

# TENG GAO

[tgaoteng@gmail.com](mailto:tgaoteng@gmail.com) | [ORCID](#) | [GitHub](#) | [Google Scholar](#)

## EDUCATION

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<b>Harvard University</b> (Cambridge, MA, USA)	Sep. 2020 – May 2024
Ph.D. in Bioinformatics and Integrative Genomics (GPA: 4.00/4.00)	
Thesis advisors: Peter J. Park and Peter V. Kharchenko	
Committee: Nir Hacohen, Vijay G. Sankaran, Kamila Naxerova	
 <b>Washington University</b> (St. Louis, MO, USA)	Sep. 2014 – May 2018
B.S. Double Major in Computer Science and Biology (GPA: 3.99/4.00)	
<i>Summa Cum Laude</i>	
Honor thesis advisor: Christopher Maher	

## RESEARCH POSITIONS

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<b>Boston Children's Hospital &amp; Broad Institute of MIT and Harvard</b>	Jun. 2024 – Present
Damon Runyon-HHMI Fellow (Advisor: Vijay G. Sankaran)	
• Studying hematopoietic stem cell biology in bone marrow transplantation using single-cell multiomics	
 <b>Harvard Medical School, Department of Biomedical Informatics</b>	Mar. 2021 – May 2024
Graduate Researcher (Advisors: Peter J. Park and Peter V. Kharchenko)	
• 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	
 <b>Memorial Sloan Kettering Cancer Center, Computational Oncology</b>	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	
 <b>Washington University in St. Louis, McDonnell Genome Institute</b>	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.”	
 <b>Roche Molecular Systems</b>	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 <i>S. aureus</i> through de novo genome assembly	
 <b>Wake Forest Institute for Regenerative Medicine</b>	May 2016 – Aug. 2016
Summer Scholar (Advisors: Anthony Atala and Sang Jin Lee)	
• Established a mathematical model for biomaterial viscoelasticity in 3D biofabrication	

## PUBLICATIONS

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

### Selected Publications

1. **Gao T<sup>‡</sup>**, Sankaran VG<sup>‡</sup> (2024). “Disease Background Influences Fate of Transplanted Stem Cells.” *Nature* (News & Views), October 23. <https://doi.org/10.1038/d41586-024-03112-y>. [Paper]

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

## Other Publications

5. Liu J, Tran D, Xue L, Wiley BJ, Vlasschaert C, Watson CJ, MacGregor HAJ, Zong X, Chan ICC, Das I, Uddin MM, Niroula A, Griffin G, Ebert BL, Mack T, Pershad Y, Sharber B, Berger M, Zehir A, Ptashkin R, Levine RL, Papaemmanuil E, Joseph V, **Gao T**, Kemel Y, Mandelker D, Stopsack KH, Pharoah PDP, Mukherjee S, Ding L, Cao Y, Walter MJ, Blundell JR, Chatterjee N, Offit K, Godley LA, Link DC, Stadler ZK, Bick AG, Natarajan P, Bolton KL (2024). “Germline genetic variation impacts clonal hematopoiesis landscape and progression to malignancy”. *Nature Genetics* (2025). <https://doi.org/10.1038/s41588-025-02250-x>. [\[Paper\]](#)
6. Olsen TK, Otte J, Mei S, Embaie BT, Kameneva P, Cheng H, **Gao T**, Zachariadis V, Tsea I, Björklund Å, Kryukov E, Hou Z, Johansson A, Sundström E, Martinsson T, Fransson S, Stenman J, Fard SS, Johnsen JI, Kogner P, Adameyko I, Enge M, Kharchenko PV, Baryawno N (2024). “Joint single-cell genetic and transcriptomic analysis reveal pre-malignant SCP-like subclones in human neuroblastoma”. *Molecular Cancer* 23, 180 (2024). <https://doi.org/10.1186/s12943-024-02091-y>. [\[Paper\]](#)
7. 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. [\[Paper\]](#)
8. 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. [\[Paper\]](#)
9. 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. [\[Paper\]](#)
10. 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, Boucail 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](#)]

11. **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](#)]
12. 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

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Speaker, Emerging Leaders in Cancer Research Seminar Series, Roswell Park Cancer Center – Buffalo, NY	Jul. 2024
Speaker, Biomedical Informatics PhD Program Recruitment Event – Boston, MA	Feb. 2024
Speaker, Altos Labs San Diego Institute of Science Annual Retreat – San Diego, CA	Dec. 2023
Poster presenter, Cold Spring Harbor Laboratory Genome Informatics Conference – New York, NY	Dec. 2023
Lightning talk speaker, NIH Somatic Mosaicism across Human Tissues (SMaHT) Network Midyear Meeting	Dec. 2023
Speaker, New York University Applied Bioinformatics Laboratory Single-Cell Club – New York, NY	Sep. 2022
Speaker, Single-Cell Cancer Biology Gordon Research Conference – Easton, MA	Jun. 2022
Speaker, Broad Institute Single-Cell Seminar Series – Cambridge, MA	Feb. 2022
Speaker, American Society of Hematology (ASH) 62nd Annual Meeting and Exhibition – San Diego, CA	Dec. 2020

## HONORS & AWARDS

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Damon Runyon-HHMI Fellowship Award, Damon Runyon Cancer Research Foundation – New York, NY	Feb 2025
Rising Young Scientist Award (\$1000), Karin Grunebaum Cancer Research Foundation – Boston, MA	May 2023
1 <sup>st</sup> 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

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### 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

Steering Committee Member, Internationals @ Broad affinity group, Broad Institute	Feb. 2025 – Present
Scientist in Residence, Broad Discovery Center Meet-a-Scientist Educational Program, Broad Institute	Sep. 2024 – Present
Student Committee Member, Bioinformatics and Integrative Genomics Ph.D. program, Harvard University	Sep. 2023 – May 2024
Peer Mentor, Bioinformatics and Integrative Genomics Ph.D. program, Harvard University	Aug. 2022 – May 2024
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), *Nature Communications*, *Frontiers in Immunology*  
Conferences: *BICOB-2022 14th International Conference on Bioinformatics and Computational Biology*

## TEACHING EXPERIENCES

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Harvard Medical School (Cambridge, MA, USA) Teaching Fellow, Concepts in Genome Analysis ( <a href="#">BMIF 201</a> )	Sep. 2022 – Dec. 2022
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**Washington University** (St. Louis, MO, USA)

Teaching Assistant, Elementary to Intermediate Statistics and Data Analysis ([Math 3200](#))

Aug. 2017 – Dec. 2017