

# MENGTING GU

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## EDUCATION

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<b>School of Arts &amp; Sciences, Yale University</b> <i>Ph.D., Computational Biology and Bioinformatics</i> Concentrations: Algorithms and Machine Learning, Functional Genomics	2013-2019
<b>School of Engineering, Yale University</b> <i>M.S., Computer Science, GPA 4.0</i>	2014-2016
<b>Tsinghua University</b> <i>B.A., School of Economics and Management</i> <i>B.S., School of Life Sciences and Biotechnology</i>	2009-2013
<b>The University of Hong Kong</b> <i>Exchange</i>	2011-2012

## EXPERIENCES

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<b>Visa Research</b> <i>Staff Research Scientist</i> <ul style="list-style-type: none"><li>· Research: Uniform word embeddings across multiple languages</li><li>· Improve Visa fraud detection system over the financial data warehouse at Visa</li><li>· Develop predictive models for essential parties in the payment and commerce system</li></ul>	06/2019 - Present <i>Palo Alto, CA</i>
<b>Yale University</b> <i>Graduate Student Researcher</i> <ul style="list-style-type: none"><li>· Developed convolution-based method to detect gene regulators at genome-wide scale</li><li>· Software adopted by scientific research consortiums like ENCODE to analyze large-scale genomic data</li><li>· Manuscript accepted in <i>Nature Methods</i>, preprint available on bioRxiv.</li><li>· Using deep-learning models to predict psychiatric disease risk based on individual genome</li><li>· Co-first author manuscript published in <i>Science</i>, front cover.</li></ul>	08/2013 - 05/2019 <i>New Haven, CT</i>
<b>StatLab, Yale University</b> <i>Consultant</i> <ul style="list-style-type: none"><li>· Support all levels of data analysis at Yale University, including consultations on research plans, experiments designs, and data analysis strategies.</li><li>· Develop materials for and lead university-wide workshops like workshops on R, Python, Matlab, etc.</li></ul>	07/2015 - 07/2018 <i>New Haven, CT</i>

## TEACHING

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<b>Yale University</b> <i>Teaching Assistant</i> <ul style="list-style-type: none"><li>· Undergraduate/Graduate Course: Biomedical Data Science, Mining and Modeling</li><li>· Instructor: Dr. Mark Gerstein, Albert L. Williams Professor of Biomedical Informatics</li></ul>	01/2017 - 05/2017 <i>New Haven, CT</i>
<b>Yale University</b> <i>Teaching Assistant</i> <ul style="list-style-type: none"><li>· Undergraduate/Graduate Course: Designing the Digital Economy</li><li>· Instructor: Dr. E. Glen Weyl, Principal Researcher at Microsoft Research</li></ul>	08/2016 - 12/2016 <i>New Haven, CT</i>

## SELECTED PUBLICATIONS

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A Sethi\*, **M Gu**\*, E Gumusgoz, L Chan, KK Yan, J Rozowsky, I Barozzi, V Afzal, J Akiyama, I Plajzer-Frick, C Yan, C Pickle, M Kato, T Garvin, Q Pham, A Harrington, B Mannion, E Lee, Y Fukuda-Yuzawa, A Visel, DE. Dickel, K Yip, R Sutton, LA. Pennacchio and M Gerstein<sup>†</sup>. A cross-organism framework for supervised enhancer prediction with epigenetic pattern recognition and targeted validation. *Accepted in Nature Methods, forthcoming*

EYK Ho, Q Cao, **M Gu**, RWL Chan, Q Wu, M Gerstein, KY Yip. Shaping the nebulous enhancer in the era of high-throughput assays and genome editing. *Briefings in bioinformatics* (2019)

FCP Navarro, H Mohsen, C Yan, S Li, **M Gu**, W Meyerson, M Gerstein. Genomics and data science: an application within an umbrella. *Genome biology* 20.1 (2019): 109

D Wang\*, S Liu\*, J Warrell\*, H Won\*, X Shi\*, F Navarro\*, D Clarke\*, **M Gu**\*, P Emani\*, M Xu, YT Yang, JJ Park, SK Rhie, K Manakongtreecheep, H Zhou, A Nathan, J Zhang, M Peters, E Mattei, D Fitzgerald, T Brunetti, J Moore, PsychENCODE Consortium<sup>†</sup>, N Sestan, AE Jaffe, K White, Z Weng, DH Geschwind<sup>†</sup>, J Knowles<sup>†</sup>, M Gerstein<sup>†</sup>. Comprehensive functional genomic resource and integrative model for the adult brain. *Science* (2018), 362 (6420)

P McGillivray, D Clarke, W Meyerson, J Zhang, D Lee, **M Gu**, S Kumar, H Zhou, M Gerstein<sup>†</sup>. Network Analysis as a Grand Unifier in Biomedical Data Science. *Annual Review of Biomedical Data Science* (2018), 1: 153-180.

V Despic, M Dejung, **M Gu**, J Krishnan, J Zhang, L Herzel, K Straube, MB Gerstein, F Butter, KM Neugebauer<sup>†</sup>. Dynamic RNA-protein interactions underlie the zebrafish maternal-to-zygotic transition. *Genome Research* (2017), 27:1184-1194

L Guan, Q Yang, **M Gu**, L Chen, X Zhang<sup>†</sup>. Exon expression QTL (eeQTL) analysis highlights distant genomic variations associated with splicing regulation. *Quantitative Biology* (2014), 2(2):71-79.

## CONFERENCE PRESENTATIONS

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ISCB conference on Regulatory & Systems Genomics (RSGDREAM 2018, New York, NY)	12/2018
CSH-Asia Systems Biology of Gene Regulation & Genome Editing (Suzhou, China)	10/2018
ENCODE Consortium Annual Meeting 2018 (Palo Alto, CA)	02/2018
American Society of Human Genetics Annual Meeting (ASHG 2017, Orlando, FL)	10/2017

## ACADEMIC SERVICE

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ICML 2020 Workshop on Computational Biology Program Committee  
BIOKDD 2020 Program Committee  
Grace Hopper Conference (GHC 2020) Artificial Intelligence Program Committee  
ENCODE Consortium enhancer prediction challenges steering committee  
Reviewer: IEEE SMARTCOMP 2019; Smart Health (Journal); PLOS One

## INVITED SEMINARS

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NEC lab (Princeton)	05/2019
University of Massachusetts Boston, Computer Science Department	04/2019
IBM Research (Thomas J. Watson Research Center, NY)	04/2019
Microsoft Research (New England)	01/2019

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\* These authors contribute equally