Zikun Yang

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EDUCATION

SHANGHAI JIAO TONG UNIVERSITY **Sept 2022 - Present**

School of Life Sciences and Biotechnology

Major in Biology Science **(ZHIYUAN HONORS PROGRAM)**

- GPA:3.79/4.3
- Functional Genomics(96), Organic Chemistry(92), Mathematical Analysis II(90), Application of Data Science(studying)
- Zhiyuan Scholarship

PUBLICATION

- Mao Y X, Li Y, **Yang Z**, et al. Comparative transcriptome analysis between rhesus macaques (Macaca mulatta) and crab-eating macaques (M. fascicularis)[J]. *Zoological Research*, **2024**, 45(2): 299.
- Zhang, S., Xu, N., Fu, L., Yang, X., Li, Y., **Yang, Z.**, ... & Mao, Y. (2024). Comparative genomics of macaques and integrated insights into genetic variation and population history. *bioRxiv*, 2024-04.

RESEARCH EXPERIENCE

Bioinfomatic Scientific Training in **MAO'S LAB** **- SJTU** **Jun 2022 - present**

- **keywords:** Comparative Genomics, Phylogeny Analysis, transcriptome analysis
- I fluently utilize Python and bash in Linux system to compute and analyse large-scale genome/transcriptome data.
- Below are representative work:
- **CNV Identification and Analysis:** Based on previous RNA-seq data, *FAM220A*, a gene associated with the positive regulation of protein binding activity, displayed differential expression in multiple tissues between human and macaque. To explain the expression difference from genetic aspect, I analysed the copy number of *FAM220A* in human, macaque and even apes, built the phylogenic tree of these duplicated genes and eventually identified 2 ape-specific segmental duplications in human. The findings are published on *Zoological Research*. This work patially explained the differential expression of *FAM220A* between human and macaque and offered an example of how structural variants can significantly impact gene expression.
- **Quantification of duplicated gene expression:**Duplicated genes, characterized by highly similar DNA sequences, pose a challenge for accurate expression quantification through read mapping alone. I developed a Python Snakemake pipeline for processing bulk RNA-seq data. This pipeline aims to differentiate the expression of duplicated genes. Our data includes human healthy tissue data(prostate, kidney, liver, brain and so on) and cancer data(prostate, kidney and so on).The program is still in progress.

ACADEMIC PROJECTS

SJTU Participation in Research Program (PRP) **Sept 2023 - Mar 2024**

Project Member

- Under mentor's guidance, we genotyped gene knockout fetal mice and took brain tissues to determine whether there is development difference of the cerebral cortex between KO and control mice through immunofluorescence staining .
- Techniques used: PCR, fetal mice dissection etc.
- Excellent Defense Project

ACTIVITIES

SJTU Student Science and Technology Association **Mar 2023 - present**

Secretary

- responsible for the arrangement and execution of the school entrepreneurship competition field service.

ADDITIONAL

- Personal Page:Eric-Y-S.github.io
- Technical Skills: R, C++(Basic), Python(Proficient)
- Language Skills: English (CAT4:636,CET6:625,practised in oral presentation), Mandarin (Native)

REFERENCE

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