Jenny Chen, PhD

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CURRENT

Data Science Postdoctoral Fellow, Harvard University, Cambridge, MA
Uncovering the genetic basis of the evolution of innate behaviors across closely related species, jointly in the labs of Sean Eddy and Hopi Hoekstra.

EDUCATION

MIT	PhD, Bioinformatics and Integrative Genomics	09/2011 – 06/2018
Stanford University	MS, Biomedical Informatics	01/2010 – 06/2011
Stanford University	BS (with distinction), Biomedical Computation	09/2006 – 06/2011

AWARDS & FELLOWSHIPS

2018	Harvard Data Science Postdoctoral Fellowship. *2 years of funding.*
2017	MIT Graduate Women of Excellence Award. *For service contributions to MIT.*
2017	HST Director's Award. *For contributions to the education of HST students.*
2014	Third Place (of 246 entries), MIT Big Data Challenge. *$500.*
2013	IDEA[2] Award for Best Research Proposal, HST. *1 semester of funding.*
2011-2013	National Human Genome Research Institute Training Grant. *3 years of funding.*
2011	Vice Provost Undergraduate Education Award, Stanford. *1 year of Master's funding.*
2010	CS Undergraduate Research Grant, Stanford. *Summer funding.*

RESEARCH EXPERIENCE

Aviv Regev Lab, Broad Institute, Cambridge, MA   09/12 – 06/2018
Developing statistical models and computational tools for inferring biological function from evolutionary signatures of gene expression and transcription across mammalian species.

Gill Bejerano Lab, Stanford University, CA   03/10 – 07/11
Designed computational and statistical methods to discover transcription factor binding site motifs from ChIP-seq datasets and predict functional cis-regulatory modules.

Stanford Cardiovascular Biomechanics Research Lab, Stanford University, CA   09/08 – 12/09
Simulated blood flow through models of coronary artery stenoses using computational fluid techniques in order to characterize hemodynamics in stenoses of different geometries and severities.

Stanford Center for Clinical and Science Research, Stanford University, CA   06/07 – 06/08
Performed genotyping and maintenance of transgenic mice used for melanoma research.

PUBLICATIONS

Chen J, Swofford R, Johnson J, Cummings BB, Rogel N, Lindblad-Toh K, Haerty W, di Palma F, and A Regev. A quantitative model for characterizing the evolutionary history of mammalian gene expression. *Forthcoming; preprint available:* http://www.biorxiv.org/content/early/2017/12/04/229096.

Ye CJ*, **Chen J***, Villani AC, Subramaniam M, Gate RE, Bhangale T, Lee MN, Raj T, Raychowdhury R, Li W, Rogel N, Imboywa SH, Chipendo PI, McCabe C, Lee MH, Frohlich IY, Stranger Be, De Jager PL, Regev A, Behrens T, and N Hacohen. Genetic analysis of isoform usage in the human antiviral response reveals influenza-specific regulation of ERAP2 transcripts under balancing selection. *Genome Research,* 2018 November. *Contributed equally.

Munschauer M, Nguyen CT, Sirokman K, Hartigan CR, Hogstrom L, Engreitz JM, Ulirsch JC, Fulco CP, Subramanian V, **Chen J**, Schenone M, Guttman M, Carr SA, and ES Lander. The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. *Nature*, 2018 September.

Schiebinger G*, Shu J*, Tabaka M*, Cleary B*, Subramanian V, Solomon A, Liu S, Lin S, Berube P, Lee L, **Chen J,** Brumbaugh J, Rigollet P, Hochedlinger K, Jaenisch R, Regev A, and ES Lander. Reconstruction of developmental landscapes by optimal-transport analysis of single-cell gene expression sheds light on cellular reprogramming. *In review*; preprint available: http://www.biorxiv.org/content/early/2017/09/27/191056.

Dixit A*, Parnas O*, Li B, **Chen J**, Fulco CP, Jerby-Arnon L, Marjanovic ND, Dionne D, Burks T, Raychowdhury R, Adamson B, Norman TM, Lander ES, Weissman JS, Friedman N, and A Regev. Perturb-seq: dissecting molecular circuits with scalable single-cell RNA profiling of pooled genetic screens. *Cell*, 2016 December.

Engreitz JM, Haines JE, Perez EM, Munson G, **Chen J**, Kane M, McDonel PE, Guttman M, and ES Lander. Neighborhood regulation by lncRNA promoters, transcription and splicing. *Nature*, 2016 November.

Chen J, Shishkin A, Zhu X, Kadri S, Hanna J, Regev A, and M Garber. Evolutionary analysis across mammals reveals distinct classes of long noncoding RNAs. *Genome Biology*, 2016 January.

Shishkin AA, Giannoukos G, Ciulla D, Busby M, Surka C, **Chen J**, Bhattacharrya RP, Patel MM, Hun DT, Gnirke A, Guttman M, and J Livny. Simultaneous generation of large numbers of strand-specific RNA-Seq cDNA libraries in a single reaction. *Nature Methods*, 2015 March.

Bochkis I, Przybylski D, **Chen J**, and A Regev. Changes in nucleosome occupancy associated with metabolic alterations in aged mammalian liver. *Cell Reports*, 2014 October.

Camp JG, Frank CL, Lickwar CR, Guturu H, Rube T, Wenger AM, **Chen J**, Bejerano G, Crawford GE, and JF Rawls. Microbiota modulate transcription in the intestinal epithelium without remodeling the accessible chromatin landscape. *Genome Research*, 2014 June.

Tuteja G, Moreira KB, Chung T, **Chen J**, Wenger AM, and G Bejerano. Automated Discovery of Tissue-Targeting Enhancers and Transcription Factors from Binding Motif and Gene Function Data. *PLoS Computational Biology*, 2014 January.

Wenger AM, Clarke SL, Guturu H, **Chen J**, Schaar BT, McLean CY, and G Bejerano. PRISM offers a comprehensive genomic approach to transcription factor function prediction. *Genome Res*, 2013 Feb.

SELECTED TALKS

Chen J, Johnson J, Linblad-Toh K, Haerty W, DiPalma F, and A Regev. A Model for Expression Evolution Across the Mammalian Lineage. Selected talk at *Ecological & Evolutionary Genomics*, Gordon Research Conference. July 2017.

Chen J, Johnson J, Linblad-Toh K, Haerty W, DiPalma F, and A Regev. A Model for Expression Evolution Across the Mammalian Lineage. Selected talk at *Biology of Genomes*, Cold Spring Harbor, NY. May 2017.

CONFERENCE PRESENTATIONS

Chen J, Shishkin A, Zhu X, Kadri S, Hanna J, Regev A, and M Garber. Evolutionary analysis across mammals reveals distinct classes of long noncoding RNAs. Poster session presented at *Genome Informatics*, Cold Spring Harbor, NY. October 2015.

Chen J, Chun Y, Villani AC, Lee MN, Raj T, Li W, Imboywa SH, Chipendo PI, Lee MH, De Jager P, Benoist CO, Bhangale T, Ortmann W, Behrens T, Hacohen N, and A Regev. Comparative analysis of computational pipelines for RNA sequencing in genetical genomic studies. Poster session presented at the *American Society of Human Genetics 2014 Annual Meeting*, San Diego, CA. October 2014.

Chen J, Chun Y, Villani AC, Lee MN, Raj T, Li W, Imboywa SH, Chipendo PI, Lee MH, De Jager P, Benoist CO, Bhangale T, Ortmann W, Behrens T, Hacohen N, and A Regev. Gene expression variation in the response of human monocyte-derived dendritic cells to influenza and IFNb stimulation. Poster session presented at *Biology of Genomes*, Cold Spring Harbor, NY. May 2014.

Chen J, Wenger AM, Guturu H, and G Bejerano. "Analysis of Transcription Factor ChIP-Seq Data Sets," Poster session presented at *Stanford Computer Science Undergraduate Research Presentations*, Stanford, CA. August 2011.

Chen J, Shih J, Kim HJ, Taylor CA. "Pressure and Flow Characterization For Idealized Models of Stenotic Coronary Arteries," Poster session presented at the *2010 Annual ASME Bioengineering Conference*, Naples, FL. June 2010.

TEACHING EXPERIENCE

Instructor (G), Molecular Biology and Genetics in Modern Medicine (HST.160)   Fall 2016
Developed curriculum, created all course materials, organized guest lectures, and taught course for 60 first-year MD and PhD students.

Teaching Assistant, Molecular Biology and Genetics in Modern Medicine (HST.160)   Fall 2013 – 2015
Led discussion sections, graded problem sets and exams, and managed all administrative aspects.

ACADEMIC SERVICE

Appointed Member, Presidential Advisory Cabinet, MIT   Fall 2017 – present
The Presidential Advisory Cabinet consists of four undergraduate and four graduate students who serve the MIT president in an advisory capacity on issues concerning the student body.

Appointed Member, Committee on Student Life, MIT   Fall 2016 – 2017
The faculty Committee on Student Life considers proposals that would change policies pertinent to student life and makes recommendations to the Dean for Student Life.

Appointed Member, Women's Advisory Group to the Office the President, MIT   Fall 2015 – 2016
The Women's Advisor Group advises the Office of the President on areas of concern to women at MIT.

Public Service Director, HST, MIT   Fall 2012 – Spring 2014
Led and organized public service opportunities for HST graduate students.

LEADERSHIP EXPERIENCE

Graduate Resident Tutor, Baker House, MIT   Fall 2015 – 2018
Foster a supportive and safe living environment and build a community for 60 undergraduate students.

Outreach Educator, Broad Institute   Fall 2016 – 2018
Create and teach outreach courses about genetics and evolution to local middle school students.

Program Director, WMBR (MIT Radio), MIT   Spring 2013 – 2016
Responsible for content of programming at WMBR, MIT Radio.