ALAN YUE YANG TEO

Data ML/AI scientist | computational biologist

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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.

PUBLICATIONS

Teo, AYY., Gautier, M., ..., Courtine, G., Squair, JW., & Skinnider, MA.(2024). Identification of perturbation-responsive regions and genes in comparative spatial transcriptomics atlases. [Preprint].
https://doi.org/10.1101/2024.06.13.598641

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Skinnider, MA., Gautier, M., **Teo, AYY.**, ..., Anderson, MA., Squair, JW. & Courtine, G.(2024). Single-cell and spatial atlases of spinal cord injury in the *Tabulae Paralytica*. Nature.
https://doi.org/10.1038/s41586-024-07504-y

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Naderi, P., **Teo, AYY.**, Karagkouni, D., Pita-Juárez, Y., Morgan, S., Slack, F., Vlachos, I. & Winston Hide (2023). PanomiR: A systems biology framework for analysis of multi-pathway targeting by miRNAs. Briefings in Bioinformatics 24(6).
https://doi.org/10.1093/bib/bbad418

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Jeon, AJ., **Teo, AYY.**, ..., Tucker-Kellogg, G., Foo, RSY., & Chow, PKH (2023) Multi-region sampling with paired sample sequencing analyses reveals sub-groups of patients with novel patient-specific dysregulation in Hepatocellular Carcinoma. BMC Cancer, 23(1).
https://doi.org/10.1186/s12885-022-10444-3

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Jeon, AJ., Anene-Nzelu, CG., **Teo, AYY.**, ..., & Chow, PKH (2023) A genomic enhancer signature associates with hepatocellular carcinoma prognosis. JHEP Reports, 5(6), p. 100715.
https://doi.org/10.1016/j.jhepr.2023.100715

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Nair, A., **Teo, AYY.**, Augustine, G. J. & Graf, M. (2023) A functional logic for neurotransmitter co-release in the cholinergic forebrain pathway. Proceedings of the National Academy of Sciences, 120(28).
https://doi.org/10.1073/pnas.2218830120

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Teo, AYY., 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

EDUCATION

PhD, Computational and Quantitative Biology (EDCB)
École Polytechnique Fédérale de Lausanne (EPFL)
NeuroRestore

📅 Feb 2022 –   📍 Switzerland

Visiting Student Research Collaborators (VSRC)
Princton University Graduate School

📅 July 2024   📍 Princeton, NJ

B.Sc (Hons) Major in Computational Biology
National University of Singapore

📅 Aug 2017 – May 2021   📍 Singapore

Exchange Semester
University of California, Santa Cruz

📅 Jan 2020 – Apr 2020   📍 Santa Cruz, CA

RESEARCH EXPERIENCE

EPFL, NeuroRestore (Role: PhD, Doctoral Assistant)
Advisors: Gregoire Courtine, Jordan Squair

📅 Feb 2022 – Current   📍 Switzerland

- Elucidating the changes in molecular and cellular architecture of spinal cord with respect to spinal cord injury (SCI) and targeted epidural spinal stimulation (TESS)-enabled walking after SCI
- Deciphering the molecular and cellular profiles of the spinal cord injury using a combination of machine learning algorithms and single-cell sequencing technologies

National Cancer Centre of Singapore (Role: Research Officer)
Advisors: Pierce Chow, Greg Tucker-Kellogg, Roger Foo

📅 May 2021 – Dec 2021   📍 Singapore

- Multi-region sampling analysis to characterize patient-specific transcriptomic dysregulation
- Precision medicine application: Novel patient stratification based on patient-specific transcriptomic profile

Genome Institute of Singapore, National Cancer Centre of Singapore
Advisors: Roger Foo, Greg Tucker-Kellogg

📅 April 2020 – May 2021   📍 Singapore

- Characterizing differential multi-omic tumor heterogeneity between HBV-infected and non-viral hepatocellular carcinoma
- Comparing inter and intra tumor heterogeneity of mulit-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.

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.

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

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.

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

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

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Advanced
java, Matlab, Python, 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

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

LANGUAGES

English (Native Speaker)

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Chinese (Native Speaker)

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OTHER INTERESTS

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