TENG GAO

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EDUCATION

Harvard University (Cambridge, MA, USA)   Sep. 2020 – May 2024 (Expected)
Ph.D. Candidate in Bioinformatics and Integrative Genomics (GPA: 4.00/4.00)
Thesis advisors: Peter V. Kharchenko and Peter J. Park
Committee: Nir Hacohen, Vijay Sankaran, Kamila Naxerova

Washington University (St. Louis, MO, USA)   Sep. 2014 – May 2018
B.S. Double Major in Computer Science and Biology (GPA: 3.99/4.00)
Summa Cum Laude
Honor thesis advisor: Christopher Maher

RESEARCH POSITIONS

Harvard Medical School, *Department of Biomedical Informatics*   Mar. 2021 – Present
Graduate Researcher (Advisors: Peter V. Kharchenko and Peter J. Park)
- Developed Numbat, a novel computational method to infer genome aberrations and single-cell phylogeny from scRNA-seq data
- Applied Numbat to characterize pediatric neuroblastoma and age-related mosaic chromosomal alterations in normal tissues
- Developing new computational methods for the analysis of subcellular RNA organization from spatial transcriptomics data

Memorial Sloan Kettering Cancer Center, *Computational Oncology*   May 2018 – Aug. 2020
Computational Biologist I-II (Advisors: Elli Papaemmanuil and Kelly Bolton)
- Led large-scale study on clonal hematopoiesis and therapy-related leukemia in 32,000 cancer patients

Washington University in St. Louis, *McDonnell Genome Institute*   Sep. 2016 – May 2018
Undergraduate Researcher (Advisor: Christopher Maher)
- Co-developed INTEGRATE-Vis, a python visualization package for patient-specific gene fusions discovered in RNA-seq data
- Honor thesis: "ceFinder: Machine learning based prediction of novel competing endogenous RNAs."

Roche Molecular Systems   May 2017 – Aug. 2017
Bioinformatics Intern (Manager: Dwight Kuo)
- Developed RNA-Seq analysis pipelines for novel miRNA biomarker discovery and differential expression in prostate cancer
- Identified a novel antibiotic resistance gene cassette in Methicillin-resistant S. aureus through de novo genome assembly

Wake Forest Institute for Regenerative Medicine   May 2016 – Aug. 2016
Summer Scholar (Advisors: Anthony Atala and Sang Jin Lee)
- Established a mathematical model for biomaterial viscoelasticity in 3D biofabrication

PUBLICATIONS   (*: equal contributions; ‡: co-corresponding authors)

Selected Publications

1. **Gao T**, Eleni MK, Ljungström V, Heinzel A, Tischler AS, Oberbauer R, Loh PR, Adameyko I, Park PJ‡, Kharchenko PV‡ (2023). "A pan-tissue survey of mosaic chromosomal alterations in 948 individuals". *Nature Genetics* 10.1038/s41588-023-01537-1. [Paper] [Code]

2. **Gao T**, Soldatov R, Sarkar H, Kurkiewicz A, Biederstedt E, Loh PR, and Kharchenko PV (2022). "Haplotype-aware analysis of somatic copy number variations from single-cell transcriptomes". *Nature Biotechnology 41*, 417–426. 10.1038/s41587-022-01468-y. [Paper] [Code]

3. **Gao T**, Ptashkin R, Bolton KL, Sirenko M, Fong C, Spitzer B, Menghrajani K, Ossa JEA, Zhou Y, Bernard E, Levine M, Martinez JSM, Zhang Y, Franch SE, Patel M, Braunstein LZ, Kelly D, Yabe M, Benayed R, Caltabellotta NM, Philip J, Paraiso E, Mantha S, Solit DB, Diaz LA Jr, Berger MF, Klimek V, Levine RL, Zehir A, Devlin SM, Papaemmanuil E (2021). "Interplay between chromosomal alterations and gene mutations shapes the evolutionary trajectory of clonal hematopoiesis". *Nature Communications 12*, 338. 10.1038/s41467-020-20565-7. [Paper] [Code]

4. Bolton KL, Ptashkin RN*, **Gao T***, Braunstein L, Devlin SM, Kelly D, Patel M, Berthon A, Syed A, Yabe M, Coombs CC, Caltabellotta NM, Walsh M, Offit K, Stadler Z, Mandelker D, Schulman J, Patel A, Philip J, Bernard E, Gundem G, Ossa JEA, Levine M, Martinez JSM, Farnoud N, Glodzik D, Li S, Robson ME, Lee C, Pharoah PDP, Stopsack KH, Spitzer B, Mantha S, Fagin J, Boucai L, Gibson CJ, Ebert BL, Young AL, Druley T, Takahashi K, Gillis N, Ball M, Padron E, Hyman DM, Baselga J, Norton L, Gardos S, Klimek VM, Scher H, Bajorin D, Paraiso E, Benayed R, Arcila ME, Ladanyi M, Solit DB, Berger MF, Tallman M, Garcia-Closas M, Chatterjee N, Diaz LA Jr, Levine RL, Morton LM, Zehir A, Papaemmanuil E (2020). "Cancer therapy shapes the fitness landscape of clonal hematopoiesis". *Nature Genetics 52*, 1219–1226. 10.1038/s41588-020-00710-0. [Paper]

5. **Gao T***, Gillispie GJ*, Copus JS, Pr AK, Seol YJ, Atala A, Yoo JJ, and Lee SJ (2018). "Optimization of gelatin–alginate composite bioink printability using rheological parameters: a systematic approach". *Biofabrication 10*, 034106. 10.1088/1758-5090/aacdc7. [Paper]

Other Publications

6. Franch SE, Mehine M, Ptashkin RN, Bolton KL, Bandlamudi C, Srinivasan P, Zhang L, Goodell MA, Gedvilaite E, Menghrajani K, Sánchez-Vela P, Mandelker D, Comen E, Norton L, Benayed R, **Gao T**, Papaemmanuil E, Taylor B, Levine R, Offit K, Stadler Z, Berger MF, Zehir A (2023). "Associations between cancer predisposition mutations and clonal hematopoiesis in patients with solid tumors". *JCO Precision Oncology* 2023:7. 10.1200/PO.23.00070. [Paper]

7. Spitzer B, Rutherford KD, Gundem G, McGovern EM, Millard NE, Arango Ossa JE, Cheung IY, **Gao T**, Levine MF, Zhang Y, Medina JSM, Feng Y, Ptashkin RN, Bolton KL, Farnoud N, Zhou Y, Patel MA, Asimomitis G, Cobbs CC, Mohibullah N, Huberman KH, Arcilla ME, Kushner BH, Modak S, Kung AL, Zehir A, Levine RL, Armstrong SA, Cheung NKV, Papaemmanuil E (2022). "Bone marrow surveillance of pediatric cancer survivors identifies clones that predict therapy-related leukemia". *Clinical Cancer Research 28*, 1614–1627. 10.1158/1078-0432.CCR-21-2451. [Paper]

8. Bolton KL, Koh Y, Foote MB, Im H, Jee J, Sun CH, Safonov A, Ptashkin R, Moon JH, Lee JY, Jung J, Kang CK, Song K-H, Choe PG, Park WB, Kim HB, Oh M-D, Song H, Kim S, Patel M, Derkach A, Gedvilaite E, Tkachuk KA, Wiley BJ, Chan IC, Braunstein LZ, **Gao T**, Papaemmanuil E, Esther NB, Pessin MS, Kamboj M, Diaz LA Jr, Ladanyi M, Rauh MJ, Natarajan P, Machiela MJ, Awadalla P, Joseph V, Offit K, Norton L, Berger MF, Levine RL, Kim ES, Kim NJ, Zehir A (2021). "Clonal hematopoiesis is associated with risk of severe Covid-19". *Nature Communications 12*, 5975. 10.1038/s41467-021-26138-6. [Paper]

9. Zhang J, **Gao T**, Maher CA (2017). "INTEGRATE-Vis: a tool for comprehensive gene fusion visualization". *Scientific Reports 7*. 10.1038/s41598-017-18257-2. [Paper] [Code]

PRESENTATIONS & INVITED TALKS

NIH Somatic Mosaicism across Human Tissues (SMaHT) Network Midyear Meeting	Dec. 2023
New York University Applied Bioinformatics Laboratory Single-Cell Club – New York, NY	Sep. 2022
Single-Cell Cancer Biology Gordon Research Conference – Easton, MA	Jun. 2022
Broad Institute Single-Cell Seminar Series – Cambridge, MA	Feb. 2022
American Society of Hematology (ASH) 62nd Annual Meeting and Exhibition – San Diego, CA	Dec. 2020

HONORS & AWARDS

Rising Young Scientist Award ($1000), Karin Grunebaum Cancer Research Foundation – Boston, MA   May 2023
1st place, Silicon Valley AI & Genomics Hackathon, Google, NVIDIA and NCBI – San Francisco, CA   Jun. 2017
Thomas Scholarship, Washington University – St. Louis, MO   Sep. 2015

ACADEMIC SERVICE

Mentoring

Krishna Dasari (Undergraduate student, Yale; Summer scholar, Park Lab, Harvard Medical School)   Jun. 2023 – Aug. 2023
- Project: Estimating oncogene dosage sensitivity from pairwise comparisons of tumor subclones

Outreach

Student Committee Member, Bioinformatics and Integrative Genomics Ph.D. program, Harvard University   Sep. 2023 – Present
Peer Mentor, Bioinformatics and Integrative Genomics Ph.D. program, Harvard University   Aug. 2022 – Present
Team Lead, Sling Health Incubator Network, Washington University   Sep. 2014 – Oct. 2016
Co-founder and Vice President, Washington University Popular Science Magazine, Washington University   Sep. 2014 – May 2016

Peer Review

Journals: *Bioinformatics*, *Cell Reports*, *Nature Genetics* (co-reviewer), *Frontiers in Immunology*
Conferences: *BICOB-2022 14th International Conference on Bioinformatics and Computational Biology*

TEACHING EXPERIENCES

Harvard Medical School (Cambridge, MA, USA)   Sep. 2022 – Dec. 2022
Teaching Fellow, Concepts in Genome Analysis (BMIF 201)

Washington University (St. Louis, MO, USA)   Aug. 2017 – Dec. 2017
Teaching Assistant, Elementary to Intermediate Statistics and Data Analysis (Math 3200)