Justin Cha

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Education

Cornell University   August 2021 – Present
PhD student
Dr. Frank Pugh Laboratory; Computational Biology

> The Pugh Lab is a leader in developing protocols for high-resolution chromatin immunoprecipitation (ChIP-exo) sequencing. I am currently developing software to detect and classify sites where proteins bind to DNA using patterns in the binding occupancy. I am also currently researching the LGE1/BRE1 complex and how modifications affect its binding patterns.

Georgia Institute of Technology   August 2014 – May 2018
BS with Highest Honors
Major in Biomedical Engineering; Minor in Physics
GPA: 3.7/4.0

Experience

Broad Institute of Harvard and MIT – Cambridge, MA
Associate Computational Biologist II   September 2018 – July 2021

> At the Broad Institute, I am a member of the Getz Lab, one of the world's leading labs for cancer genomics. I have worked on several exciting projects pushing at the forefront of the field. One was an analysis of genomic progression in head and neck squamous cell carcinoma (HNSCC). For this project, I made use of a novel set of computational methods to reconstruct the trajectory of genomic events from exome sequencing data. This allowed us to see which mutations and other variants tend to occur early on in the progression of cancer, which will be useful in treatment development and prognosis.

Integrative Systems Biology Lab – Atlanta, GA
Undergraduate Researcher   August 2016 – May 2018

> In the Integrative Systems Biology Lab at Georgia Tech, I worked with Dr. Denis Tsygankov on a project to simulate the biomechanics of solid tumors. For this project, I developed a tool to simulate densely packed cell populations under high pressure using time-evolving Voronoi diagrams, which is useful for analyzing tumor growth under specified conditions.

Georgia Institute of Technology – Atlanta, GA   January 2017 – May 2017
Data Analyst

> As a data analyst for the Biomedical Engineering department of Georgia Tech, I worked with Professor James Rains to analyze the market data for hospitals in the United States. I created a UI using Matlab to easily analyze subsets of the data and used trends to identify market hotspots for medical devices.

Publications
- "Genomic profiling of smoldering multiple myeloma identifies patients at a high risk of disease progression.," Journal of Clinical Oncology, 2020, 38(21), 2380-2389

Submission, revision, and review
- "Comprehensive analysis of tumour initiation, spatial and temporal progression under multiple lines of treatment," 2018
- "Event timing analysis establishes the genetic progression of HPV-positive head and neck squamous cell carcinoma (HNSCC), distinguishes progressions among further subgroups of HNSCC, and uncovers the development of intra-tumor genetic heterogeneity.," 2020
- "Genomic landscape of metastatic breast cancer (MBC): comprehensive cell-free DNA analysis from over 10,000 patients and comparison with primary breast cancer," 2020

Presentations
- "Mechanisms of Primary and Acquired Resistance to Venetoclax in Chronic Lymphocytic Leukemia (CLL)," American Association for Cancer Research, 2020
- "Genomic landscape of metastatic breast cancer (MBC): comprehensive cell-free DNA analysis from over 10,000 patients and comparison with primary breast cancer," San Antonio Breast Cancer Symposium, 2020

Training
- Open Science Grid (OSG) User School; Madison, WI; all expenses paid

Skills
Programming Languages: Python, JavaScript, Matlab, SQL, Julia
Quantitative: Data analysis, Statistics, Genomics
Communication: Technical presentation/writing, Data visualization, Teaching

Links
- https://github.com/broadinstitute/PhylogicNDT
- https://github.com/broadinstitute/getzlab-SignatureAnalyzer