

Katarzyna (*Kasia*) Bryc, PhD

CONTACT INFORMATION	23andMe, Inc. Research Team 1390 Shorebird Way Mountain View, CA 94043	<i>Web:</i> kasiabryc.com <i>Phone:</i> (513) 720-1862 <i>E-mail:</i> kasia1@gmail.com <i>Updated: October 13, 2014</i>
RESEARCH INTERESTS	Theoretical and applied population genetics, human population structure and admixture inference, eigenanalysis in population structure estimation.	
ACADEMIC EXPERIENCE	Harvard Medical School , Boston, Massachusetts USA <i>Postdoctoral Research Fellow</i> September 2010 to March 2014 <i>Advisor:</i> Professor David Reich Estimating heterozygosity from low-coverage sequence data, delineating the complex admixture deconvolution of African Americans, and improving the understanding of the use of PCA in detection of substructure.	
EDUCATION	Cornell University , Ithaca, New York USA PhD, Biometry January 2011 <i>Advisor:</i> Professor Carlos D. Bustamante <i>Dissertation title:</i> “Genome-wide patterns of population structure and ancestry among continental and admixed populations” M.S., Biometry January 2009 <i>Advisor:</i> Professor Carlos D. Bustamante Stanford University , Stanford, California USA B.S., Mathematical and Computational Science June 2005 <i>Advisor:</i> Professor Brad Efron	
FELLOWSHIPS AND AWARDS	NIH F32: Postdoctoral Fellowship September 2011 – August 2014 Ruth Kirschstein National Research Service Award: “Insights from ancient and recent population mixture relevant to medical genetics” The American Society of Human Genetics 2012 Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research 2011 Trainee Research Semifinalist Award 2009 Trainee Research Award Finalist 2008 Predoctoral Basic Trainee Award Semifinalist	
PROFESSIONAL EXPERIENCE	23andMe , Mountain View, California USA <i>Population Geneticist</i> March 2014 to present <ul style="list-style-type: none">• Conducted population genetic research leveraging the 23andMe genotype-phenotype database: established the genetic landscape of the US.• R&D ancestry-related methods for Product improvements and updates.• Point person for ancestry-related questions in PR.• Evaluated academic collaborator proposals. 23andMe , Mountain View, California USA <i>Visiting Postdoctoral Research Fellow</i> September 2013 to March 2014 <ul style="list-style-type: none">• With Dr. Eric Durand and Dr. Joanna Mountain• Examination of self-identified versus genetic ancestry in the United States.	

Cincinnati Children's Hospital Medical Center, Cincinnati, Ohio USA

Biostatistics Research Assistant **January 2006 to August 2006**

- Designed methodology for a large microarray study looking for predictors of negative outcomes for epilepsy drug treatments in children.
- Provided statistical support for researchers.

Stanford University, Stanford, California USA

Anthropology and Genetics Research Assistant **June 2005 to August 2005**

- Professor Joanna Mountain
- Studied the population genetics of the Hadza of Tanzania, Africa.

Stanford University, Stanford, California USA

Statistics Research Assistant **June 2004 to August 2004**

- Professor Susan Holmes
- Designed a simulation for Affymetrix of the action of enzyme Klenow exo-

TEACHING
EXPERIENCE

Instructor, **Cornell University**, Ithaca, New York USA

Biometry 601: Statistical Methods I **Fall Semester 2006**

Graduate student teaching assistant for a graduate level introductory statistics course. Responsible for recitation section, office hours, and grading.

Biometry 602: Statistical Methods II **Spring Semester 2007**

Graduate student teaching assistant for a graduate level introductory statistics course. Responsible for recitation section, office hours, and grading.

Biometry 683: Introduction to Probability and Statistics **Fall Semester 2007**

Graduate student teaching assistant for a graduate level, intensive course on introductory probability and statistics. Responsible for recitation section, office hours, solution sets and grading.

PUBLICATIONS

14. **Bryc K**, Bryc W, Silverstein JW. *Separation of the largest eigenvalues in eigenanalysis of genotype data from discrete subpopulations*. Theoretical Population Biology. 20 Aug 2013.
13. **Bryc K**, Patterson N, Reich D. *A Novel Approach to Estimating Heterozygosity from Low-Coverage Genome Sequence*. Genetics. 9 Aug 2013.
12. Brisbin A, **Bryc K**, Byrnes J, Zakharia F, Omberg L, Degenhardt J, Reynolds A, Ostrer H, Mezey JG, Bustamante CD. *Principal Components-based assignment of ancestry along each chromosome in individuals with admixed ancestry from two or more populations*. Human Biology. 2012 Aug.
11. Kidd JM, Gravel S, Byrnes J, Moreno-Estrada A, Musharoff S, **Bryc K**, Degenhardt JD, Brisbin A, Sheth V, Chen R, McLaughlin SF, Peckham HE, Omberg L, Bormann Chung CA, Stanley S, Pearlstein K, Levandowsky E, Acevedo-Acevedo S, Auton A, Keinan A, Acua-Alonzo V, Barquera-Lozano R, Canizales-Quinteros S, Eng C, Burchard EG, Russell A, Reynolds A, Clark AG, Reese MG, Lincoln SE, Butte AJ, De La Vega FM, Bustamante CD. *Population genetic inference from personal genome data: impact of ancestry and admixture on human genomic variation*. Am J Hum Genet. 2012 Oct 5.

10. Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, Mallick S, Schraiber JG, Jay F, Prfer K, de Filippo C, Sudmant PH, Alkan C, Fu Q, Do R, Rohland N, Tandon A, Siebauer M, Green RE, **Bryc K**, Briggs AW, Stenzel U, Dabney J, Shendure J, Kitzman J, Hammer MF, Shunkov MV, Derevianko AP, Patterson N, Andrs AM, Eichler EE, Slatkin M, Reich D, Kelso J, Pbo S. *A high-coverage genome sequence from an archaic Denisovan individual*. Science. 2012 Oct 12.
9. Gao H, **Bryc K**, Bustamante CD. *On identifying the optimal number of population clusters via the deviance information criterion*. PLoS One. 2011 Jun 28.
8. De La Vega FM, **Bryc K**, Degenhardt J, Musharoff S, Kidd JM, Seth V, Stanley S, Brisbin A, Keinan A, Clark A, Bustamante CD. *Genome sequencing and analysis of admixed genomes of African and Mexican ancestry: implications for personal ancestry reconstruction and multi-ethnic medical genomics*. Genome Biology. 2010 October 11.
7. **Bryc K**, Velez C, Hammer M, Karafet T, Ostrer H, Bustamante CD. *Genome-wide patterns of population structure and admixture among Hispanic/Latino populations*. PNAS, May 2010.
6. VonHoldt BM, Han E, Pollinger J, Lohmueller K, Earl DA, Parker HG, Quignon P, Boyko A, Auton A, Reynolds A, **Bryc K**, Brisbin A, Knowles J, Mosher DS, Spady TC, Elkhouloun A, Pilot M, Grecco C, Randi E, Bannasch D, Kays R, Wilton A, Shearman J, Cargill M, Jones PG, Zuwei Q, Zhou W, Zhang Y, Bustamante CD, Ostrander EA, Novembre J, and Wayne RK. *Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication*. Nature, March 2010.
5. **Bryc K**, Nelson MR, Oksenberg JR, Hauser SL, Williams S, Bustamante CD, Tishkoff SA. *Genome-wide patterns of population structure and admixture in Africans and African Americans*. PNAS, January 2010.
4. Auton, A, **K Bryc**, AR Boyko, K Lohmueller, K Wright, J Novembre, A Reynolds, A Indap, J Degenhardt, KS King, MR Nelson, CD Bustamante. *Global distribution of genomic diversity underscores rich complex history of continental human populations*. Genome Research. 2009 May 1.
3. Bovine HapMap Consortium. *Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds*. Science. 2009 Apr 24.
2. Novembre J, Johnson T, **Bryc K**, Kutalik Z, Boyko AR, Auton A, Indap A, King KS, Bergmann S, Nelson MR, Stephens M, Bustamante CD. *Genes mirror geography within Europe*. Nature. 2008 Aug 31.
1. Nelson MR, **Bryc K**, King KS, Indap A, Boyko AR, Novembre J, Briley LP, Maruyama Y, Waterworth DM, Waeber G, Vollenweider P, Oksenberg JR, Hauser SL, Stirnadel HA, Kooner JS, Chambers JC, Jones B, Mooser V, Bustamante CD, Roses AD, Burns DK, Ehm MG, Lai EH. *The Population Reference Sample, POPRES: A Resource for Population, Disease, and Pharmacological Genetics Research*. Am J Hum Genet. 2008 Aug 27.
5. **Bryc K**, Williams A, Patterson N, Musani S, Sale M, Chen W, Divers J, Ng M, Bowden DW, Wilson JG, Reich D. *Differential relatedness of African Americans to populations within West Africa*. Presented at the annual meeting of The American Society of Human Genetics, November 8, 2012, San Francisco, California. [ASHG Research Trainee Award Semifinalist]

SELECTED
CONFERENCE
PRESENTATIONS

4. **Bryc K**, Patterson N, Reich D. *Estimating heterozygosity rates of low-coverage sequence genomes by leveraging joint spectra*. Presented at the 12th International Congress of Human Genetics/61st Annual Meeting of The American Society of Human Genetics, October 12, 2011, Montreal, Canada. [ASHG Trainee Award Semifinalist]
3. **Bryc K**, Velez C, Hammer M, Hernandez R, Reynolds A, Auton A, Karafet T, Ostrer H, Bustamante CD. *Genome-wide patterns of population structure and admixture among Hispanic/Latino populations*. Presented at the annual meeting of The American Society of Human Genetics, October 21, 2009, Honolulu, Hawaii. [ASHG Trainee Award Finalist]
2. Brisbin A, **Bryc K**, Degenhardt J, Reynolds A, Auton A, Mezey JG, Ostrer H, Bustamante CD. *Identifying ancestry of genomic regions in admixed individuals*. Presented at the annual meeting of The American Society of Human Genetics, October 21, 2009, Honolulu, Hawaii.
1. **Bryc K**, Nelson M, Oksenberg J, Hauser S, Bustamante CD, Tishkoff S. *Genome-wide patterns of population structure and admixture in Africans and African Americans*. Presented at the annual meeting of The American Society of Human Genetics, November 13, 2008, Philadelphia, Pennsylvania. [ASHG Trainee Award Semifinalist]

TECHNICAL
SKILLS

Programming

C, C++, Python, Perl, UNIX shell scripting, R, T_EX, L^AT_EX, and B_IB_TE_X.

Population Genetics

STRUCTURE, Eigenstrat/Eigensoft, ms, FRAPPE, SABRE, LAMP, ADMIXTURE, BEAGLE, HAPMIX, PLINK and others

SERVICE

Journal Reviewer

American Journal of Human Genetics
Bioinformatics
BMC Medical Genomics
Genes
Genetics
Genome Biology and Evolution
Molecular Biology and Evolution
PLoS Genetics
PLoS ONE

CITIZENSHIP

USA; Poland (EU)