

Zhiqi Tang

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EDUCATION

University of Toronto, Toronto, Canada

2019-09 to 2023-04

Faculty of Arts & Science

Major: Quantitative Biology | GPA: 3.02/4.0

Minor: Environmental Biology, Classical Civilization

Degree: Honours Bachelor of Science

Nanyang Technological University, Singapore

2023-08 to 2024-06

School of Biological Sciences (SBS)

Track: Bioinformatics | GPA: 4.08/5.0

Degree: Master of Science in Biomedical Data Science

SUMMARY

Bioinformatics Graduate with a Master's degree in Biomedical Data Science and a Bachelor's degree in Quantitative Biology. Have several past experiences at implementing bioinformatics pipeline, conducting statistical analysis, and communicating results in written reports and oral presentations. Passionate in technical problem solving and active learning in the application of bioinformatics methods.

COURSE ACTIVITIES

EEB313 Quantitative Methods in R for Biology (Course offered by U of T)

Participant

- In this general course on R for biology, I learned basic skills for data manipulation, visualization, modelling, and statistical analysis.
- As the final project for this course, me and other team members conducted a project on the correlation between African malaria cases and mosquito species richness. Data was acquired from a public dataset. My tasks included initial data transformation (filtering through available data and preparing the data format for later usage), preliminary data investigation via graphs/tables, and implementation of some statistical models. The resulting mixed effect model suggested that there is no strong correlation between the two variables, and this is communicated to the rest of the class with an oral presentation.

EEB405 Temperate Field Experience (Course offered by U of T)

Participant

- Within this two-week field trip course taught at Koffler Scientific Reserve, I visited several natural habitats in the reserve and learned about experimental design and approaches from KSR researchers; In-door activities included literature review (with a focus on critical thinking of experimental setups) and coding sessions on processing and transforming ecological raw data.
- As the final project for this course, I designed and conducted an independent project to investigate the correlation between plant and detritivore richness. Species richness data was estimated from collected soil samples and processed in RStudio for correlation analysis. The results were illustrated in a

presentation with figures and tables.

EEB430 Modeling in Ecology and Evolution (Course offered by U of T)

Participant

- In this epidemiology, genetics and ecology themed course, I practiced building, analyzing and interpreting mathematical models. The focus is on Deterministic Dynamical models (Recursions and Differential equations) and assignments usually include implementing and simulating these models in Python.
- As the final project for this course, I created a variant of the Lotka-Volterra model of interspecific competition and analyzed it in Python. I added mathematical terms to the original model, to represent the flow of individuals joining and leaving the population, such that the variant model can help to investigate the effect of density-dependent migration on interspecific competition. Results indicated that this effect makes the two species more likely to co-exist.

OTHER ACTIVITIES

Statistical data science for public health and biomedicine research program **2022-07 to 2022-09**

Participant

- In this training program, I practiced machine learning related coding skills.
- As a final project, me and the other group member compared the accuracy of several machine learning models in predicting future covid-induced mortality based on vaccination status data from online open-source datasets.

Internship at SCELSE (Master Program Final Year Project) **2024-01 to 2024-05**

Research Assistant

- In this internship, I worked under two professors and contributed to their research project. The project was guided with regular meetings and discussions, and I was tasked with proceeding the project based on these directions.
- The project is interested in the distribution of the composition of microbes in nature and put the focus on gut microbiome data acquired via shotgun metagenomic sequencing. Initial investigations collected data from individual papers on the subject, usually from their NCBI archives; Later progressions sought data from public databases with more samples. A general processing pipeline was developed to increase the comparability of the data sources and most operations were carried out in RStudio.
- The result was in-conclusive as the results across multiple data sources were inconsistent. This might suggest that there are no universal patterns in the microbiome compositions, but data quality issues and potential biases greatly limited the interpretability of the outcomes. These results were eventually presented with a thorough oral presentation and a written report for grading.

Internship at SCELSE **2024-08 to 2024-12**

Research Assistant

- For this internship, I participated in a research project to investigate the interactions that caused *S. aureus* takeover in a colony with *C. acnes* and *S. epidermidis*, a phenomenon that often leads to diseases in the natural human skin. In our hypothesis involving the biological market theory, the takeover happened due to *C. acnes*' need for anaerobic environment and *S. aureus*' superior oxygen consumption rate, allowing it to replace *S. epidermidis*' role in the community.
- To provide additional evidence towards this hypothesis and confirm that oxygen consumption played

a key role in these interactions, I developed a cellular automata model (in MATLAB) with rules modified from Conway's game of life, imitating the real conditions and testing our assumptions. The model was repeatedly modified and improved according to the ongoing experiments, and additional functions are being implemented to allow further investigations on the topic.

- Simulation results suggest that *S. aureus*' higher oxygen consumption rate does provide advantages and could lead to its dominance, supporting the hypothesis.

RA at NTU SBS, AnniZ lab

2025-01 to Present

Research Associate

- I am currently working on a project regarding horizontal gene transfer (HGT) and selective sweep in the human gut, at professor Anni Zhang's lab. The project primarily focused on HGT as it is deeply related to the adaptation and evolution of gut microbial communities, which then correlates to human individual health, as suggested by numerous studies. At the beginning of this project I am attempting to establish a stable computational method to detect HGT, given microbial genomic data extracted from the human gut and elsewhere.

SKILLS

Language competence: Chinese Mandarin (native), English (fluent),

Coding skills: RStudio (ggplot2, phyloseq, DADA2, dplyr, etc.),

Python (numpy, sympy, seaborn, matplotlib, etc.), MATLAB