# Li Ye

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#### **EDUCATION**

University of Michigan, Ann Arbor
M.S. in Bioinformatics (GPA: 4.0)

Ann Arbor, MI

Ocean University of China (Project 985)

B.S. in Biological Science (Rank: 1/55)

O8/2016 – 06/2020

Qingdao, China

#### **WORKING EXPERIENCES**

Data Engineer
Aptiv

O2/2023 – Present
Troy, MI

- Utilized Python packages (Numpy, SciPy, Matplotlib) to translate vehicle CAN bus data into humanreadable values for visualization, encapsulated the code into classes and methods, and converted the script into an executable file (.exe).
- Relied on Suds, a Simple Object Access Protocol (SOAP)-based python web service client, to package Web Services Description Language (WSDL) requests for efficient querying in our web management system (Polarion), and automatically send email notifications with query results upon completion.
- Developed Python scripts for a data processing pipeline, which analyzes .mat files containing vehicle signal data to evaluate Advanced Driver Assistance System (ADAS) features (Adaptive Cruise Control, Lane Departure Warning, etc.).
- Assisted other team engineers with vehicle data collection.

Bioinformatics Analyst 05/2022 – 08/2022

Bioinformatics and Sequencing Section at the Michigan Department of Health and Human Services (MDHHS)

Lansing, MI

- Implemented an HIV drug resistance pipeline to identify HIV-1 low frequency drug resistance mutations with the data generated at MDHHS, optimized the pipeline for speed and generated reports specific to the lab's needs.
- Developed R functions to check whether patient samples contain multiple SARS-CoV-2 infections, e.g.
   Delta and Omicron concurrent infection, which would allow accurate reporting on strains and recommendations for effective treatment.
- Designed a course "Best Practices in Pipeline Development with R" to provide a standard or set of guidelines for R beginners.

### **Bioinformatics Analyst**

04/2021 - 08/2021

Shanghai Biotree Biotech Company

Shanghai, China

- Carried out routine analysis of Non-targeted Metabolomics data by LC-MS and GC-MS. Analyses involved statistical approaches, radar plot, correlation analysis, chord diagram, bubble plot and pathway enrichment analysis.
- Completed subsequent analysis and personalized analysis according to clients' need, including ROC curve, PERMANOVA and volcano plot with labels.
- Participated in upgrade and development of pipelines utilizing R and R Markdown.

# **Bioinformatics Analyst**

09/2020 - 04/2021

Shanghai OE Biotech Company

Shanghai, China

- Performed analysis of microbial diversity (16S, 18S, ITS) data by next-generation sequencing (NGS).
   Analyses involved OTU clustering, community's structure, alpha diversity, beta diversity, correlation heatmap, random forest prediction for classification and phylogenetic tree construction.
- Aided in upgrade and development of pipelines utilizing Docker. Utilized Docker to create an image of RDA/CCA analysis and then pushed it to Harbor. Connecting this new Docker image with the Cloud Platform, the company could improve the efficiency and flexibility of subsequent analysis and personalized analysis.

#### RESEARCH EXPERIENCES

Research Assistant (Advisor: Dr. Marcin Cieslik, Co-advisor: Dr. Russell Ryan) 01/2022 – 05/2022

Comparison of enhancer activation between specific stages of normal B-cell development and B-ALL

Ann Arbor, MI

- Isolated different cell population from a published scATAC-Seq dataset.
- Generated "BigWig" coverage track utilizing tool ArchR.
- Re-aligned the BAM files to another reference with Cell Ranger ATAC.
- Published in Blood Cancer Discovery, 2022 (Refer to PUBLICATIONS)

#### **Undergraduate thesis project OUC (Advisor: Dr. Xiaoting Huang)**

10/2019 - 05/2020

The regulatory mechanism of scallop hypoxia-inducible factor (PyHIF) in response to heat stress

Qingdao, China

- Collected HIF homologous sequences of different species from NCBI and UniProt databases.
- Identified *PyHIF* gene and characterized structure of *PyHIF* gene using BLAST, SMART and Pfam.
- Constructed phylogenetic tree and compared HIF proteins among representative species using MEGA software.
- Analyzed *PyHIF* gene expression characteristics in the larval development, adult different tissues and under thermal stress.

### Student Research Developing Program OUC-SRDP (Team leader, Advisor: Dr. Zhiqiang Wu)

11/2017 – 11/2018

Toxic Effect and Action Mechanism of Polycyclic Aromatic Hydrocarbons (PAHs) with Low Concentration on Cartilaginous Fish Digestive Enzyme Qingdao, China

- Designed and managed experimental workflows.
- Maintained experimental records, and conducted data analysis.
- Quantified soluble protein concentrations, and determined the minimum toxic dosage of PAHs for crude enzyme assays.

## **TEACHING**

#### **Teaching Assistant (Developmental Biology)**

03/2020 - 06/2020

Ocean University of China

Qingdao, China

- Recorded student attendance.
- Evaluated and graded assignments.
- Tutored students.
- Informed students about the procedures for completing and submitting coursework.
- Provided feedback to the professor to enhance the overall teaching quality.

#### **PUBLICATIONS**

Kodgule R., Goldman JW, Monovich AC, Saari T, Aguilar AR, Hall CN, Rajesh N, Juhi Gupta, Chu S-C A, **Li Ye**, et al. ETV6 Deficiency Unlocks ERG-Dependent Microsatellite Enhancers to Drive Aberrant Gene Activation in B-Lymphoblastic Leukemia. *Blood Cancer Discov*. 2022; BCD-21-0224. doi: 10.1158/2643-3230.BCD-21-0224.

#### **AWARDS**

•	Office of Graduate and Postdoctoral Studies Master's Student Award	2022
•	OUC the First Class Scholarship Award	2019
•	OUC the Second Class Scholarship Award	2018
•	OUC the Third Class Scholarship Award	2017
•	Outstanding Student Award	2017

## **SKILLS**

Python, R, Linux Shell, Slurm, Git, SQL, Docker, C++, MATLAB, LaTeX