TYLER M. CHINSKY
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Education

- **Johns Hopkins University** Baltimore, MD
  Master of Science, Bioinformatics *June 2022 – May 2024*

- **University at Buffalo SUNY** Buffalo, NY
  Bachelor of Science, Bioinformatics and Computational Biology *February 2022*
  Cum Laude
- **Mansfield High School** Mansfield, MA
  Diploma, High School *May 2015*

Research Experience

Computational Biologist, Dana-Farber Cancer Institute Boston, MA
Advisors: Saud AlDubayan, Eliezer Van Allen, Dept. of Breast Oncology *September 2022 – Present*

- Independently led multiple projects over a range of topics in cancer genomics, including uncovering the somatic genetic architecture of ER+ metastatic breast cancer, understanding the influence of germline elements on disease presentation, determining the efficacy of clinical, associating tumor's genetic characteristic with immunotherapy response and more.
- Performed large-scale genomic analysis using cloud computing tools (Terra, Google Cloud) and developed more than 10 workflows for common genomic tasks including sequence alignment, population and individual variant calling (short and structural variants), OncoPanel analysis, , genome and transcriptome wide association analysis, statistical analysis and developed novel methods for data mining. The workflows are extensively documented and are shared amongst team members.
- Acquired additional data to improve the statistical power of existing projects through initiating conversations with internal and external collaborators as well as curating data from publicly available databases such as the sequencing read archive. Presented research progress and learnings from conferences in multiple lab meetings and assisted with onboarding new members.

Computational Biologist, University at Buffalo SUNY CTRC Buffalo, NY
Advisors: Animesh Sinha and Kristina Seiffert *August 2020 – August 2022*

- Identified the association of certain HLA alleles as disease drivers of an autoimmune disease using predisposition markers, microarray sequencing, and functional analyses. Discovered sets of genes which categorize into divers based on disease status and/or HLA status of the patient, in addition to those which protect given the same categories. Furthermore, discovered how certain pathway mutation predispose the patient for having a higher polygenic risk score, and risk for developing Pemphigus vulgaris (PV).
- Developed and constructed pipelines to analyze microarray and RNA-seq data from *Pemphigus vulgaris*, utilizing multiple tools and libraries filter out noise from the raw reads and obtain images/matrices for each analysis.
- Designed and executed an experiment to functionally validate both the NGS work performed, and signatures found during analysis

Associate Research Technician, University at Buffalo SUNY Buffalo, NY
Advisor: Michael Yu *May 2021 – January 2022*

- Researched arginine methylation in RNA of budding flocculant yeast in the presence of one or more remodeling proteins
- Trained under Dr. Yu and his graduate students to gain and develop laboratory skills to utilize for future research projects
- Conducted *in vivo* experiments looking to verify HMT protein methylation levels in the presence and absence of Snf2, Ime4, and elF1A
- Applied *ex vivo* techniques to analyze protein expression of HMT proteins between Snf2, Ime4, and elF1A

Associate Computational Biologist, University at Buffalo SUNY Buffalo, NY
Advisor: Gerald Koudelka *January 2021 – May 2021*

- Conducted thorough research to identify consensus regions within specific bacteriophage DNA regions
- Constructed R programs to assist analysis of secondary structure prediction of Shiga toxin producing lambda bacteriophages
- Studied under Dr. Koudelka learning and amassing bioinformatics skills for future research projects

Laboratory Technician Assistant, Rochester Institute of Technology Rochester, NY
Advisor: Gosnell School of Life Sciences *August 2018 – March 2019*

- Successfully prepared, set up, and cleaned instructional laboratories as per professors' requests, while adhering to state and local regulations
- Prepared media, reagents, and buffers for instructional laboratories according to department and professor needs
- Demonstrated proficiency in maintaining and preparing bacterial and eukaryotic cell cultures for instructional use

Associate Computational Biologist, Rochester Institute of Technology Rochester, NY
Advisor: Feng Cui *August 2015 – October 2016*

- Conducted research on chromatin organization associated with DNA binding of tumor suppressors.
- Received training under the guidance of Dr. Cui and his graduate students, developing and enhancing bioinformatics skills for future research projects.
- Analyzed ChIP-Seq data to identify genomic inhibition regions for tp53 DNA binding sites, and gene expression information to determine pathway inhibition and activation on DNA binding regions.

Teaching Experience

Associate Research Mentor, University at Buffalo SUNY Buffalo, NY
Yu Laboratory: *August 2021 – January 2022*

- Mentored two sophomore undergraduate students alongside Dr. Yu in his laboratory, fostering the development of their laboratory skills.
- Provided guidance and explanations on the basic techniques and processes of biological scientific research, effectively communicating complex concepts to students.
- Encouraged constructive comprehension of learning from failed experiments, instilling a growth mindset in the students.
- Trained the two undergraduates on proper scientific notebook-keeping techniques, including maintaining a digital copy of figures, images, and tables.
- Demonstrated strong comprehension of techniques and methods through effective teaching and training of others.

Instructor, iD Tech Camps Boston, MA
Computer Security, Data Analysis, and Machine Learning Courses *May 2018 – August 2018*

- Designed and implemented coursework to teach high school students python, C++, and Java
- Taught 20 students per week for 12 weeks throughout the summer
- Implemented a multifaceted approach using auditory, kinesthetic, and visual aspects to ensure every student was able to learn the materials while still having fun
- Assisted other classes as needed when a different learning approach was needed

Publications

Peer-reviewed: (* - Equal Contribution, underline – First Authorships)

1. Alexander Bowitch, **Tyler M. Chinsky**, Michael C. Yu, Denise M. Ferkey. *The C. elegans OCTR-1 and Human Alpha-2A Adrenergic Receptors are Methylated within the Third Intracellular Loop by Human PRMT5 in vitro.* microPublication Biology, doi:10.17912/micropub.biology.000546 (2022)

2. Anutthaman Parthasarathy, Narayan H. Wong, Amanda N. Weiss, Susan Tian, Sara E. Ali, Nicole T. Cavanaugh, **Tyler M. Chinsky**, Chelsea E. Cramer, Aditya Gupta, Rakshanda Jha, Loryn K. Johnson, Elizabeth D. Tuason, Lauren M. Klafehn, Varada Krishnadas, Ryan J. Musich, Jennifer M. Pfaff, Spencer C. Richman, Alexandria J. Shumway, André O. Hudson. *SELfies and CELLfies: Whole Genome Sequencing and Annotation of Five Antibiotic Resistant Bacteria Isolated from the Surfaces of Smartphones, An Inquiry Based Laboratory Exercise in a Genomics Undergraduate Course at the Rochester Institute of Technology.* Journal of Genomics, 7, 26–30. https://doi.org/10.7150/jgen.31911 (2019)

Submitted Manuscripts:

1. Mark B. Leick, Seunghun Han, Kathleen M.E. Gallagher, Harrison J. Silva, Grace Martin, Rebecca C. Larson, **Tyler M. Chinsky**, Hoyin Chu, Christopher Reilly, Michael C. Kann, Bryan D. Choi, Sabrina Camp, Riaz Gillani, Merle Phillips, Tamina Kienka, Stefanie R. Bailey, Charlotte E. Graham1, Max Jan, Nicholas S. Moore, Nora Horick, Justin Budka, Simone Filosto, Rhine R. Shen, Eliezer Van Allen, Saud AlDubayan, Marcela V. Maus. *Germline variants in hemophagocytic lymphohistiocytosis associated genes and CAR-T cell toxicity*. Under Review, Journal Submission (March 2023)

Abstracts

Peer-reviewed: (P – Presenter)

1. Anis A Hamid, **Tyler M. Chinsky**, Matías Vergara, Emily Grist, Gerhardt Attard, Eliezer Van Allen, Saud AlDubayan, Christopher J Sweeney. *Landscape and impact of germline pathogenic variants (PVs) in metastatic hormone sensitive prostate cancer (mHSPC): ancillary study of E3805 CHAARTED.* Journal of Clinical Oncology, 41, 16_suppl, 5082-5082. doi: 10.1200/JCO.2023.41.16_suppl.5082 Submitted to the American Society of Clinical Oncology (ASCO) 2023 Meeting, (February 2023)

2. **Tyler M. Chinsky (P)**, Ricky Chen, Sarah Holan, Harshitha B. Suresha, Kristina R. Sieffert, Animesh A. Sinha. *Investigation of transcriptionally regulated differential gene expression as a potential protection signature in the Pemphigus vulgaris disease model.* Poster Presentation, SUNY University at Buffalo Jacobs School of Medicine and Biomedical Sciences Research Symposium, (January 2022)

Honors and Awards

Latin Honors – Cum Laude, University at Buffalo SUNY	*2022*
Emerson Student Undergraduate Research Fellowship, Rochester Institute of Technology	*2016*
Dean's List, SUNY Empire State	*2020*
FIRST Robotics Scholarship, Rochester Institute of Technology	*2015 – 2018*