

Sarah Catherine Nelson

University of Washington
Box 359461
Seattle, WA 98195

sarahcn@uw.edu
206.543.1850 (work)
206.588.5104 (mobile)

EDUCATION AND TRAINING

University of Washington, Seattle, WA

PhD candidate in Public Health Genetics, 9/14 – present (candidacy granted 2/16)

- Dissertation research on direct-to-consumer genetic testing customers' uses of their uninterpreted data in third party systems; Advisor: Stephanie M. Fullerton

Graduate Certificate in Science, Technology, and Society Studies (STSS), 9/15 – present

Master of Public Health in Public Health Genetics, 9/12 – 6/14 (3.94 GPA)

- Received interdisciplinary training in the ethical, legal, social, and scientific aspects of applying genetic knowledge and technologies to individual and population-level health
- Completed thesis examining use of metaphor among research participants considering return of genetic results
 - Semifinalist for 2014 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research
 - PHG nominee for UW Graduate School Distinguished Thesis Award (8/14)
- Gained experience in qualitative methods through MPH practicum project, analyzed comments in a survey of genetics' professionals views on race, ancestry, and genetics

University of North Carolina at Greensboro, Greensboro, NC, 8/01–12/04

BS in Biology, Minors in Psychology and Dance

- Graduated *summa cum laude*, Chancellor's List (GPA 3.95 or above) 4 of 5 semesters
- Merit Awards Scholar: Edith Butler Centennial Scholarship covering 4 years out-of-state tuition
- UNCG Student Excellence Award for academic achievement, spring 2004
- Senior Honors Project: "The Genetics of ADHD," supported by Undergraduate Research Assistantship, spring 2004. Culminated in co-presentation of a poster at the World Congress on Psychiatric Genetics in Dublin, Ireland, 10/04.
- Inducted into *Phi Beta Kappa* and *Tri Beta* (biological sciences) academic honor societies
- Fall semester 2003 abroad at Deakin University, Melbourne, Australia
- APA's *Summer Science Institute*, summer 2002, held at Columbia University, NY, NY

University of Washington, Summer Institute in Statistical Genetics, summer 2010

- Modules taken: GWAS Data Cleaning and Population Genetics

Duke University, Bioinformatics Workshop, Durham, NC, 8/06

WORK AND ADDITIONAL RESEARCH EXPERIENCE

Research Scientist 4, University of Washington, Genetic Analysis Center, Seattle, WA, 8/09 –present

- Performed data cleaning, imputation, and bioinformatics analyses for the Hispanic Community Health Study/Study of Latinos (HCHS/SOL)
- Developed and implemented high-throughput genotype imputation pipeline, for over 20 genome-wide association studies (GWAS) in the GENEVA and GARNET consortia
- Participated in development of “GWASTools,” an R package for GWAS quality control
- Generated many written resources, including three first-author papers; a comprehensive document on DNA strand issues; and numerous imputation and data cleaning reports

Research Staff (part-time), University of Washington, Department of Pediatrics, 01/15 –7/15

- Conducted qualitative coding and analysis of interviews in research project on a web tool for self-management of results from genome sequencing
- Organize and administered online SharePoint site for collaboration amongst research team
- Conducted phone interviews with participants during a preparatory independent study period

Data Technician, Duke University, Center for Human Genetics, Durham, NC, 1/05 – 8/09

- Conducted data management, quality control, and bioinformatics support for several genetic association studies (case-control and family-based)
- Gained expertise in UNIX (shell scripts, vi editor) and Oracle relational databases (structured query language, database loading and management)
- Prepared figures, tables, and summaries for manuscripts, presentations, and grant proposals
- Received “CHG Stars” employee recognition award, Team Player category, 3rd quarter ‘08

Research Assistant, NC Task Force on Genomics and Public Health, Raleigh, NC, 8/04 – 4/05

- Compiled literature search of genetic associations for diseases with public health implications
- Assisted with the organization of “Genetics in Epidemiology” symposium, held 3/18/05

Research Assistant, Oak Ridge National Lab, Mammalian Genetics Facility, Oak Ridge, TN, 6/02-8/02

- Supported by the US DOE Education and Research Undergraduate Learning Fellowship (ERULF)
- Assisted with development of protocols for insulin and glucose tolerance testing in a novel mouse model for obesity and type 2 diabetes
- Published in the Journal of Undergraduate Studies (DOE Office of Sciences)
- Presented poster at the AAAS annual conference in Denver, Colorado, 2/03

COMMUNITY AND CAMPUS ENGAGEMENT

UW Genomics Salon, organizing committee, 06/17-present

UW Institute for Public Health Genetics, student representative, 09/14 – 06/16

STEAMVent, Community Meet-up group, moderated session on direct-to-consumer genetics, 12/14

Northwest Association for Biomedical Research, Seattle non-profit promoting public understanding of research. Participant in, volunteer for, and co-moderator of various community engagement events.

UW Forum on Science Ethics and Policy, member

UW Tower Green Team, environmental conservation and education club, member

DNA Day Essay Judge, 2007, 2013, 2015, 2016. Judged high school submissions for American Society of Human Genetics annual essay contest

PRESENTATIONS AND CONFERENCES

Nelson, S.C., Fullerton, S.M. (2017). Third-party tools for consumer-driven interpretation of personal genetic data: sources of meaning-making for citizen scientists. (**Presentation**). Presented at the 4th ELSI Congress, Farmington, CT.

Received trainee travel award to attend.

Nelson, S.C., Fullerton, S.M. (2016). Content analysis of third party interpretation tools for direct-to-consumer genetic testing data. (Poster, Abstract 3115W). Presented at the 66th American Society of Human Genetics Annual Meeting, Vancouver, BC, October 2016.

Nelson, S.C., Levine, D.M., Storer, B., Zhao, L.P., Warren, E.H., Martin, P.J., & Hansen, J.A. (2015). Evaluation of alternative imputation strategies for mega-analysis of multiple genotyping cohorts: maximizing imputation yield while minimizing artifacts (Poster, Abstract 1364F). Presented at the 65th American Society of Human Genetics Annual Meeting, Baltimore, MD, October 2015.

Nelson, S.C. The "Raw Data Diet:" Patient/consumer access to un-interpreted genetic data (Poster). Sage Bionetworks Paris Assembly, Paris, France, April 2015.

Selected as "Sage Scholar" to attend Assembly with paid expenses.

Nelson, S.C. et al. Weapons, boxes, and credit reports: Metaphorical language in discussions of receiving exome and whole genome sequencing results (**Platform Presentation**). 64th American Society of Human Genetics Annual Meeting, San Diego, CA, October 2014.

Semi-finalist for Epstein Trainee Award, paid attendance fee and travel stipend.

Nelson, S.C. et al. Imputation-Based Genomic Coverage Assessments of Current Human Genotyping Arrays (Poster, Abstract 936W). Presented at the 63rd Annual Meeting of The American Society of Human Genetics, Boston, MA, October 2013.

Nelson S.C. From Subject to Participant to...Principal Investigator? The rise of citizen science in genetics research (Talk). Presented at the University of Washington Scholar's Studio "Lightning Talks," Seattle, WA, November 2012.

Nelson, S.C., Browning, S.R., Browning, B.L., et al. "Next Generation" Imputation: Widening the Genome-Wide Association Study (Talk). WNAR-Graybill 2012 Conference. Presented at Colorado State University, Fort Collins, CO, June 2012.

Nelson, S.C. et al. "Next Generation" Imputation: Assessing the 1000 Genomes Project reference panel and imputation into multi-ethnic cohorts (Poster, Abstract 621F). Presented at the 12th International Congress of Human Genetics/61st Annual Meeting of The American Society of Human Genetics, Montreal, Canada, October 2011.

Nelson, S.C., Laurie, C.C., Crosslin, D.R., Browning, B.L., Marazita, M.L. Effects of ignoring relatedness among study subjects in genotype imputation analyses (Poster, Abstract 3030). Presented at the 60th Annual Meeting of The American Society for Human Genetics, Washington, D.C, November 2010.

SELECTED* PUBLICATIONS

Nelson, S.C. Geneticists should offer data to participants (World View article). *Nature* **539**, 7–7 (2016).

Conomos, M. P. *et al.* Genetic Diversity and Association Studies in U.S. Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. *Am. J. Hum. Genet.* **98**, 165–184 (2016).

Nelson, S. C., Crouch, J. M., Bamshad, M. J., Tabor, H. K. & Yu, J.-H. Use of metaphors about exome and whole genome sequencing. *Am. J. Med. Genet. A* **170**, 1127–1133 (2016).

Nelson, S. C. et al. Improved imputation accuracy in Hispanic/Latino populations with larger and more diverse reference panels: applications in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). *Hum. Mol. Genet.* (2016).

- Nelson, S. C.**, Yu, J.-H. & Ceccarelli, L. How Metaphors About the Genome Constrain CRISPR Metaphors: Separating the ‘Text’ From Its ‘Editor’. *Am. J. Bioeth.* **15**, 60–2 (2015).
- Nelson, S. C. et al.** Imputation-based genomic coverage assessments of current human genotyping arrays. *G3 Genes, Genomes, Genet.* **3**, 1795–807 (2013).
Featured in G3 2013 year-in-review booklet
- Nelson, S. C.**, Doheny, K. F., Laurie, C. C. & Mirel, D. B. Is ‘forward’ the same as ‘plus’?...and other adventures in SNP allele nomenclature. *Trends Genet* **28**, 361–363 (2012).
- Laurie, C. C. *et al.* Detectable clonal mosaicism from birth to old age and its relationship to cancer. *Nat Genet* **44**, 642–650 (2012).
- Gogarten, S. M. *et al.* GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. *Bioinformatics* **28**, 3329–3331 (2012).
- Minear, M. A. *et al.* Polymorphic variants in tenascin-C (TNC) are associated with atherosclerosis and coronary artery disease. *Hum Genet* **129**, 641–654 (2011).
- Chen, H. C. *et al.* Genome-wide linkage analysis of quantitative biomarker traits of osteoarthritis in a large, multigenerational extended family. *Arthritis Rheum* **62**, 781–790 (2010).
- Shah, S. H. *et al.* Neuropeptide Y gene polymorphisms confer risk of early-onset atherosclerosis. *PLoS Genet* **5**, e1000318 (2009).
- Sutton, B. S. *et al.* Comprehensive genetic analysis of the platelet activating factor acetylhydrolase (PLA2G7) gene and cardiovascular disease in case-control and family datasets. *Hum Mol Genet* **17**, 1318–1328 (2008).
- Wang, L. *et al.* Peakwide mapping on chromosome 3q13 identifies the kalirin gene as a novel candidate gene for coronary artery disease. *Am J Hum Genet* **80**, 650–663 (2007).
- Connelly, J. J. *et al.* GATA2 is associated with familial early-onset coronary artery disease. *PLoS Genet* **2**, e139 (2006).

*Complete list: <http://www.ncbi.nlm.nih.gov/sites/myncbi/sarah.nelson.2/bibliography/46024915>

OTHER SCIENCE WRITING

Attended “The OpEd Project” workshop on public expertise leadership, 4/16

Open Reading Frame, blog about dissertation and related topics, 11/15 – present

<http://myopenreadingframe.com/>

Three quarters of graduate level science and technical writing classes at the University of Washington
Contributed content to Nature educational website Scitable: *Essentials of Genetics* sections on DNA sequencing and microarrays. <http://www.nature.com/scitable/ebooks/Essentials-in-Genetics-8>

Nelson, S.C. Astronomers Search For Rocky, Habitable Planets In Other Solar Systems. Northwest Science & Technology, Spring 2010 issue. <http://www.nwst.org>

Nelson, S.C. CHG Researchers Intensify Genetic Studies of Chiari Type I Malformation. Duke Center for Human Genetics website. (2009)

Nelson, S.C. Comparative Methylation Hybridization. *Nature Education* **1(1)**.
<http://www.nature.com/scitable>. (2008)