

EDUCATION

Stanford University*Sep 2014-Present*

- PhD student in Computer Science under Professor Anshul Kundaje

Massachusetts Institute of Technology*Sep 2009-June 2013*

- B.S. Computer Science with Molecular Biology, Minor in Mathematics, GPA 5.0/5.0

HONORS & AWARDS

Microsoft Women's Fellowship	2016
MIT SuperUROP Outstanding Research Award	2013
American Institute of Chemical Engineers Sophomore Academic Excellence Award ¹	2011
IGCSE Physics: highest score in India	June 2007
IGCSE Geography: highest score in India	June 2007
IGCSE Extended Mathematics: highest score in India	June 2006

EXPERIENCE

Kundaje Lab - Computer Science PhD Student*Sep 2014 - present*

- Conceived of and developed DeepLIFT (patent pending), the first comprehensive interpretation engine for deep learning models in genomics. Demonstrated the effectiveness of DeepLIFT on diverse genomic and epigenomic tasks, where it achieves far superior performance relative to conventional methods. See Talks.
- Built frameworks to facilitate training deep learning models on genomic data. Applied deep learning to predict genomic regulatory features from sequence.

Palantir Technologies Healthcare Team - Forward Deployed Engineer*June 2013 - Sep 2014*

- Did primary development for Healthcare team's first enterprise deployment.
- Played critical role in winning 30 million dollar contract with a Fortune-500 company.
- Created a way to integrate Palantir's two major platforms into a cohesive experience - a rare feature which Palantir repeatedly highlighted at company-wide meetings.
- Built multiple code libraries as side-projects for use both team-wide and company-wide.
- Am inventor on two pending patents resulting from my work at Palantir.
- Consistently received 4/5 rating in bi-annual reviews (indicating that I went above-and-beyond what was expected of me and made significant contributions impacting multiple deployments). In the reviews, my lead (Lekan Wang) said I had at times done the work of 2-3 coders and had set a new standard for productivity among my teammates.

MIT Computational Biology Group (Kellis Lab) - Undergraduate Researcher*Sep 2012 - June 2013*

- Applied a Hidden Markov Model (HMM) to identify transcription factor binding sites using patterns in the shape of histone modification signal data, resulting in improved specificity. Work was conducted without the supervision of a graduate student.
- Recognized with MIT's SuperUROP Outstanding Research award.

MIT Boyer Lab - Undergraduate Researcher*June 2011 - Sep 2012*

- Analyzed high-throughput sequencing data on cardiac cells using statistical techniques to study regulatory relationships concerning enhancers, motif binding patterns, RNA-seq expression patterns, and long non-coding RNAs.
- Independently selected which statistical tests to apply, which controls to use, and how to process the data in a way that would allow the desired questions to be asked. As I matured as a researcher I would test my own hypotheses on the data and present results to my Postdoctoral colleague. Publication summarized below; bulk of work done as a rising junior.

¹Prior to switching to Computer Science with Molecular Biology, I studied Chemical Engineering

- Performed comparative analysis of peak-calling algorithms (the BioMicroCenter is the primary bioinformatics facility for the MIT biology department).

TALKS

Computational Evolutionary and Human Genomics (CEHG) Symposium - Feb 2016, Stanford

- Not Just a Black Box: Interpretable Deep Learning for Genomics and Epigenomics. Abstract [here](#).
- Authors: **Avanti Shrikumar**, Peyton Greenside, Nasa Sinnott-Armstrong, Anshul Kundaje.

Epigenomics - Feb 2016, Puerto Rico

- Similar content to CEHG 2016 talk.

PUBLICATIONS

Cell - Sep 2012

- Wamstad JA, Alexander JM, Truty RM, **Shrikumar A**, Li F, Eilertson KE, Ding H, Wylie JN, Pico AR, Capra JA, Erwin G, Kattman SJ, Keller GM, Srivastava D, Levine SS, Pollard KS, Holloway AK, Boyer LA#, Bruneau BG# (2012) **Dynamic and coordinated epigenetic regulation of developmental transitions in the cardiac lineage**. Cell 151, 206-220. #co-corresponding authors.
- 209 citations as of March 2016.
- Collaboration with Gladstone Institutes. I performed the main bioinformatics analysis at MIT.

Full list at <https://web.stanford.edu/~avanti/resume.html>

TEACHING AND COMMUNICATION

Python reading group - Dec 2015-Present

- Organized and led a reading group for my colleagues to study advanced features of python
- Gave impromptu lectures on topics the group wanted to learn more about

Genetics training camp - Sep 2015

- Prepared and led tutorial sessions on bioinformatics analyses, starting with basic Unix.
- Tailored course to incoming first-year genetics students, most of whom had never programmed before.

CS 373 (Computational Biology) - Spring 2015

- Wrote problem sets, held office hours and graded assignments for first iteration of the course.
- Took initiative in organizational and administrative tasks to ensure that the course was a success.

Theater

- Have acted in school productions since primary school; most recent performance received special mention in the Stanford Daily.
- Directed for a small theatrical production at MIT.

SKILLS

Programming

- Strong emphasis on good design, in contrast to the "hacky" culture of bioinformatics.
- Languages (in order of familiarity): Python, Java, Perl, R, MATLAB, SQL/PostgreSQL.

Web development

- Basic Javascript, CSS and HTML
- Built web-based tool for final project of UI Design class at MIT, prototyped two web applications for deal proposals at Palantir.

INTERESTING

- Calculator art with parametric equations (search "calculator penguin" on YouTube)
<http://www.youtube.com/watch?v=r-I5M--fvJQ>
- Simulations of Rubik's Cube and Sudokube (personal project in high school)
<http://www.youtube.com/watch?v=fLvs5nvT2j8>