

Herbert & Florence Irving Assistant Professor of Cancer Data Research  
Assistant Professor of Biomedical Engineering  
Affiliated Faculty, Department of Computer Science  
Affiliated Member, Data Science Institute  
Member, Herbert Irving Comprehensive Cancer Center  
Columbia University  
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## EDUCATION

- 2010-2014, Ph.D., Bioinformatics, Boston University, Boston MA, USA.
- 2009 - 2010, M.S., Electrical Engineering (Machine Learning and Signal Processing), Boston University, Boston MA, USA.
- 2004 - 2008, B.S., Electrical Engineering (Signal Processing), minor in Industrial Engineering, Sharif University of Technology, Tehran, Iran.

## POSITIONS

- Herbert & Florence Irving Assistant Professor of Cancer Data Research (in the Irving Institute for Cancer Dynamics), Columbia University, 2020 - present
- Assistant Professor (tenure track), Department of Biomedical Engineering, Columbia University, 2020 - present
- Postdoctoral Research Fellow, Memorial Sloan Kettering Cancer Center, New York, NY, Mentor: Dr. Dana Pe'er, 2016 - 2019
- Postdoctoral Research Scientist, Department of Biological Sciences, Columbia University, New York, NY, Dr. Dana Pe'er (moved to MSK), 2014 - 2016
- Research Intern, Microsoft Research, Redmond, WA, Dr. Bill Bolosky. Summer 2014
- Visiting Researcher, Department of Statistics, Harvard University, Cambridge, MA, Dr. Edoardo Airoldi, 2013-2014
- Research Assistant, Department of Biomedical Engineering, Boston University, Boston, MA, Dr. James Galagan. 2010-2014

## HONORS AND AWARDS

- Early-Career Innovator in Science Award in Cancer Immunology, Takeda and the New York Academy of Sciences (*one awardee across the globe*), 2024.
- Allen Distinguished Investigator Award, Allen Institute, 2023.
- NHGRI Award for Supporting Talented Early Career Researchers in Genomics (R01), 2023.
- CZI Science Diversity Leadership Award, Chan Zuckerberg Initiative and the National Academies of Sciences, Engineering, and Medicine, 2022.
- NSF CAREER Award, 2022.
- Provost's Grant for junior faculty contributing to the diversity goals of Columbia University, 2022.
- Columbia Research Initiatives in Science & Engineering (RISE) Award, 2021.
- Irving Endowed Assistant Professorship in Cancer Data Research, Columbia University, 2020.

- Tri-Institutional Breakout Prize for Junior Investigators, Weill Cornell Medicine, Rockefeller University, and Memorial Sloan Kettering Cancer Center, 2019.
- Next Generation in Biomedicine (20 scientists selected worldwide), Broad institute of MIT and Harvard, 2018.
- NIH NCI Pathway to Independence Award (K99/R00), 2018.
- American Cancer Society Postdoctoral Fellowship, 2017.
- IBM Best Student Paper Award, New England Statistics Symposium (NESS), 2014.
- TEDMED Front Line Scholarship, 2014.
- Best Poster Presentation Awards: 10th Annual Machine Learning Symposium, The New York Academy of Sciences, 2016; Memorial Sloan Kettering Postdoctoral Research Symposium, 2016; Boston Bacterial Meeting, Harvard University, 2013; Bioinformatics Student Symposium, Boston University, 2013.
- Presidential Award for Exceptional Students, Iran, 2004.
- Silver Medal, 16th National Physics Olympiad, Iran, 2003.
- Prize in 11th Intl. Competition of First Step to Nobel Prize in Physics for high school students, Polish Academy of Sciences (first awardee from Iran), 2003.
- Silver Medal, National Khwarizmi Student Research Contest, Iran, 2002.

## PUBLICATIONS

*Note:* ^ indicates corresponding and senior author(s). \* equal contributions. Underlining indicates lab trainees.

### Manuscript Pre-prints, Submitted, and Under Review

1. Maurer K\*, Park CY\*, Mani S, Borji M, Penter L, Jin Y, Zhang JY, Shin C, Brenner JR, Southard J, Krishna S, Lu W, Lyu H, Abbondanza D, Mangum C, Olsen LR, Neuberg DS, Bachireddy P, Garhi SL, Li S, Livak KL, Ritz J, Coiffeur RJ, Wu CJ^, Azizi E^. [Coordinated Immune Cell Networks in the Bone Marrow Microenvironment Define the Graft versus Leukemia Response with Adoptive Cellular Therapy](#), *In revision in Science Immunology*.
2. Park C\*, Mani S\*, Beltran-Velez N, Maurer K, Gohil S, Li S, Huang T, Knowles DA, Wu CJ, Azizi E^. [DIISCO: A Bayesian framework for inferring dynamic intercellular interactions from time-series single-cell data](#). *In revision in Genome Research*.
3. Boyeau P\*, Hong J\*, Gayoso A, Kim M, McFaline-Figueroa JL, Jordan MI, Azizi E, Ergen C^, Yosef N^, [Deep generative modeling of sample-level heterogeneity in single-cell genomics](#), *bioRxiv*. 2024.
4. Nazaret A\*, Fan JL\*, Lavallée V-P\*, Cornish AE, Kiseliovas V, Masilionis I, Chun J, Bowman RL, Eisman SE, Wang J, Shi L, Levine RL, Mazutis L, Blei D, Pe'er D^, Azizi E^, [Deep generative model deciphers derailed trajectories in acute myeloid leukemia](#). *bioRxiv*. 2023.11. 11.566719.
5. He S, Zhu Y, Chauhan S, Tavakol DN, Lee JH, Berris RB, Xu C, Lee JH, Lee C, Cai S, McElroy S, Vunjak-Novakovic G, Timer R, Azizi E, Xu B, Lao Y-H^, Leong KW^. [Human vascular organoids with a mosaic AKT1 mutation recapitulate Proteus syndrome](#). *bioRxiv*. 2024.
6. Gu J, Iyer A, Wesley B, Tagliatalata A, Leuzzi G, Hangai S, Decker A, Gu R, Klickstein N, Shuai Y, Jankovic K, Parker-Burns L, Jin Y, Zhang JY, Hong J, Niu S, Chou J, Landau DA, Azizi E, Chan EM, Ciccio A, Gaublotte JT. [CRISPRmap: Sequencing-free optical pooled screens mapping multi-omic phenotypes in cells and tissue](#). *bioRxiv*. 2023:2023-12. *In revision in Nature Biotechnology*.
7. He S, Xu C, Lao YH, Chauhan S, Xiao Y, Willner MJ, Jin Y, McElroy S, Rao SB, Gogos JA, Tomer R, Azizi E, Xu B, Leong KW. [Mapping morphological malformation to genetic dysfunction in blood vessel organoids with 22q11. 2 Deletion Syndrome](#). *bioRxiv*. 2021.

## Peer-Reviewed Journal Publications

8. [He S\\*](#), [Jin Y\\*](#), [Nazaret A\\*](#), [Shi L](#), [Chen X](#), Rampersaud R, Dhillon BS, Valdez I, [Friend LE](#), [Fan JL](#), [Park CY](#), Mintz Y-H, [Carrera D](#), [Fang KW](#), [Mehdi K](#), [Rohde M](#), McFaline-Figueroa JL, Blei D, Leong KW, Rudensky AY<sup>^</sup>, Plitas G<sup>^</sup>, [Azizi E<sup>^</sup>](#). [Starfysh integrates spatial transcriptomic and histologic data to reveal heterogeneous tumor-immune hubs](#). *Nature Biotechnology*, 2024.
9. [Fuller J](#), Abramov A, Mullin D, Beck J, Lemaitre P, [Azizi E<sup>^</sup>](#). [A Deep Learning Framework for Predicting Patient Decannulation on Extracorporeal Membrane Oxygenators: Development and Model Analysis Study](#). *JMIR Biomedical Engineering*. 2024.
10. Liu Y, [Jin Y](#), [Azizi E<sup>^</sup>](#), Blumberg AJ<sup>^</sup>. [CellStitch: 3D Cellular Anisotropic Image Segmentation via Optimal Transport](#). *BMC Bioinformatics*. 24, 480. 2023.
11. Tavakol DN, Nash TR, Kim Y, [He S](#), Fleischer S, Graney PL, Brown JA, Liberman M, Tamargo M, Harken A, Ferrando AA, Amundson S, Garty G, [Azizi E](#), Leong KW, Brenner SJ, Vunjak-Novakovic G. [Modeling and countering the effects of cosmic radiation using bioengineered human tissues](#). *Biomaterials*. 2023 Aug 11:122267.
12. Wang Y\*, [Fan JL\\*](#), Melms JC\*, Amin AD, Georgis Y, Barrera I, Ho P, Tagore S, Abril-Rodriguez G, [He S](#), [Jin Y](#), Biermann J, Hofree M, Caprio L, Berhe S, Khan S, Henick BS, Ribas A, Macosko EZ, Chen F, Taylor AM, Schwartz GK, Carvajal RD, [Azizi E<sup>^</sup>](#), Izar B<sup>^</sup>, [Multi-modal single-cell and whole-genome sequencing of small, frozen clinical specimens](#). *Nature Genetics*. 55, 19-25.2023.
13. Biermann J, Melms JC, Amin AD, Wang Y, Caprio LA, Karz A, Tagore S, Barrera I, Ibarra-Arellano MA, Andreatta M, Fullerton BT, [et al. including [Azizi E](#)]. [Dissecting the treatment-naive ecosystem of human melanoma brain metastasis](#). *Cell*. 2022 Jul 7;185(14):2591-608.
14. Bachireddy P\*<sup>^</sup>, [Azizi E\\*<sup>^</sup>](#), Burdziak C, Nguyen VN, Ennis C, Maurer K, [Park CY](#), Choo Z-N, Li S, Gohil, SH, Ruthen NG, Ge Z, Keshin D, Cieri N, Livak K, Kim HT, Neuberger DS, Soiffer RJ, Ritz J, Alyea E, Pe'er D<sup>^</sup>, Wu CJ<sup>^</sup>. [Mapping the evolution of T cell states during response and resistance to adoptive cellular therapy](#). *Cell Reports*, 37, no. 6: 109992, 2021. (Featured in top 10 Best of Cell Reports 2021-2022).

## Peer-Reviewed Conference Publications

15. [Nazaret A\\*<sup>^</sup>](#), [Hong J\\*<sup>^</sup>](#), [Azizi E<sup>^</sup>](#), Blei D<sup>^</sup>. [Stable Differentiable Causal Discovery](#), *Proceedings of International Conference in Machine Learning (ICML) 2024* (top venue in machine learning; acceptance rate: 27%).
16. [Park C\\*](#), [Mani S\\*](#), Beltran-Velez N, Maurer K, Gohil S, Li S, Huang T, Knowles DA, Wu CJ, [Azizi E<sup>^</sup>](#). [DIISCO: A Bayesian framework for inferring dynamic intercellular interactions from time-series single-cell data](#). *Proceedings of Conference on Research in Computational Molecular Biology (RECOMB) 2024* (top venue in computational biology; acceptance rate: 16%).
17. [Zhang M](#), [Hoffer-Hawlik K](#), Izar B, [Azizi E<sup>^</sup>](#). GGERAPHF: Graph Generative Poisson Hierarchical Factorization. *ICML Workshop on Computational Biology*. 2023.
18. [Lia I](#), Vaikunthan M, Redenti A, Im J, Danino T, McFaline-Figueroa JL; [Azizi E<sup>^</sup>](#). BacTIME: Computational inference of bacterial interactions with the tumor microenvironment. *ICML Workshop on Computational Biology*. 2023.
19. [Nazaret A\\*](#), [Fan JL\\*](#), Pe'er D, [Azizi E<sup>^</sup>](#), [Probabilistic basis decomposition for characterizing temporal dynamics of gene expression](#), *ICML Workshop on Computational Biology*. 2022.
20. [Jin Y\\*](#), [Toberoff A\\*](#), [Azizi E<sup>^</sup>](#), [Transfer learning framework for cell segmentation with incorporation of geometric features](#), *NeurIPS LMRL Workshop*, 2020.

## Publications as a postdoctoral fellow

21. Alonso-Curbelo D, Ho YJ, Burdziak C, [et al. including **Azizi E**], [A gene–environment-induced epigenetic program initiates tumorigenesis](#). *Nature*. 2021 Feb;590(7847):642-8.
22. Price JC, **Azizi E**, Naiche LA, Parvani JG, Shukla P, Kim S, Slack-Davis JK, Pe'er D, Kitajewski JK, Notch3 signaling promotes tumor cell adhesion and progression in a murine epithelial ovarian cancer model, *Plos one*, 15(6) : e0233962, 2020. PubMed PMID: 32525899.
23. Burdziak C\*, **Azizi E\***, Prabhakaran S, & Pe'er D, [A Nonparametric Multi-view model for Estimating Cell Type-Specific Gene Regulatory Networks](#). *arXiv 1902.08138*, 2019.
24. Hemmers S, Schizas M, **Azizi E**, Dikiy S, Zhong Y, Feng Y, Altan-Bonnet G, Rudensky AY. [IL-2 production by self-reactive CD4 thymocytes scales regulatory T cell generation in the thymus](#). *Journal of Experimental Medicine*. 2019 Nov 4;216(11):2466-78.
25. Viny AD, Bowman RL, Liu Y, [et al. including **Azizi E**]. [Cohesin members Stag1 and Stag2 display distinct roles in chromatin accessibility and topological control of HSC self-renewal and differentiation](#). *Cell Stem Cell*. 2019 Nov 7;25(5):682-96.
26. **Azizi E\***, Carr AJ\*, Plitas G\*, Cornish AE\*, Konopacki C, Prabhakaran S, Nainys J, Wu K, Kiseliovas V, Setty M, Choi K, Fromme, R.M., Dao P, McKenney P.T., Wasti, R.C., Kadaveru, K., Mazutis L, Rudensky AY, Pe'er D, [Single-cell Map of Diverse Immune Phenotypes in the Breast Tumor Microenvironment](#), *Cell* 174 (5): 1293-1308, 2018 (Featured as **Cover Story**; over 1600 citations to date)
27. Diallo AB , Nguifo EM, Dhifli W, **Azizi E**, Prabhakaran S, Tansey W, Selected Papers from the Workshop on Computational Biology: Joint with the International Joint Conference on Artificial Intelligence and the International Conference on Machine Learning, *Journal of Computational Biology* 26(6) : 507-508, 2019. PubMed PMID: 31184954
28. **Azizi E\***, Prabhakaran\* S, Carr A, Pe'er D, [Bayesian Inference for Single-cell Clustering and Imputing](#), *Genomics and Computational Biology* 3 (1), 46, 2017.
29. Prabhakaran S\*, **Azizi E\***, Carr A, Pe'er D, [Dirichlet Process Mixture Model for Correcting Technical Variation in Single-Cell Gene Expression Data](#), *Proceedings of The 33rd International Conference on Machine Learning (ICML)*, *PMLR* 48:1070-1079, 2016 (Top venue in machine learning, acceptance rate: 24%; Recipient of Datamir Poster Presentation Award, NYAS Machine Learning Symposium 2016).

## Publications as a graduate student:

30. Dekhang R, Wu C, Smith KM, Lamb TM, Peterson M, Bredeweg EL, Ibarra O, Emerson JM, Karunarathna N, Lyubetskaya A, **Azizi E**, Hurley JM, Dunlap JC, Galagan JE, Freitag M, Sachs MS, Bell-Pederson D. [The Neurospora transcription factor ADV-1 transduces light signals and temporal information to control rhythmic expression of genes involved in cell fusion](#). *G3: Genes, Genomes, Genetics*. 2017 Jan 1;7(1):129-42.
31. **Azizi E**, Airoidi EM, Galagan JE, [Learning Modular Structures from Network Data and Node Variables](#), *Proceedings of the 31st International Conference on Machine Learning (ICML)*, *PMLR* 32(2):1440-1448, 2014 (Recipient of IBM Best Student Paper Award, **NESS 2014**) (Extended version).
32. Gomes AL, Abeel T, Peterson M, **Azizi E**, Lyubetskaya A, Carvalho L, Galagan J. [Decoding ChIP-seq with a double-binding signal refines binding peaks to single-nucleotides and predicts cooperative interaction](#). *Genome research*. 2014 Oct 1;24(10):1686-97.
33. Galagan JE, Minch K\*, Peterson M\*, Lyubetskaya A\*, **Azizi E\***, Sweet L\*, Gomes A\*, Rustad T, Dolganov G, Glotova I, et al., [The Mycobacterium tuberculosis regulatory network and hypoxia](#), *Nature*. 2013 Jul 11; 499 (7457): 178-183. doi: 10.1038/nature12337. (Azizi listed as co-second author; advisor listed as first author).
34. **Azizi E**. Joint learning of modular structures from multiple data types. *NeurIPS workshop on frontiers of network analysis*. 2013.

## Doctoral Thesis

35. E. Azizi, Modeling gene regulatory networks through data integration, *Ph.D. Thesis*, Boston University, 2014.

## Publications as an undergraduate student

36. Kianfar S, Azizi E, Kianfar F. A Comparison of Two Estimators for Solutions to Greedy Algorithm in Scheduling Depletable Sources. *International Conference on Risk Management & Engineering Management*. 2008.
37. Azizi E, Mohimani GH, Babaie-Zadeh M. Adaptive Sparse source separation with application to speech signals. *IEEE International Conference on Signal Processing and Communications* 2007 Nov 24 (pp. 640-643). IEEE.

## TEACHING

- Spring 2024 BMCSE 4480 Statistical Machine Learning in Genomics
- Spring 2023 BMENE 4480 Statistical Machine Learning in Genomics
- Spring 2022 BMENE 4480 Statistical Machine Learning in Genomics
- Fall 2020 BMENE 4480 Statistical Machine Learning in Genomics

## MENTORSHIP

- **Postdoctoral Trainees:** *Current:* Aaron Zweig (IICD; co-mentored with David Knowles); Lingting Shi (IICD; co-mentored with José McFaline-Figueroa). *Former:* Xueer Chen (IICD).
- **Doctoral Students:** *Current:* Cameron Y. Park (BME), Linyue Joy Fan (BME), Achille Nazaret (CS, co-advised with David Blei); Yinuo Jin (BME), Justin Hong (CS), Ioana Lia (BME; co-advised with José McFaline-Figueroa); Kevin Hoffer-Hawlik (BME, co-advised with José McFaline-Figueroa); Mingxuan Zhang (CUMC, co-advised with Andrea Califano). *Former:* Siyu He (BME; co-advised with Kam Leong).
- **Master Students:** *Current:* Khushi Desai (CS), Joshua Myers (BME), Michael Pressler (BME). *Former:* Jia Yi (Ady) Zhang (BME), Xumin Shen (BME), Crystal Shin (BME), Shouvik Mani (CS), Lauren Friend (BME).
- **Research interns sponsored from outside Columbia:** Marc Chevrier (France Polytechnique), Lea Bohbot (France Polytechnique), Abdullah Naqvi (CCNY), Tu Duyen Nguyen (France Polytechnique), Anabel Ojeda (Adelphi), Hannah Khanshali (CCNY), Pranik Chainani (Yale).
- **Undergraduate trainees:** *Current:* Jessie Huang, Danielle Maydan, Kaylee Fang, *Former:* Veronica Woldehanna, Jose Pomarino Nima, Tamjeed Azad, Alex Toberoff, Joshua Fuller, Max David Gupta, Ruxandra Tonea, James Wang, Sopho Kevlishvili, Isha Arora, David Carrera, Noa Kalfus (Barnard), William O'Brien, Siddhant Sanghi.
- **High school research interns:** Princess Della Tsivor, Rachel Africk, Kaleem Mehdi, Madeline Rohde.

## INVITED TALKS SINCE 2020

1. Cancer Immunotherapy: from bench to bedside and back Nature Conference, DFCI, Boston MA, June 2024.
2. NCI Data Science Seminar Series, May 2024.
3. NCI Spring School on Algorithmic Cancer Biology (SSACB), April 2024
4. Probing Human Disease Using Single-Cell Technologies Fusion Conference, Feb 2024.
5. American Society of Hematology (ASH) Annual Meeting, San Diego, December 2023.
6. The 18th Machine Learning in Computational Biology (MLCB2023), Seattle WA, December 2023 [Keynote].
7. MD Anderson Cancer Center's 2023 Leading Edge of Cancer Research Symposium, November 2023.
8. JKTG Foundation Symposium on Metastasis, Spatial Analytics and Combination Therapies, Bethesda MD, October 2023.

9. American Cancer Society Comedy Against Cancer fundraising event, Stamford CT, September 2023.
10. Single Cell Mapping in Development & Cancer Symposium, NYU Langone Department of Pathology, September 2023
11. EMBL-EBI Precision medicine in the era of high-resolution biology & artificial intelligence, Cambridge MA, September 2023.
12. Lipari Summer School: Computational Single-Cell Analysis with application in Biology and Medicine, July 2023.
13. Cell Growth and Proliferation Gordon Research Conference, July 2023.
14. Tumor-Immune Systems Biology Symposium, MSKCC, May 2023.
15. MSKCC Computational Oncology Seminar Series, April 2023.
16. NCI Cancer AI Research: Computational Approaches Addressing Imperfect Data Workshop, April 2023.
17. CSHL Probabilistic Modeling in Genomics, March 2023.
18. Transplantation and Cellular Therapy meeting of ASTCT and CIMTBR, February 2023.
19. Weill Cornell Medicine ICB Seminar Series, October 2022.
20. JSM 2022 Special Session on Statistical methods for single cell genomics and spatial transcriptomics, August 2022.
21. Probing Human Disease Using Single-Cell Technologies Fusion Conference, May 2022
22. University of Pennsylvania Bioengineering Graduate Research Symposium, April 2022, [Keynote].
23. Women in Science at Columbia (WISC) Graduate Research Symposium, April 2022, [Keynote].
24. Dept. of Bioinformatics and Computational Biology, University of Texas MD Anderson Cancer Center, March 2022.
25. NIAID Data Science Seminar, December 2021.
26. UNC Computational Medicine Seminar, November 2021.
27. Johns Hopkins Biomedical Engineering Seminar Series, November 2021.
28. Redirected Immune Cell Therapies Webinar, The New York Academy of Sciences, September 2021.
29. University of Washington Machine Learning in Computational Biology Seminar Series, May 2021.
30. NYU Biomedical Engineering Colloquium, April 2021.
31. ENAR Invited session on Bulk deconvolution and single-cell data analysis, March 2021.
32. NYU Pathology Department Research Seminar Series, March 2021.
33. 2nd Annual Symposium on Epigenetics, Immunity and Cancer, Universities of Pennsylvania, Columbia and Temple (virtual), Jan 2021.
34. Systems Biology Seminar Series, Boston University, March 2020.
35. Annual Engineering in Medicine Symposium, Columbia University, Feb 2020.

## RESEARCH FUNDING

### Current

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**R21HG012639**

NIH/NHGRI

**PI: Azizi**

9/21/2023-8/30/2025

1.7 months

Total: \$435,475

**Title:** Computational toolbox for spatial transcriptomic analysis of complex tissues

**Description:** The goal of this study is to develop a suite of interpretable machine learning frameworks and software for analyzing spatial transcriptomic data from any tissue type.

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<b>R01HG012875</b> NIH/NHGRI	<b>PI: Azizi</b> 02/17/2023 - 12/31/2027	2.4 months	Total: \$2,219,971
<b>Title:</b> Machine learning methods for interpreting spatial multi-omics data			
<b>Description:</b> The goal of this proposal is to develop the first computational toolbox for integrating multi-modal spatially resolved transcriptomic, proteomic, and epigenomic data in addition to histological images of tissues, to enable a comprehensive characterization of microenvironments, their regulatory programs, and associated genetic alterations in any tissue type.			
<b>Allen Distinguished Investigator Award</b> The Paul G. Allen Frontiers Group	<b>PI: Simunovic, McFaline, Azizi</b> 12/01/2023-12/30/2026	0.36 months	Total: \$1,500,000
<b>Title:</b> Sex hormone morphogenesis: a new frontier in studying organ development			
<b>Description:</b> To develop a multiplexed in vitro platform that combines quantitative stem cell models of gastrulation, single cell genome perturbation approaches, and machine learning to define the coupling between sex hormones and early organ development across species.			
<b>Science Diversity Leadership Award</b> Chan Zuckerberg Institute	<b>PI: Azizi</b> 12/01/2022 - 11/30/2027	2.0 months	Total: \$1,150,000
<b>Title:</b> Computational modeling of dysregulated mechanisms in the spatial breast tumor microenvironment			
<b>Description:</b> To construct a quantitative model for dysregulated mechanisms in the triple-negative breast tumor microenvironment.			
<b>CAREER CBET 2144542</b> NSF	<b>PI: Azizi</b> 2/15/2022-1/31/2027	0.25 months	Total: \$500,030
<b>Title:</b> CAREER: Integrative modeling of intercellular interactions in the tumor microenvironment			
<b>Description:</b> The goal of this study is to construct a computational model of spatial heterogeneity and intercellular interactions in the breast tumor microenvironment through the integration of spatial transcriptomics and imaging using novel machine learning methods.			
<b>Gift Funding</b> Africk Family Foundation	<b>PI: Azizi</b> 2/1/2020-12/31/2024	0.25 months	Total: \$200,000
<b>Title:</b> Computational Cancer Biology Research			
<b>Description:</b> The goal of the gift funding was to kickstart high-risk projects in the Computational Cancer Biology Laboratory directed by Azizi and propel the lab's interdisciplinary research in developing novel machine learning methods for studying the process of tumor progression in cancer patients using single-cell genomic data.			
<b>MacMillan CSNCG</b> MacMillan Family Foundation	<b>PI (Theme 2): Knowles, Co-I: Azizi</b> 9/21/2023-8/30/2026	0.36 months	Total: \$125,206
<b>Title:</b> Mathematical approaches to establishing dark genome causality			
<b>Description:</b> The goal of Theme 2 is to infer cell-type specific gene regulatory and disease causal networks underlying cancer progression and drug resistance.			
<b>R01CA266446</b> NIH/NCI	<b>PI: Izar; Co-I: Azizi</b> 9/1/2022-8/31/2027	0.36 months	Total: \$2,453,430
<b>Title:</b> The role of the CD58:CD2 axis in cancer immune evasion and resistance to immunotherapy			
<b>Description:</b> The goal of this study is to identify resistance mechanisms and therapy dependencies across the genomic spectrum of uveal melanoma.			
<b>SCOR-22937-22</b> Leukemia & Lymphoma Society	<b>PI: Soiffer, Wu; Co-I: Azizi</b> 10/1/2022 – 9/20/2027	0.36 months	Total: \$5,000,000
<b>Title:</b> Understanding and Overcoming Mechanisms of Immune Evasion after Allogeneic Transplant			
<b>Description:</b> This project will leverage recently developed advances in single cell genomic analysis to characterize critical immune cell interactions within the marrow microenvironment in the setting of adoptive immunotherapy to identify predictive biomarkers and specific antigenic targets of GvL.			

## Completed

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<b>R00CA230195</b> NIH/NCI	<b>PI: Azizi</b> 5/1/2020-10/30/2023	9.0 months	Total: \$747,000
<b>Title:</b> Integrative framework for identifying dysregulated mechanisms in the tumor-immune microenvironment <b>Description:</b> The goal of this study is to perform an unbiased characterization of cell populations in the tumor microenvironment and their dysregulated mechanisms, with an interdisciplinary framework of single-cell resolution transcriptional and epigenetic measurements, that are integrated with principled computational tools.			
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<b>R21CA263381</b> NIH/NCI	<b>PI: Izar; Co-I: Azizi</b> 7/8/2021-6/30/2023	0.12 months	Total: \$445,500
<b>Title:</b> Dissecting drug resistance in serial uveal melanoma biopsies using integrated, multi-modal single-cell profiling and novel machine learning tools. <b>Description:</b> The goal of this study was to use single-cell genomic, genome-editing and machine-learning tools to define drug resistance to MEKi and potential synthetic lethal vulnerabilities across the distinct genomic landscape of uveal melanoma			
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<b>HICCC-SEAS Seed Grant</b> Columbia University	<b>PI: Azizi, Stockwell</b> 1/1/2023-12/31/2023	0.12 months	Total: \$80,000
<b>Title:</b> Identifying 3D tumor metabolic neighborhoods using mass spectrometry imaging and machine learning <b>Description:</b> The goal of this study is developing technologies and algorithms for 3D mapping of the distributions of lipids/metabolites at single cell resolution in solid tumors			
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<b>Provost junior faculty grant</b> Columbia University	<b>PI: Azizi</b> 1/1/2022-12/31/2022	0.12 months	Total: \$25,000
<b>Title:</b> Machine learning for characterizing spatial dynamics in tumor tissues <b>Description:</b> The goal of this study is to develop a 3D segmentation tool for spatial transcriptomic data from complex tumor tissues.			
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<b>Columbia RISE Internal Grant</b> Columbia University	<b>PI: Azizi, Izar</b> 6/1/2021-5/31/2022	0.12 months	Total: \$80,000
<b>Title:</b> Dissecting drug resistance in serial uveal melanoma biopsies using integrated, multi-modal single-cell profiling and novel machine learning tools <b>Description:</b> The goal of this study is to study impact of MEKi-therapy on metastatic uveal melanoma at single-cell resolution.			
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<b>HICCC IPPP grant</b> Columbia HICCC (NCI P30 CA013696)	<b>PI: Azizi, Reshef</b> 9/15/20-9/14/21	0.24 months	Total: \$80,000
<b>Title:</b> Identification of a targetable macrophage maturation defect in human intestinal graft-versus-host disease by using advanced single-cell technologies and machine learning tools <b>Description:</b> This study aimed to characterize the phenotype and function of tissue-resident macrophages as well as their spatial and functional relationships with T cells and intestinal epithelium in human gut GVHD at single-cell level.			
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<b>DSI-HICD Seed Fund</b> Columbia Data Science Institute	<b>PI: Azizi, Gaublomme</b> 01/01/20 - 12/31/21	0.96 months	Total: \$175,000
<b>Title:</b> Probabilistic modeling of intercellular interactions that drive ferroptosis susceptibility of therapy-resistant cancer cells <b>Description:</b> The goal of this study is to develop probabilistic models to elucidate the role of intercellular interactions in driving susceptibility of treatment-resistant mesenchymal tumor cells to ferroptotic vulnerability, in liver cancer.			
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## MEDIA AND PRESS

- Takeda and The New York Academy of Sciences Announce 2024 Innovators in Science Award [[Summary Video](#)] [[Ceremony](#)] [[Press release](#)] [[Columbia Story](#)] [[Award announcement](#)]
- Chan Zuckerberg Science Diversity Leadership [[Link](#)] [[Columbia story](#)]