



YUE YANG TEO

science admirer | machine learning enthusiast | computational biologist
Science is nothing but our feeble attempt at understanding the universe.

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PERSONAL PROFILE

I am a science enthusiast that is obsessed with understanding and quantifying everything. One of the greatest fields that have always confounded me is biology. This led me to computational biology, to utilize applied mathematics, or computing, to understand biology. What started out as pure curiosity has brought me to research facilities all over the world, from building biological networks to modelling diseases with machine learning. These experiences have solidified my dedication to scientific research and my passion for modelling and analyzing biological systems. Being a strong proponent of AI and data-driven research, my scientific vision is to model biological systems using machine learning and further fields such as computational neuroscience, bioengineering, and precision medicine. Given my passion for research and vision in science, I am ready to kick-start my academic career and embark on my graduate school journey!

EDUCATION

B.Sc (Hons) Major in Computational Biology

National University of Singapore

Aug 2017 – May 2021 (Expected)

Singapore

Exchange Semester

University of California, Santa Cruz

Jan 2020 – Apr 2020

Santa Cruz, CA

RESEARCH EXPERIENCE

Genome Institute of Singapore

Advisors: Roger Foo, Greg Tucker-Kellogg

April 2020 – Current

Singapore

- Characterizing differential multi-omic tumor heterogeneity between HBV-infected and non-viral hepatocellular carcinoma
- Comparing inter and intra tumor heterogeneity of multi-region samples between HBV-infected and non-viral hepatocellular carcinoma at the transcriptomic and metabolomic level.
- Identifying unifying genes, pathways and metabolites contributing to inter/intra-tumor heterogeneity

BIDMC, Harvard Medical School

Advisor: Winston Hide

March 2020 – July 2020

Boston, MA

- Prioritizing disease-related miRNAs using known miRNA:mRNA interactions and pathway clusters
- Enriched pathways are used to map pathway clusters.
- Fisher analysis of pathway clusters with known miRNA:mRNA interactions prioritizes miRNA related to disease of interest.
- Second author of poster at ISMB 2020.

UCSC Genome Institute

Advisor: Benedict Paten

January 2020 – April 2020

Santa Cruz, CA

- Investigating deep neural networks for nanopore sequencing basecalling methods
- Deciphered the nanopore sequencing signal features utilized by commercial deep learning models for the basecalling.

Sackler Faculty of Medicine, Tel Aviv University

Advisor: Noam Shomron

📅 June 2019 – Dec 2019

📍 Tel Aviv, Israel

- Identifying cancer-related genes with deep learning classification
- Deep learning classification is done using a QRNN model with NGS data of cancer vs healthy patients.
- GRAD-CAM methodology is used to analyze the deep learning model's parameters.
- Authored a chapter in Deep Sequencing Data Analysis

Lee Kong Chian School of Medicine, Nanyang Technological University

Advisor: George Augustine

📅 Dec 2018 – Dec 2019

📍 Singapore

- Modeling the computational role of cholinergic input in a claustral RNN
- The firing-rate network model is built using electrophysiological data collected from claustral neurons in brain slices.
- Model showed that cholinergic input toggle network encoding efficiencies of different subpopulations in the claustrum
- Second author of a paper in manuscript

National University of Singapore

Advisor: Lim Kah Leong

📅 May 2018 – Dec 2018

📍 Singapore

- Identifying molecular links between Type II Diabetes and Parkinson's Disease using network analysis
- Protein-protein interaction (PPI) network built using STRING database.
- Analysis is done using graph theory algorithms (Random-walk-with-restart) with PPI constructed.

PUBLICATIONS

Nair, A., Graf, M. **Teo, Y.** & Augustine, G. J. (2021) A functional logic for neurotransmitter co-release in the cholinergic forebrain pathway.
<https://doi.org/10.1101/2021.02.25.432623>

Teo, Y., Danilevsky, A. & Shomron, N. (2021) Overcoming Interpretability in Deep Learning Cancer Classification. Methods Mol Biol. 2021;2243:297-309.
https://doi.org/10.1007/978-1-0716-1103-6_15

POSTERS

Yeganeh, P.N., **Teo Y.**, Morgan, S., Vlachos, I. & Hide, W. (2020) CARAWAY: Capturing miRNA-controlled coordinated pathway activity. Intelligent Systems for Molecular Biology Conference 2020.

Nair, A., **Teo, Y.**, Graf, M., & Augustine, G.J. (2019). Opposing cholinergic gain control of the claustrum. Society for Neuroscience 49th Annual Meeting. Society for Neuroscience.

Nair, A., **Teo, Y.**, Graf, M., & Augustine, G.J. (2019). Opposing cholinergic gain control of the claustrum. Gordon Research Conference for Modulation of Neural Circuits and Behavior 2019.

AWARDS

Best Presentation Award.

Integrated Science Congress 2018

National University of Singapore, Singapore.

RESEARCH PROGRAMME

Interdisciplinary Special Programme in Science

National University of Singapore

📅 Aug 2017 – Dec 2018

📍 Singapore

LEADERSHIP EXPERIENCE

Cluster Leader

Prince George's Park Residence

📅 Aug 2020 – Dec 2020

📍 Singapore

- Managed a cluster of student residents residing on campus at the Prince George's Park Residence.

Project Leader

Social Committee, Raffles Hall

📅 Aug 2017 – Aug 2019

📍 Singapore

- Planned projects for social events across the entire residence at Raffles Hall.
- Aimed to facilitate bonding between residents of different blocks.
- Helped to integrate international student residents in Raffles Hall.

Military Specialist Cadet School Instructor (Infantry)

Singapore Armed Forces

📅 Feb 2015 – Dec 2016

📍 Singapore

- Trained cadets to become infantry sergeants at the Specialist Cadet School of the Singapore Armed Forces.
- Conducted management, leadership and physical training.
- Taught navigation, weapon technicality, urban and non-urban combat skills.

RESEARCH INTERESTS

Machine Learning, Artificial Intelligence, Bioinformatics, Precision Medicine, Data Science, Computational Biology, Big Data in Biology, Computational Neuroscience, Mathematical Modeling of Biology, Cloud Computing for Biological Data

PROGRAMMING LANGUAGES

Basic

Javascript, HTML

Intermediate

C, C++, R, LaTeX, bash, Mathematica, Hadoop, Spark, PostgreSQL, AWS, Kubernetes

Advanced

java, Matlab, Python, Microsoft Windows OS, Linux OS, R

TECHNICAL SKILLS

Dry Lab

Machine Learning (Tensorflow, Pytorch), Artificial Intelligence, Regression Analysis, Statistical Analysis, Image Analysis, Computer Vision, Bioinformatics, Natural Language Processing, Data Structures & Algorithms, Big Data, Database Systems, Graph Theory

Wet Lab

Cell culture, Optogenetics, Western Blotting, DNA-sequencing, RNA-sequencing

LANGUAGES

English (Native Speaker)

Chinese (Native Speaker)

OTHER INTERESTS

Science Fiction, Science Podcasts, Board games, Video games, Football(Soccer), Floorball, Basketball, Trekking, Travelling