

Zhi-Lin Pan

BIOSCIENCES STUDENT

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Education

National Yang-Ming University

Undergraduate Student in Life Sciences

Taipei, Taiwan

Sep. 2015 - Present

Suspension: Aug. 2018 - Aug. 2019

- Honor Student (ranked top 1): 3 semesters
- Professor Kuang-Dong Wu Outstanding Genetics Scholarship
- Relevant Coursework: Biochemistry, Cell and Molecular Biology, Genetics, Genomics, Immunobiology, Neurobiology, R and Python Programming, Data Structure and Algorithms, Biostatistics, Honor Calculus, Linear Algebra, Deep Learning

Research Experience

Undergraduate Researcher

Taipei, Taiwan

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

Projects: Identify and characterize transcriptional regulation in mammalian tissues and cancer

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

Mar. 2018 – July 2018

- Built a multivariate linear regression model and applied to GTEx 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

- 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

- 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

International Genetically Engineered Machine Competition (iGEM)

Taipei, Taiwan & Boston, MA

Gold Medal (Overgrad), NYMU-Taipei 2016 iGEM team

Oct. 2015 – Nov. 2016

Project: Integrated Orchard Safeguard

- Designed the main project, gene circuits and wet experiments
- Conducted molecular cloning and fungal transformation
- Interviewed researchers in the field of entomopathogenic fungi, CRISPR/Cas9, etc.
- Participated in wiki and poster documentation writing

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

Skills

Languages

R & R Markdown (daily), Python, Matlab, awk & sed

Environments

Linux/Unix, Mac OS, AWS Cloud Computing/Ronin

Bioinformatics

NGS tools (bedtools, Salmon, tximport, tximeta, DESeq2, limma-voom, GFOLD, BLAST, etc.), pathway analysis tools (GSEA, goseq, g:Profiler, EnrichmentMap), Git