

Zhi-Lin Pan

BIOSCIENCES STUDENT

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Education

National Yang-Ming University

Undergraduate Student in Life Sciences

Taipei, Taiwan

2015 - 2018, 2019 - 2020

- Honor Student (ranked top 1): 3 semesters
- Professor Kuang-Dong Wu Outstanding Genetics Scholarship
- International Genetically Engineered Machine (iGEM) 2016 Gold medal
- Relevant Coursework: Biochemistry, Cell and Molecular Biology, Genetics, Genomics, Immunobiology, Neurobiology, R and Python Programming, Data Structure and Algorithms, Biostatistics, Honor Calculus, Linear Algebra

Research Experience

Undergraduate Researcher

Taipei, Taiwan

Supervisor: Prof. Cho-Yi Chen, National Yang-Ming University

Project: Identify and characterize pre- and post-transcriptional regulation in mammalian tissues and human cancer [Github: **HNCS-3'UTR**]

Oct. 2019 - Present

- Identify transcripts regulated by alternative polyadenylation, alternative promoter, and alternative splicing from RNA-seq
- Detect and characterize the circadian rhythmicity of identified transcripts
- Characterize 3'UTR landscape in head and neck cancer cells under ER-stress

Project: Analysis of multi-tissue transcriptomes reveals candidate genes and pathways influenced by cerebrovascular diseases [Github: **GTEC-CVD**]

Mar. 2018 - July 2018

- Built a multivariate linear regression model and applied to GTEC RNA-seq data
- Conducted limma-voom differential expression analysis and Gene Set Enrichment Analysis
- Interpreted the results and identified links between cerebrovascular diseases and tissue expression

Research Internship

Pittsburgh, PA

Supervisors: Prof. Silvia (Shuchang) Liu & Prof. George Tseng, University of Pittsburgh

Mar. 2019 - Aug. 2019

Project: Nonparametric robust order-based machine learning framework for accurate inter-study prediction of categorical and continuous outcomes [Github: **ROML**]

- Selected and converted features with k top scoring pair (kTSP) algorithm
- Developed and diagnosed random forest models for prediction of cancer outcomes
- Implemented simulations based on realistic statistical models and estimated parameters

Research Internship

Singapore

Supervisor: Dr. Jonathan Göke, Genome Institute of Singapore

Aug. 2018 - Jan. 2019

Project: Machine learning predicts tumor metastatic potential [Github: **TCGA-ML**]

- Quantified raw transcript reads and summarized into gene-level values using Salmon and Tximport
- Applied machine learning algorithms to predict tumor metastasis potential from TCGA pancancer RNA-seq
- Evaluated models by feature selection and engineering using differential expression and pathway analysis

Summer Internship

Hong Kong

Supervisor: Prof. Jiguang Wang, Hong Kong University of Science and Technology

June 2017 - Aug. 2017

Project: Identification of noncoding somatic variants in paired primary-recurrent brain tumors

- Received training of large sequencing data manipulation in Unix environment
- Called variants from whole-genome sequencing data of glioblastoma samples
- Detected clusters of frequent mutations in noncoding regions using 'hotspot' analysis

Skills

Languages R & R Markdown (daily), Python, Matlab, awk & sed
Environments Linux/Unix, Mac OS, AWS Cloud Computing/Ronin

Publications

1. Analysis of multi-tissue transcriptomes reveals candidate genes and pathways influenced by cerebrovascular diseases

Zhi-Lin Pan, Cho-Yi Chen

bioRxiv 806893; October 2019; doi: <https://doi.org/10.1101/806893>

2. Robust Order-based Machine Learning framework: a non-parametric predictive model with order-based feature selection for transcriptomic data

Zhi-Lin Pan^{*}, Wei Zong^{*}, Kelly Cahill, Yuchen Pan, Silvia Liu, George Tseng

^{*}: co-first authors; paper in preparation