

Amy L. Williams

CONTACT INFORMATION Cornell University *Phone:* +1 (801) 842-8654
Biological Statistics & Computational Biology Dept *E-mail:* awilliams@cornell.edu
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Ithaca, NY 14853

CITIZENSHIP USA

EDUCATION **Massachusetts Institute of Technology**, Cambridge, Massachusetts, USA
Ph.D., Computer Science **February 2010**
• Advisors: Professors David K. Gifford and David E. Housman
S.M., Electrical Engineering and Computer Science **June 2005**
• Advisor: Professor Michael D. Ernst
University of Utah, Salt Lake City, Utah, USA
B.S., Computer Science (with Honors) **May 2003**
• Advisor: Professor Wilson Hsieh
B.S., Mathematics **May 2003**

ACADEMIC EXPERIENCE **Cornell University**, Ithaca, New York, USA
Assistant Professor **August 2014 to Present**
Nancy and Peter Meinig Family Investigator in Life Sciences
Columbia University, New York, New York, USA, *and*
Howard Hughes Medical Institute, Chicago, Illinois, USA
*Work conducted at **Columbia University***
Postdoctoral Research Fellow **August 2013 to July 2014**
• Advisor: Professor Molly Przeworski
Harvard Medical School, Boston, Massachusetts, USA
Postdoctoral Research Fellow **October 2009 to July 2013**
• Advisors: Professors David Reich and David Altshuler
Massachusetts Institute of Technology, Cambridge, Massachusetts, USA
Graduate Student and Research Assistant **January 2004 to October 2009**
• Advisors: Professors David K. Gifford and David E. Housman
Teaching Assistant **January 2005 to May 2005**
• 6.170, Spring Semester 2005: Laboratory in Software Engineering
– Undergraduate course in software engineering principles
University of Utah, Salt Lake City, Utah, USA
Undergraduate Research Assistant **May 2002 to May 2003**
• Advisors: Professors Wilson Hsieh and Peter Shirley

AWARDS AND
FELLOWSHIPS

Alfred P. Sloan Research Fellowship, 2015
ASHG Trainee Research Semifinalist Award, 2011
Ruth L. Kirschstein National Research Service Award (NRSA), 2010
NIH post-doctoral fellowship (2010 – 2013)
NSF Graduate Research Fellowship, 2003
Pre-doctoral fellowship (2003 – 2006)
Dean's List, University of Utah, 1998 – 2002
C.M. Collins Engineering Scholarship, University of Utah, 2002
Early undergraduate admission following high school junior year, 1998

PUBLICATIONS

***Corresponding author**

Ramstetter MD, Dyer TD, Lehman DM, Duggirala R, Blangero J, Mezey JG, **Williams AL***. *Inferring identical by descent sharing in sample ancestors promotes high resolution relative detection* (**In preparation**).

Basu-Roy S, Dyer TD, Lehman DM, Duggirala R, Blangero J, **Williams AL***. *Inferring parental genomes and parent-of-origin using genotypes from siblings*. (**In preparation**).

Ramstetter MD*, Dyer TD, Lehman DM, Duggirala R, Blangero J, Mezey JG, **Williams AL***. *A performance assessment of relatedness inference methods using genome-wide data from thousands of relatives* (**In revision, Genetics**), 2017. [bioRxiv pre-print available]

Palmer ND, Goodarzi MO, Langefeld CD, ... [22 authors] ... **Williams AL**, ... [21 authors] ... Watanabe RM, Wagenknecht LE. *Genetic Variants Associated with Quantitative Glucose Homeostasis Traits Translate to Type 2 Diabetes in Mexican Americans: The GUARDIAN (Genetics Underlying Diabetes in Hispanics) Consortium*. **Diabetes** **64(5):1853-66**, May 2015.

Williams AL*, Genovese G, Dyer T, et al. for the T2D-GENES Consortium. *Non-crossover gene conversions show strong GC bias and unexpected clustering in humans*. **eLife** **2015;4:e04637**, Apr 2015.

The SIGMA Type 2 Diabetes Consortium: Estrada K, Aukrust I, Bjørkhaug L, Burt NP, Mercader JM, García-Ortiz H, Huerta-Chagoya A, Moreno-Macías H, Walford G, Flannick J, **Williams AL**[†], et al. *Association of a Low-Frequency Variant in HNF1A With Type 2 Diabetes in a Latino Population*. **JAMA** **311(22):2305-14**, Jun 2014.

[†]**Preformed sample selection for exome sequencing and contributed to association analyses**

The SIGMA Type 2 Diabetes Consortium: Williams AL[‡], Jacobs SBR, Moreno-Macías H, et al. *Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico*. **Nature** **506:97-101**, Feb 2014.

[‡]**Led the genetics analysis and wrote the genetics portions of paper.**

The 1000 Genomes Project Consortium[§]. *An integrated map of genetic variation from 1,092 human genomes*. **Nature** **491:56-65**, Nov 2012.

[§]**Developed HAPMIX extension and applied it to the Latino populations.**

Williams AL*, Patterson N, Glessner J, Hakonarson H, Reich D. *Phasing Many Thousands of Genotyped Samples*. **Am J Hum Genet**, **91:238-51**, Aug 2012.

Fejerman L, Chen GK, Eng C, Huntsman S, Hu D, Williams A, Pasaniuc B, John EM, Via M, Gignoux C, Ingles S, Monroe KR, Kolonel LN, Torres-Mejía G, Pérez-Stable EJ, Burchard EG, Henderson BE, Haiman CA, Ziv E. *Admixture mapping identifies a locus on 6q25 associated with breast cancer risk in US Latinas*. **Hum Mol Genet**, **21:1907-17**, Apr 2012.

Williams AL*, Housman DE, Rinard MC, Gifford DK. *Rapid Haplotype Inference for Nuclear Families*. **Genome Biol**, **11:R108**, Oct 2010.

Williams A, Thies W, Ernst MD. *Static Deadlock Detection for Java Libraries*. In **Proceedings of the 2005 European Conference on Object-Oriented Programming (ECOOP)**. Glasgow, Scotland, UK. Jul 2005.

Williams A, Barrus S, Morley K, Shirley P. *An efficient and robust ray-box intersection algorithm*. **Journal of Graphics Tools**, **10:49-54**, Jun 2005.

CONFERENCE
TALKS

“*Inferring the genomes of mothers and fathers using genotype data from a set of siblings*”
Family History Technology Workshop February 2017

“*Pedigree reconstruction in the era of many thousands of samples*”
Probabilistic Modeling in Genomics September 2016

“*Inferring local ancestry by jointly analyzing admixed samples*” (**Invited Speaker**)
Probabilistic Modeling in Genomics October 2015

“*Inferring local ancestry by jointly analyzing admixed samples*” (**Invited Speaker**)
Models and Inference in Population Genetics Workshop September 2015

“*Fine-scale properties of non-crossover gene conversion in humans.*” (**Invited Speaker**)
New York Area Population Genomics Workshop January 2015

“*The fine-scale landscape of meiotic non-crossover gene conversion.*”
64th Annual Meeting of The American Society of Human Genetics October 2014

“*A genome-wide estimate of the meiotic gene conversion rate in humans.*”
Biology of Genomes May 2013

“*Identification of a novel genome-wide significant association with type 2 diabetes risk in Mexican and Mexican Americans.*”
62nd Annual Meeting of The American Society of Human Genetics November 2012

“*Phasing of Many Thousands of Genotyped Samples.*”
61st Annual Meeting of The American Society of Human Genetics October 2011
Semifinalist for Trainee Research Award

“*Static Deadlock Detection for Java Libraries.*”
European Conference on Object-Oriented Programming (ECOOP) July 2005

INVITED TALKS	<p><i>“Relatedness inference in modern samples: Leveraging multi-way signals to improve resolution”</i></p> <ul style="list-style-type: none"> – Weill Cornell Medicine March 2017 <p><i>“Towards large-scale disease and ancestry analyses in diverse samples”</i></p> <ul style="list-style-type: none"> – Population Architecture using Genomics and Epidemiology (PAGE) Steering Committee Meeting November 2015 <p><i>“Haplotype inference of large datasets and applications to gene conversion and disease studies”</i></p> <ul style="list-style-type: none"> – Brigham Young University March 2014 – Cornell University February 2014 – New York University February 2014 – University of Chicago February 2014 <p><i>“Meiotic gene conversion in humans: rate, sex ratio, and GC bias”</i></p> <ul style="list-style-type: none"> – University of Chicago June 2013 <p><i>“Analyzing gene conversion event rate and structure”</i></p> <ul style="list-style-type: none"> – Texas Biomedical Research Institute April 2013 <p><i>“Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico”</i></p> <ul style="list-style-type: none"> – Icahn School of Medicine at Mount Sinai November 2013 – Texas Biomedical Research Institute April 2013 – Harvard Medical School March 2013 – Broad Institute Annual Retreat November 2012 <p><i>“Phasing of Many Thousands of Genotyped Samples”</i></p> <ul style="list-style-type: none"> – Harvard Medical School March 2013 – Columbia University February 2013 – Broad Institute of Harvard and MIT February 2013
PROFESSIONAL SERVICE	<p>Reviewer, National Heart Lung and Blood Institute (NHLBI) 2016</p> <p>Special Emphasis Panel</p> <p>Reviewer, National Human Genome Research Institute (NHGRI) 2015</p> <p>Special Emphasis Panel</p> <p>Reviewer, American Society of Human Genetics 65th Annual Meeting 2015</p> <p>Reviewer, International Society for Computational Biology/ECCB 2015</p> <p>Member, American Society of Human Genetics 2009-Present</p> <p>Ad hoc reviewer for manuscripts submitted to the following journals: 2010-Present</p> <ul style="list-style-type: none"> – Nature Genetics – Proceedings of the National Academy of Sciences – Genome Research – Molecular Biology and Evolution – PLoS Genetics – Genetics – Annals of Human Genetics – Bioinformatics – PLoS Computational Biology – European Journal of Human Genetics – Diabetologia – PLoS ONE

CORNELL UNIVERSITY SERVICE	– Senator, CALS Faculty Senate	2017-Present
	– Program Committee, Computational Biology and Medicine Graduate Field Tri-Institutional program of Cornell University, Weill Cornell Medical College, and Sloan-Kettering Institute	2016-Present
	– Faculty Search Committee, Biological Statistics & Computational Biology	2015-2016
	– Consulted Life Science Advisory Committee concerning computational biology on campus	10/7/2015
	– Admissions Committee, Computational Biology Graduate Field	2014-Present
	– Faculty Search Committee, Molecular Biology and Genetics Dept.	2014-2015
– Advising 8 undergraduate students majoring in Biometry & Statistics	2015-Present	

Updated April 12, 2017