MENGTING GU

2137 University Ave, Mountain View, CA • 203-397-6155 • gumengting333@gmail.com

EDUCATION

School of Arts & Sciences, Yale University

Ph.D, Computational Biology and Bioinformatics
Concentrations: Algorithms and Machine Learning, Functional Genomics

School of Engineering, Yale University

M.S., Computer Science, GPA 4.0

Tsinghua University

B.A., School of Economics and Management

B.S., School of Life Sciences and Biotechnology

The University of Hong Kong

Exchange

EXPERIENCES

Visa Research 06/2019 - Present

Staff Research Scientist

Palo Alto, CA

- · Research: Uniform word embeddings across multiple languages
- · Research: Modeling dynamic transaction graphs using graph attention networks
- · Improve Visa fraud detection system over the financial data warehouse at Visa
- · Develop predictive models for essential parties in the payment and commerce system

Yale University 08/2013 - 05/2019

Graduate Student Researcher

- New Haven, CT
- Developed convolution-based method to detect gene regulators at genome-wide scale
 Software adopted by scientific research consortiums like ENCODE to analyze large-scale genomic data
- · Co-first author manuscript published in Nature Methods
- · Using deep-learning models to predict psychiatric disease risk based on individual genome
- · Co-first author manuscript published in *Science*, front cover.

StatLab, Yale University

07/2015 - 07/2018

Consultant

New Haven, CT

- · Support all levels of data analysis at Yale University, including consultations on research plans, experiments designs, and data analysis strategies.
- · Develop materials for and lead university-wide workshops like workshops on R, Python, Matlab, etc.

TEACHING

Yale University

Teaching Assistant

01/2017 - 05/2017

New Haven, CT

- · Undergraduate/Graduate Course: Biomedical Data Science, Mining and Modeling
- · Instructor: Dr. Mark Gerstein, Albert L. Williams Professor of Biomedical Informatics

Teaching Assistant

 \cdot Undergraduate/Graduate Course: Designing the Digital Economy

· Instructor: Dr. E. Glen Weyl, Principal Researcher at Microsoft Research

SELECTED PUBLICATIONS

A Sethi*, M Gu*, E Gumusgoz, L Chan, KK Yan, J Rozowsky, I Barozzi, V Afzal, J Akiyama, I Plajzer-Frick, C Yan, C Novak, M Kato, T Garvin, Q Pham, A Harrington, B Mannion, E Lee, Y Fukuda-Yuzawa, A Visel, DE. Dickel, K Yip, R Sutton, L.A. Pennacchio and M Gerstein[†]. Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. *Nature Methods* 17.8 (2020): 807-814

J Zhang*, D Lee*, V Dhiman*, P Jiang*, J Xu*, P McGillivray*, H Yang*, J Liu, W Meyerson, D Clarke, M Gu, S Li, S Lou, J Xu, L Lochovsky, M Ung, L Ma, S Yu, Q Cao, A Harmanci, KK Yan, A Sethi, G Gürsoy, M R Schoenberg, J Rozowsky, J Warrell, P Emani, Y T Yang, T Galeev, X Kong, S Liu, X Li, J Krishnan, Y Feng, J Rivera-Mulia, J Adrian, J R Broach, M Bolt, J Moran, D Fitzgerald, V Dileep, T Liu, S Mei, T Sasaki, C Trevilla-Garcia, S Wang, Y Wang, C Zang, D Wang, R J Klein, M Snyder, D M Gilbert, K Yip, C Cheng, F Yue, X S Liu, K P White, M Gerstein†. An integrative ENCODE resource for cancer genomics. Nature Communications

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* 21.3 (2020): 836-850

FCP Navarro, H Mohsen, C Yan, S Li, \mathbf{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[‡], N Sestan, AE Jaffe, K White, Z Weng, DH Geschwind[†], J Knowles[†], M Gerstein[†]. 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[†]. 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[†]. 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[†]. Exon expression QTL (eeQTL) analysis highlights distant genomic variations associated with splicing regulation. *Quantitative Biology* (2014), 2(2):71-79.

^{*} These authors contribute equally

CONFERENCE PRESENTATIONS

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

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

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