Katarzyna (*Kasia*) Bryc, PhD

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About

Skilled statistical geneticist specializing in human population genetics, data analysis, and algorithm development.

Effective team player adept at fostering cross functional collaboration to drive innovation.

Technical Skills

Python (NumPy, SciPy, scikit-learn), Jupyter, visualization tools (ggplot, matplotlib, bokeh, folium, d3), batch computing (AWS batch, GridMap), Drone, Jenkins, Metaflow, R, C, C++, Perl, UNIX shell scripting, LaTeX.

Dimension-reduction methods (PCA, tSNE, UMAP), classification methods (SVM, logistic regression), HMMs and appropriate techniques (EM, MCMC), network detection.

Population genetic algorithms: phasing, imputation, IBD, and population structure and demographic inference.

Experience

23andMe, Sunnyvale, California USA

Senior Scientist, Population Genetics **2016 to 2023**

Product Development

- Developed algorithms and pipelines for novel and enhanced ancestry products, resulting in two patent applications[1,2], and numerous released features[3,4,5,6].
- Guided the challenging technical redevelopment of ancestry features through significant platform (Illumina OmniExpress+ to GSA-based chip) and website front-end redesign.
- Acquired numerous external reference datasets for algorithm development, and created resources to facilitate in-house use of these data.

Leadership

- Recruited, trained, and scaled a Population Genetics R&D team to eight highly effective scientists. Mentored nearly a dozen new team members; cultivated a productive and successful group from startup through IPO.
- Developed and streamlined research surveys covering ancestry and ethnicity phenotypes after consultation with internal and external stakeholders.
- Developed data transfer frameworks that aligned privacy and security teams, and revised policy to ensure security of data while minimizing overhead for researchers.

Research

- Awarded NIH Small Business Innovation Research grant and led successful research on admixture mapping in non-Europeans[1]; collaborated on an internal research project to discover novel associations with disease in genetically diverse populations[*(in prep)*].
- Facilitated academic research collaborations to drive insights into populations in the Americas, and the genetic legacy of historical individuals[1] and events[2].

23andMe, Mountain View, California USA

Visiting Postdoctoral Research Fellow and *Population Geneticist* **2013 to 2016**

- Established innovative postdoctoral academic collaboration partnership between industry and academia, and joined 23andMe Research Team.

- Published high-impact population genetic research leveraging the 23andMe genotype-phenotype database. This research illuminated the complex relationship between self-identified ancestry and genetic ancestry of groups in the US[1,2].
- R&D for ancestry product improvements, new features, and updates. Served as spokesperson and population genetics subject matter expert for the company.

Harvard Medical School, Boston, Massachusetts USA

Postdoctoral Research Fellow **2010 to 2014**

Advisor: Professor David Reich

- Developed an expectation-maximization method for estimating heterozygosity from low-coverage sequence data, delineated the complex admixture deconvolution of African Americans, and improved the understanding of the use of PCA in detection of substructure.

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

Biostatistics Research Assistant **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.

Education

Cornell University, Ithaca, New York USA

Ph.D., Biometry **January 2011**

Advisor: Professor Carlos D. Bustamante

Dissertation title: "Genome-wide patterns of population structure and ancestry among continental and admixed populations"

M.S., Biometry **January 2009**

Advisor: Professor Carlos D. Bustamante

Stanford University, Stanford, California USA

B.S., Mathematical and Computational Science **June 2005**

Advisor: Professor Brad Efron

Fellowships and Awards

Small Business Innovation Research Phase I April 2016 – March 2018

NIH Department of Health and Human Services

"Admixture-driven discovery of disease-associated genetic variants not found in Europeans"

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

Publications

For a complete list of publications including those as part of the 23andMe Research Team, please see google scholar or pubmed.

23. Harney E, Micheletti S, Bruwelheide KS, Freyman W, **Bryc K**, Akbari A, Jewett E, Comer E, Gates HL, Heywood L, Thornton J, Curry R Esselmann SA, Barca KG, Sedig J, Sirak K, Olalde I, Adamski N, Bernardos R, Broomandkhoshbacht N, Ferry M, Qiu L, Stewardson K, Fatma Zalzala JNW, Mallick S, Micco A, Mah M, Zhang Z, 23andMe Research Team, Rohland N, Mountain JL, Owsley DW, Reich D. *The genetic legacy of African Americans from Catoctin Furnace*. Science. 2023 Aug 3.

22. Jingchunzi S, O'Connell J, Hicks B, Wang W, **Bryc K**, Brady JJ, Vacic V, Freyman W, Abul-Husn NS, Auton A, 23andMe Research Team, Shringarpure S. *GWAS of cataract in Puerto Ricans identifies a novel large-effect variant in ITGA6*. In prep. 2023 Jul 25.

21. Micheletti SJ, Esselmann SA, **Bryc K**, Mountain JL. *Response to Pfenning and Lachance*. American Journal of Human Genetics. 2023 Feb 2.

20. Freyman WA, McManus KF, Shringarpure SS, Jewett EM, **Bryc K**, 23andMe Research Team, Auton A. *Fast and Robust Identity-by-Descent Inference with the Templated Positional Burrows–Wheeler Transform*. Molecular Biology and Evolution. 2021 May 5.

19. Micheletti SJ, **Bryc K**, Esselmann SA, Freyman WA, Moreno ME, Poznik GD, Shastri AJ, 23andMe Research Team, Beleza S, Mountain JL. *Genetic Consequences of the Transatlantic Slave Trade in the Americas*. American Journal of Human Genetics. 2020 Aug 6.

18. Smith RP, Kleinman A, **Bryc K**, Mountain J, Durand EY, McManus K, Esselmann SA. *White Paper 23-05: Neanderthal Ancestry Inference*. 23andMe white paper. 2020 Jul 1.

17. **Bryc K**, Durand EY Mountain J. *White Paper 23-14: Ancestry Timeline*. 23andMe white paper. 2017 Mar 10.

16. **Bryc K**, Durand EY, Macpherson M, Reich D, Mountain J. *The genetic ancestry of African Americans, Latinos, and European Americans across the United States*. American Journal of Human Genetics. 2015 Jan 8.

15. **Bryc K**, Bryc W, Silverstein JW. *Separation of the largest eigenvalues in eigenanalysis of genotype data from discrete subpopulations*. Theoretical Population Biology. 2013 Aug 20.

14. **Bryc K**, Patterson N, Reich D. *A Novel Approach to Estimating Heterozygosity from Low-Coverage Genome Sequence*. Genetics. 2013 Aug 9.

13. 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.

12. 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, Acuea-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*. American Journal of Human Genetics. 2012 Oct 5.

11. Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, Mallick S, Schraiber JG, Jay F, Prufer 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, Andres AM, Eichler EE, Slatkin M, Reich D, Kelso J, Paabo S. *A high-coverage genome sequence from an archaic Denisovan individual.* Science. 2012 Oct 12.

10. Gao H, **Bryc K**, Bustamante CD. *On identifying the optimal number of population clusters via the deviance information criterion.* PLoS One. 2011 Jun 28.

9. 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 Oct 11.

8. **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, 2010 May 5.

7. 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, Elkahloun 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, 2010 Mar 17.

6. **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, 2010 Jan 22.

5. Auton, A, **K Bryc**, AR Boyko, K Lohmueller, K Wright, J Novembre, A Renyolds, 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.

4. Bovine HapMap Consortium. *Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds.* Science. 2009 Apr 24.

3. 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.

2. 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.* American Journal of Human Genetics. 2008 Aug 27.

1. Glauser TA, **Bryc K**, Nick TG, Gilbert D, Holt E, Fordyce S, and Sharp FR. Genomic profiles in blood of children with untreated idiopathic epilepsy. In EPILEPSIA (Vol. 47, pp. 366-366). 2006 Jan.