# Justin Cha

## 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 involved in several projects investigating the fundamental characteristics of chromatin. I have investigated the role of the intrinsically disordered region in the LGE1/BRE1 ubiquitin-depositing complex in yeast, as well as the roles of specific components in the SWR1 H2A.Z-exchange complex. Currently I am working on methods for identifying and characterizing TF-TF interactions.

*Georgia Institute of Technology* May 2018
BS with Highest Honors
Major in Biomedical Engineering; Minor in Physics

## 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.

## Publications

*These authors contributed equally

- Burr, R. *et al.* (2024, in press) "Germline mutations and developmental mosaicism underlying EGFR-mutant lung cancer," *Nature Cancer*.
- Naeem, A. *et al.* (2023) "Pirtobrutinib targets BTK C481S in ibrutinib-resistant CLL but second-site BTK mutations lead to resistance," *Blood Advances.* Available at: https://doi.org/10.1182/bloodadvances.2022008447.
- Khalsa, J.*, Cha, J.*, Utro, F.*, Naeem, A.*, Murali, I.*, *et al*. (2023) "Genetic events associated with venetoclax resistance in CLL identified by whole exome sequencing of patient samples," *Blood*. Available at: https://doi.org/10.1182/blood.2022016600.
- Leshchiner, I.*, Mroz, E.*, Cha, J.*, *et al*. (2023) "Inferring early genetic progression in cancers with unobtainable premalignant disease," *Nature Cancer*. Available at: https://doi.org/10.1038/s43018-023-00533-y.
- Bustoros, M. *et al.* (2020) "Genomic profiling of smoldering multiple myeloma identifies patients at a high risk of disease progression," *Journal of Clinical Oncology*, 38(21), pp. 2380–2389. Available at: https://doi.org/10.1200/jco.20.00437.

## Presentations

- "Mutating the intrinsically disordered region of LGE1 in yeast impacts H2B ubiquitination," Cornell Computational Biology student seminar, 2022
- "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

## Posters

- "High-resolution characterization of transcription factor binding in S. cerevisiae," Great Lakes Bioinformatics, 2023
- "Inferring early genetic progression in cancers with unobtainable premalignant disease," Massachusetts General Hospital Center for Cancer Research, 2019

## Training

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

## Skills

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

## Links

- jcha40.github.io
  Personal website
- https://orcid.org/0000-0001-6026-2211
  ORCID
- https://github.com/broadinstitute/PhylogicNDT
  PhylogicNDT: A tool for clustering mutations, inferring tumor phylogeny, and inferring the order of mutations in cancer
- https://github.com/broadinstitute/getzlab-SignatureAnalyzer
  SignatureAnalyzer: A tool for identifying mutational signatures in a cohort of tumor samples
- https://github.com/jcha40/DPMCMC
  DPMCMC: A library for a tensorflow implementation of the Dirichlet Process Monte Carlo Markov Chain algorithm