SHANNON E. ELLIS

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EDUCATION

2010—2016 **PhD** | Human Genetics
Johns Hopkins University School of Medicine • Baltimore, MD
Multi-omic Data Provide a More Complete Understanding of the Autistic Brain

2006—2010 **BS** | Biology & Spanish
King's College • Wilkes-Barre, PA

TEACHING

2018—Present **Assistant Teaching Professor**
University of California San Diego • La Jolla, CA
Instructor for COGS 9 Introduction to Data Science, COGS 108 Data Science in Practice, COGS 18 Introduction to Python, and DSC180A Data Science Capstone.

Spring 2018 **Co-instructor** | Health Data Analysis Practicum
Johns Hopkins University • Baltimore, MD
Through the analysis of public health datasets and analysis, co-instructed this seminar course to enhance students' quantitative, scientific reasoning, and functional abilities in statistical analysis using the R statistical language. Provided weekly code feedback and assisted students through all course assignments.

Fall 2017 **Teaching Assistant** | Public Health Biostatistics
Johns Hopkins University • Baltimore, MD
Prepared and instructed two sections weekly (~50 students total), graded and provided feedback on all quizzes, tests, and projects, and held office hours and answered student emails throughout the semester.

Summer 2017 **Instructor** | Genetics
Johns Hopkins Center for Talented Youth • Baltimore, MD
Planned and taught an intensive three-week genetics course to 18 gifted high school students using a combination of lectures, activities, laboratories, debates, discussions, and computer simulations to engage and teach students for more than 100 classroom hours.

Spring 2013 **Teaching Assistant** | Advanced Topics in Human Genetics
Johns Hopkins School of Medicine • Baltimore, MD
Facilitated and guided discussion-based classes, met with and discussed scientific literature to help prepare in-class presentations, and wrote, administered, and graded the midterm exam 12 first year graduate students and three pediatric genetics fellows.

Mentoring

2020 Serene Issa | *Undergraduate Student*, UC San Diego
2019 Pratyush Khurana | *Undergraduate Student*, UC San Diego
Anran Li | *Undergraduate Student*, UC San Diego
Lauren Awaya | *Undergraduate Student*, UC San Diego
Ayushi Gupta | *Undergraduate Student*, UC San Diego

Zheng Tang | *Undergraduate Student*, UC San Diego
Jaidev Mirchandani | *Undergraduate Student*, UC San Diego
Qian Yin | *Undergraduate Student*, UC San Diego
Weilun Yao | *Undergraduate Student*, UC San Diego
Emily Le | *Undergraduate Student*, UC San Diego

2016 Augusto Ramirez | *Undergraduate Student*, Johns Hopkins
Elizabeth Vincent | *Graduate Student*, Johns Hopkins

2015—2016 Rebecca Panitch | *Undergraduate Student*, Johns Hopkins

2014 Heather Wick | *Graduate Student*, Johns Hopkins
Edward Pang | *Undergraduate Student*, Johns Hopkins

2013 James Miller | *Undergraduate Student*, Johns Hopkins

RESEARCH & PROJECTS

2017—Present **Curriculum Lead** | Cloud-Based Data Science
clouddatascience.org • Baltimore, MD
Developed educational content for 13 free, online courses to teach the basics of data science to individuals with no prior computational experience. Supported development of technology built to support content development. Developed and implemented in-person tutoring and support program to help individuals who have earned their GED learn the basics of data science and obtain entry-level data science jobs.

2016—2018 **Postdoctoral Fellow** | *Biostatistics*
Johns Hopkins University Bloomberg School of Public Health • Baltimore, MD
Advisor: Jeffrey T. Leek, Ph.D.
Used gene expression data from 70,000 human samples and machine learning to predict critical phenotype information.

2010—2016 **Graduate Student** | *Institute of Genetic Medicine*
Johns Hopkins University School of Medicine • Baltimore, MD
Advisor: Dan E Arking, Ph.D.
Analyzed RNA-Sequencing data and identified an upregulation of activated M2 microglia genes in autism brains.Developed a method to guide RNA-Sequencing analysis using eQTLs as a gold standard. Identified significant DNA hypermethylation at cytosines outside of the classically-studied CpG context in autism brains utilizing bisulfite sequencing.

Peer-reviewed Publications

2019 Madugundu A.K., Hyun Na C., Nirujogi R.S., Reunuse S., Kim KP, Burns KH, Langmead B., **Ellis S.E.**, Collado-Torres L., Halushka M.K., Kim M., and Pandey A. (2019). Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial cells. *Proteomics*.

2018 **Ellis S.E.**, Collado-Torres L., Jaffe A., Leek J.T. (2018). Improving the value of public RNA-seq expression data by phenotype prediction. *Nucleic Acids Research*.

Ellis S.E. and Leek J.T. (2018). How to share data for collaboration. *The American Statistician.*

2017 Andrews S., **Ellis S.E.**, Bakulski K., Sheppard B., Croen L., Hertz-Piccioto I., Newschaffer C., Feinberg A., Arking D.E., Ladd-Acosta C., and Fallin M.

(2017). Cross-tissue integration of genetic and epigenetic data offers insight into autism spectrum disorder. *Nature Communications*.

Ellis S.E., Gupta S., Moes A., West A.B., Arking D.E. (2017). Exaggerated CpH Methylation in the Autism-Affected Brain. *Molecular Autism.*

Collado-Torres L., Nellore A., Kammers K., **Ellis S.E.**, Taub M.A., Hansen K.D., Jaffe A.E., Langmead B., Leek J. (2017). Reproducible RNA-seq analysis using *recount2*. *Nature Biotechnology.*

2016 **Ellis S.E.**, Panitch R., West A.B., Arking D.E. (2016). Transcriptome Analysis of Cortical Tissue Reveals Shared Sets of Down-Regulated Genes in Autism and Schizophrenia. *Translational Psychiatry.*

2015 Huang C, Haritunians T, Okou DT, Cutler DJ, Zwick ME, Taylor KD, Datta LW, Maranville JC, Liu Z, **Ellis S**, Chopra P, Alexander JS, Baldassano RN, Cross RK, Dassopoulos T, Dhere TA, Duerr RH, Hanson JS, Hou JK, Hussain SZ, Isaacs KL, Kachelries KE, Kader H, Kappelman MD, Katz J, Kellermayer R, Kirschner BS, Kuemmerle JF, Kumar A, Kwon JH, Lazarev M, Mannon P, Moulton DE, Osuntokun BO, Patel A, Rioux JD, Rotter JI, Saeed S, Scherl EJ, Silverberg MS, Silverman A, Targan SR, Valentine J, Wang MH, Simpson CL, Bridges SL, Kimberly RP, Rich SS, Cho JH, Di Rienzo A, Kao LW, McGovern DP, Brant SR, and Kugathasan S. (2015). Characterization of Genetic Loci That Affect Susceptibility to Inflammatory Bowel Diseases in African Americans. *Gastroenterology*.

2014 Gupta, S., **Ellis, S.E.**, Ashar, F.N., Moes, A., Bader, J.S., West, A.B., and Arking, D.E. (2014). Transcriptome Analysis Reveals Deregulation of Innate Immune Response Genes and Neuronal Activity-Dependent Genes in Autism. *Nature Communications*.

2013 **Ellis, S.E.**, Gupta, S., Ashar, F.N., Bader, J.S., West, A.B., and Arking, D.E. (2013). RNA-Seq optimization with eQTL gold standards. *BMC Genomics 14*, 892.

Invited Talks

2019 **Ellis, S.E.** (Jul 29, 2019). Overcoming the barriers of entry into data science for nontraditional learners with cloud computing. *Joint Statistical Meeting*.

Ellis, S.E. (Jun 1, 2019). Teaching Data Science: A Workshop for High School Teachers. *Symposium on Data Science and Statistics*.

Ellis, S.E. (Apr 2, 2019). Making a Case for Why Programming Will Save You Time. *Annual Congress in Clinical Mass Spectrometry.*

2018 **Ellis, S.E.** (Nov 28, 2018). Designing MOOCs to Democratize Data Science Education. *Design@Large.*

Ellis, S.E. (Feb 1, 2018). Improving the value of public data with *recount2* and phenotype prediction. *Joint Statistical Meeting*.

Ellis, S.E. (Feb 1, 2018). Improving the value of public data with *recount2* and phenotype prediction. *University of Washington Biostatistics Seminar*.

2017 **Ellis, S.E.** (Oct 11, 2017). Improving the value of public data with *recount2* and phenotype prediction. *Genomics and Bioinformatics Symposium*.

Ellis, S.E. (June 5-7, 2017). *In silico* phenotyping to improve the usefulness of public data. *Graybill Conference in Statistical Genomics and Genetics*.

Ellis, S.E. (March 26-31, 2017). *In silico* phenotyping to improve the usefulness of public data. *BIRS Statistical and Computational Challenges in Large Scale Molecular Biology*.

Ellis, S.E. (Feb 16-17, 2017). Increasing the value of public data with *in-silico* phenotyping. Statistical *and Algorithmic Challenges in Microbiome Data Analysis*.

PROFESSIONAL DEVELOPMENT & SERVICE

Pedagogy Training

Spring 2017 **Participant** | Johns Hopkins Teaching Institute

Active Completed an intensive workshop in pedagogy focused on enhancing instruction in higher education. Topics covered included: Teaching as Scholarship, Inclusive Classrooms, Learning, Planning a Course, Assessment, and Evaluation.

Scientific Meetings Attended

2019 Symposium on Data Science and Statistics
2018—2019 Joint Statistical Meeting
2017 Graybill Conference in Statistical Genomics and Genetics
2017 rOpenSci Unconference
2017 BIRS Statistical & Computational Challenges in Large Scale Molecular Biology
2017 Statistical and Algorithmic Challenges in Microbiome Data Analysis
2010—2015 American Society for Human Genetics
2013—2014 Society for Neuroscience
2009—2010 American Society for Microbiology

Volunteering

2020 **Essay Judge** | Stemanities
2019, 2020 **Career Panelist** | UCSD EPIC Postdoc Bootcamp
2015—Present **Volunteer** | Icing Smiles
2015—Present **DNA Day Essay Judge** | The American Society of Human Genetics
2016—2018 **Volunteer** | Science Outside the Lines
2017 **Abstract Reviewer** | The American Society of Human Genetics

Service & Leadership

2019—Present **LPSOE in Data Science Search Committee** | Halicioğlu Data Science Institute
2019—Present **LPSOE in Machine Learning Search Committee** | Cognitive Science Department
2018—Present **Undergraduate Curriculum Committee** | Cognitive Science Department
2013—2016 **Graduate Student Representative** | Institute of Genetic Medicine
2013—2016 **Student Leader** | Barton Childs Lecture Planning Committee
2011—2015 **Committee Leader** | Graduate Program New Student Recruitment
Spring 2014 **Student Leader** | McKusick Lecture Planning Committee

Journal Reviewer

PLoS One | `journals.plos.org/plosone`
Nature Biotechnology | `www.nature.com/nbt/`
European Journal of Human Genetics | `www.nature.com/ejhg/`
Peer J | `peerj.com/`
PLOS Computational Biology | `journals.plos.org/ploscompbiol/`

Professional Societies

2018—present **Member** | American Statistical Association
2010—2017 **Member** | The American Society of Human Genetics

HONORS AND AWARDS

2017 **Teaching Award** | Johns Hopkins Center for Talented Youth
2008 **Undergraduate Research Fellowship** | National Science Foundation
2006—2010 **Presidential Scholarship** (a full academic scholarship) | King's College