

# 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
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## 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, and COGS 18 Introduction to Python.
- 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

- 2016 Augusto Ramirez | *Undergraduate Student*  
Elizabeth Vincent | *Graduate Student*
- 2015–2016 Rebecca Panitch | *Undergraduate Student*

2014 Heather Wick | *Graduate Student*  
Edward Pang | *Undergraduate Student*  
2013 James Miller | *Undergraduate Student*

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## RESEARCH

2016–2018 **Postdoctoral Fellow** | *Biostatistics*  
Johns Hopkins University Bloomberg School of Public Health • Baltimore, MD  
Advisor: Jeffrey T. Leek, Ph.D.  
Developed content, curriculum, and in-person tutoring program for a new program to train skilled workers for entry-level jobs in Data Science. 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.

## Publications

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*.

2017 Andrews S., **Ellis S.E.**, Bakulski K., Sheppard B., Croen L., Hertz-Piccioto I., Newschaffer C., Feinberg A., Arking D.E., and 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.** and Leek J.T. (2017). How to share data for collaboration. *The American Statistician*.

**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, Dhare 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,

- That 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 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

- 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*.
- usefulness **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*.

### Poster Presentations

- 2015 **Ellis, S.E.**, Gupta S., Moes A, Absher D., West A.B. & Arking D.E. (Oct. 6-10, 2015). No Evidence That Differences In Cortical DNA Methylation Contribute to Autism. *American Society for Human Genetics*.
- 2014 **Ellis, S.E.**, Gupta, S., Moes, A., West, A.B., and Arking, D.E. (Oct. 18-22, 2014). Assessing the role of methylation in autism brains. *American Society for Human Genetics*.
- 2013 **Ellis, S.E.**, Gupta, S., Ashar, F.N., Bader, J.S., West, A.B., and Arking, D.E. (Oct. 22-26, 2013). RNA-Seq optimization with eQTL gold standards. *American Society for Human Genetics*.
- Ellis, S.E.**, Arking, D.E., Iacono, D., Pletnikova, O., Rudow, G., Talbot, C., O'Brien, R., Resnick, S. and Troncoso, J.C, (Nov. 9-13, 2013). Understanding the Transcriptome of Asymptomatic Alzheimer's Disease. *Society for Neuroscience*.

2010 **Ellis, S.E.**, Doering, T.L., and Ory, J.J. (May 23-27, 2010). Microarray Analysis of a *cuf1* Strain of *Cryptococcus neoformans* Suggests Cuf1p is Involved in Both Repressor and Enhancer Activities. *American Society for Microbiology*.

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## PROFESSIONAL DEVELOPMENT

### Pedagogy Training

Spring 2017 **Participant** | Johns Hopkins Teaching Institute  
Completed an intensive workshop in pedagogy focused on enhancing instruction in higher education. Topics covered included: Teaching as Scholarship, Inclusive Classrooms, Active Learning, Planning a Course, Assessment, and Evaluation

### Scientific Meetings Attended

2018 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

### Journal Reviewer

**PLoS One**, [journals.plos.org/plosone](http://journals.plos.org/plosone)  
**Nature Biotechnology**, [www.nature.com/nbt/](http://www.nature.com/nbt/)  
**European Journal of Human Genetics**, [www.nature.com/ejhg/](http://www.nature.com/ejhg/)  
**Peer J**, [peerj.com/](http://peerj.com/)

### Volunteering

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

### Leadership Experience

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

### Professional Societies

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

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## HONORS AND AWARDS

2017 **Teaching Award** | Johns Hopkins Center for Talented Youth  
2006–2010 **Presidential Scholarship** (a full academic scholarship) | King's College

