Archive Network. My hope is that this software will gain widespread use in the model organism research community.

During my junior and senior years, I have worked in the lab of Dr. Gillian Stanfield at the University of Utah. My project has focused on identifying mutations that suppress premature sperm activation in male *C. elegans*. I carried out a series of crosses and phenotype selections as part of a genetic mapping scheme, and, at the end of my first year, several strains that displayed the suppressed phenotype were sent for sequencing in the hopes of being able to identify causal mutations. I am now beginning to utilize raw genetic sequence and mapping data to identify variants implicated in suppression. This project may help to identify the causal mutation for each of the individual suppressed strains and will culminate in the publication of my Honors thesis.

Most recently, I have become deeply interested in the large-scale analysis of genomic data. I want to refine the methods used to connect phenotypic traits back to specific genomic variants. This problem is interesting from both a biological and a computational perspective. In order to accurately and efficiently connect physiological traits to genetic differences, a massive amount of phenotypic and genotypic data must be collected and analyzed. This problem is pertinent to many facets of modern human life. Genomic information utilized in the diagnosis and treatment of certain diseases has proven to be a paradigm-shifting development in medicine. The identification of genes influencing yield or environmental robustness will be key to creating crops capable of feeding our growing population. During my tenure in a PhD program and through my career as a researcher, I will work to confront the theoretical, logistical, and scientific challenges related to problems in quantitative genetics.

I have selected Stanford because of the incredible wealth of opportunities that it will provide in achieving my educational and career goals. For instance, Stanford's Bio-X initiative offers unparalleled opportunities to expand my research into new fields. The ability to utilize biochemical and biophysical knowledge to predict the downstream effects of genetic differences is critical for the application of quantitative genetics. Through Bio-X, I will interact with and learn from leading researchers from these and related fields, multiplying the impact of my own work. Additionally, the faculty at Stanford will provide superior training and guidance as I further develop my skills in genetics, mathematics, and computer science.

In particular, I am interested in working with Dr. Lars Steinmetz who has conducted extensive research on the interaction between genes and environmental factors with respect to human disease. As co-director of the Stanford Genome Technology Center, Dr. Steinmetz has unprecedented access to emerging tools for the gathering and analysis of genomic data, which I hope to leverage in my own research. Moreover, I am interested in the work of Drs. Stephen Montgomery and Jonathan Pritchard, who have both examined gene regulation, an important component of many diseases, from population-wide and evolutionary perspectives. The research of Drs. Carlos Bustamante and Hua Tang, both of whom have utilized genetic variation to investigate the evolutionary history of humans, also interests me. The academic opportunities that Stanford will provide are truly exciting. The mentorship and experience that I will gain at Stanford will prepare me exceptionally well to undertake a career in genomic research.