

Tiffany Tu

Computational Biology and Bioinformatics PhD Student @ Duke University

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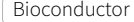
















SKILLS

Programming R (RShiny, roxygen2), Python, Unix, Javascript, HTML
Technical \LaTeX , git version control, Pack Office(Word, Excel, PowerPoint).
Coursework Statistical Inference, Population Genetics, Pharmaceutical Statistics, Biostatistics Methods I/II

EDUCATION

Current **PhD - Computational Biology and Bioinformatics**, Duke University - School of Medicine
2020 **Master of Science - Biostatistics - Statistical Genetics Track**, Columbia University Mailman School of Public Health
2017 **Bachelor of Science - Computational Mathematics; Biology Minor**, George Washington University

EXPERIENCE

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- Aug 2020** | **Real World Data Science Intern, ROCHE, Little Falls, NJ**
Jan 2020 | pREDi Data Science (Pharma Research and Early Development Informatics)
> Developed an end-to-end analytical pipeline for overall survival of specific mutation combinations by integrating clinicogenomic data to understand molecular mechanism behind drug resistance.
> Implemented a new preference score function in a Roche R package that enables selection of an appropriate comparator arm in observational studies.
> Contributed to RNA-seq differential gene expression analysis using DESeq R package to identify genes of interests for cancer immunotherapy resistance.
    
- Dec 2019** | **Bioinformatics Co-op Student, REGENERON PHARMACEUTICALS, Tarrytown, NY**
Jun 2019 | > Maintained experimental image data intake, quality control, and analysis workflow with AWS cloud computing.
> Developed a web application for searching, analysis, and display of LacZ-reporter gene expression image data to improve efficiency of pre-therapeutic target discovery research using RShiny.
> Refined an existing statistical consulting application that recommends tests based on user input and allows for user data upload and analysis by adding in 13 additional statistical tests with detailed description and use cases.
> Strengthened skills in data integrity, infrastructure design, and appropriate use of revision control.
       
- Aug 2018** | **Research Associate Level II, ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI, New York, NY**
Oct 2017 | > Performed high dimensional data reduction analyses using machine learning algorithms, such as Phenograph and t-SNE, for predictive modeling and visualization of immune cell clusters with single cell RNA-Seq data.
> Established analytical pipelines for studying how gene diversity shapes human immune responses, specifically with human leukocyte antigen (HLA)-E molecules.
> Performed wet bench experiments such as PBMC blood processing and immunohistochemistry.
> Undertook administrative tasks by maintaining lab supplies, equipment operation, and lab protocols.
   
- Aug 2017** | **Graduate Research Assistant, UNIVERSITY OF CALIFORNIA, LOS ANGELES, Los Angeles, CA**
Jun 2017 | > Recipient of NIH funded UCLA Bruins in Genomics summer research program and attended two-week structured boot camp covering topics on NGS Analysis, Hi-C, Galaxy, and RNA-Seq held by the QCB Collaboratory.
> Strengthened skills in sequencing alignment, data cleaning, and data scraping using RNA-Seq data from public sources such as ENCODE (Encyclopedia of DNA Elements).
> Worked on developing an algorithm to infer unknown genetic functions between two species with tight spectral clustering and bipartite node covariates; particularly looking at human and mouse homologs.


Aug 2016 | **Mathematical Ecology Research Student, UNIVERSITY OF WISCONSIN, LA CROSSE, La Crosse, WI**
Jun 2016 |
> Generated bird and bat population dynamic model subject to wind energy development with branching processes, population inertia, and sensitivity and elasticity simulation.
> Collaborated with USGS to generate significant results for future Upper Midwest environmental management decisions on the endangered Indiana Bat species.
> Presented poster **Demographic Modeling of Indiana Bat Population Subject to Stress by Wind Energy** at the 2016 Mathematical Association of America Joint Math Meeting in Atlanta, GA.

R MATLAB

May 2016 | **Clinical Research Intern, GEORGETOWN UNIVERSITY HOSPITAL CENTER, Washington, D.C.**
Oct 2015 |
> Contributed to medical chart review, longitudinal data analyses, patient recruitment, and patient screening.
> Increased proficiency of data entry with REDCap and refined skills on clinical trial design, risk prediction modeling, and patient communication.

REDCap EXCEL

PUBLICATIONS

> Haider H, Oldfield S, **Tu T**, Moreno R, Diendorfer J, Eager E, Erickson R. Incorporating Allee effects into the potential biological removal level. *Natural Resources Modeling*. 2017; 30:e12133

SCHOLARSHIP

2018 Canadian Bioinformatics 1-Week Workshop for Cancer Genomics; Cold Spring Harbor Laboratory, NY
2016 SAMSI 3-day Undergraduate Workshops for Astronomy; Research Triangle Park, NC
2015 Hong Kong University of Science and Technology Summer Abroad full scholarship; Hong Kong
2013-17 School of Engineering and Applied Sciences Merit-Based Scholarship; George Washington University; Washington, D.C.