Anisha Tehim

abt65@cornell.edu | (201) – 394 - 4970

EDUCATION

Cornell University **2023 - 2026**
Major: Biometry & Statistics
Minor: Computer Science
Relevant Courses: *BIOCB4830 (Quantitative Genomics & Genetics), STSCI4030 (Linear Models with Matrices), STSCI3740 (Data Mining & Machine Learning), BTRY3080 (Probability Models & Inference), BTRY3020 (Biological Statistics II), CS2110 (Object Oriented Programming & Data Structures)*

University of California, Berkeley **2022 - 2023**
Intended Majors: Computer Science & Molecular Biology
Relevant Courses: *STAT20 (Introduction to Probability & Statistics), MATH54 (Linear Algebra & Differential Equations), CS61A (Structure & Interpretation of Computer Programs)*

RESEARCH EXPERIENCE

Tri-Institutional Computational Biology Program (MSK & Weill Cornell) **Summer 2024 - Present**
Dr. Ekta Khurana's Lab, Department of Physiology & Biophysics

- Conducted single-cell RNA sequencing analysis on Castration Resistant Prostate Cancer (CRPC) to investigate tumor microenvironment and cellular interactions driving tumor growth and immune evasion
- Optimized scSorter, a K-nearest neighbors algorithm, for improved classification accuracy of CRPC subtypes by refining cell-specific marker gene parameters
- Utilized PCA and UMAP for dimensionality reduction, uncovering spatial proximities and potential molecular overlaps between CRPC subtypes and Myeloid cells
- Modeled ligand-receptor interactions between CRPC subtypes and Myeloid cells, identifying significant interactions that suggest therapeutic targeting opportunities for enhanced anti-tumor responses

Weill Cornell Medical School **November 2023 – May 2024**
Dr. Ekta Khurana's Lab, Department of Physiology & Biophysics

- Performed cellular deconvolutional analysis on tissue & cell free DNA samples from prostate cancer patients to understand how cell deconvolution algorithms can be optimized for use on cell free DNA samples

National Institute of Health, National Cancer Institute **Summer 2023**
Dr. Fathi Elloumi, Developmental Therapeutics Branch

- Developed *MyPatient* in R/RShiny for TumorMiner, allowing physicians to search cancer patient data and explore clinical and molecular features
- Created a genomic dashboard to filter and analyze biomarkers, offering insights into gene expression, methylation, and mutation data
- Implemented scoring functions inspired by Jaccard Index to match patients by clinical and molecular profiles, aiding in identifying personalized treatment options.

University of Pennsylvania, Perelman School of Medicine **Summer 2022**
Dr. Blanca Hime's Lab, Department of Biostatistics, Epidemiology, and Informatics

- Analyzed evolutionary relationships among aldo-keto reductase proteins through sequence alignments and tree structure testing, using IQ-TREE and bootstrapping to validate findings.
- Published results in the Aldo-Keto Reductase (AKR) Superfamily Database, identifying potential new members

University of Pennsylvania, Perelman School of Medicine **Summer 2021**
Dr. Blanca Hime's Lab, Department of Biostatistics, Epidemiology, and Informatics

- Analyzed two million U.S. coronavirus sequences in R, constructing data pipelines to track spike protein mutations and variant distributions to inform future vaccine development

PUBLICATIONS & CONFERENCES

Publications

- Andress Huacachino A, Joo J, Narayanan N, Tehim A, Himes BE, Penning TM. *Aldo-keto reductase (AKR) superfamily website and database: An update. Chem Biol Interact. 2024*
- Shukla S, Li D, Cho WH, Nguyen HM, Conner JL, Roskes M, Tehim A, Bayshtok G, Schoeps DM, Pachai MR, Yan J, Teri NA, Campeau E, Attwell S, Trojer P, Ostrovnaya I, Gopalan A, Khurana E, Corey E, Chi P, Chen Y. BET inhibitors as a therapeutic intervention in gastrointestinal gene signature-positive castration-resistant prostate cancer. *J Clin Invest.* [Manuscript Submitted for Publication]
- Roskes M, Martinez-Fundichely A, Cohen S, Balaban M, Wong CK, Li W, Gonzalez T, Tehim A, Xu H, ElNaggar S, Myers M, Bareja R, Dorsaint P, Gorski K, Asad M, Al Assaad M, Robinson B, Sigouros M, Barnett E, Manohar J, Tagawa S, Nanus D, Molina A, Nauseef J, Sternberg C, Mosquera JM, Scher H, Sboner A, Raphael B, Chen Y, Khurana E. Cell-free DNA whole-genomes reveal chromosomal rearrangements associated with heterogeneity and stem cell-like castration-resistant prostate cancer. *Caner Discovery.* [Manuscript Submitted for Publication]

Conferences

- F. Elloumi, W. Reinhold, S. Verma, A. Tehim, D. Taniyama, M. Mizunuma, A. Dhall, K. Reilly, K. Pacack, J. Howe, Y. Arakawa, A. Luna, M. Aladjem, A. Thomas, J. D. Rivero, Y. Pommier. *TumorMiner: A new tool for precision medicine. International Society for Computational Biology. 2024*
- M. Roskes, A. M. Fundichely, W. Li, S. Cohen, H. Xu, S. Elnaggar, A. Tehim, M. Balaban, C. K. Wong, Y. Chen, B. Raphael, E. Khurana. *Evolution of genomic and epigenomic heterogeneity in prostate cancer from tissue and liquid biopsy. International Society for Computational Biology. 2024*
- M. Kan, A. Tehim, Q. Lu, B. E. Himes. *Genome Wide Analysis of SARS-CoV-2 Variants in the United States. American Thoracic Society International Conference. 2022*

EXTRACURRICULAR ACTIVITIES

Biomedical Informatics Club **August 2024 - Present**

Founder, President

- Developing lesson plans and projects to teach members principles of bioinformatics such as running sequence alignments, GWAS, GSEA, single cell analysis techniques, KNN, Bayes Classifier, evolutionary biology techniques

Girls Who Code, Women in Computing at Cornell **2023 - Present**

Co-leader

- Leads 90-minute weekly classes to teach Python to middle school girls in the Ithaca area
- Develops lesson plans covering principles of python (control structures, loops, functions along with final project code templates)

Bioprinting@Berkeley **2022 - 2023**

Sub-team Leader, Schwann Scaffolds: Bioprinting fibrin-factor XIII hydrogel scaffolds

- Selected to present research at the Cal Undergraduate Bioengineering Symposium | *Tehim, A., Budhia S., Gee, T.,*
- *Generating a CAD Model in Fusion 360 to Model Bioprinted Fibrin-Factor XIII-HA Scaffolds*
- Skills Learned: Running the CELLINK bioprinter, modeling in Fusion360, creating hydrogels, subculturing

Girls Who Code Middle School Club **2020 – 2022**

Founder, Leader

- Started the first Girls Who Code club for Middle School girls in the Ridgewood School & organized one 1-hour virtual meeting per week and developed lesson plans to teach members principles of HTML/CSS, Scratch, and Python to facilitate the development of individual projects such as Websites, Quiz Games, & Animation

AWARDS

- CRA Outstanding Undergraduate Research Award, Honorable Mention **2024**
- RHS Award for Excellence in Biology, *awarded to one student from graduating class* **2022**
- National Merit Commended Scholar **2021**
- AP Capstone Diploma **2022**
- NCWIT Aspirations in Computing National Honorable Mention Award **2022**
- National Latin Exam, Magna Cum Laude **2019, 2020, 2021, 2022**

SKILLS

- Experienced in R (R Packages: bioconductor, shiny (for app development), DESEq, Seurat, dplyr, ggtree), Python (pandas), Bash, HTML/CSS, Java, and JavaScript
- Familiar with Machine Learning algorithms such as K-Nearest Neighbors, Naïve Bayes Classifier, Linear and Quadratic Discriminant Analysis