Xiangjie Zhao

Male | Born on May 23, 1994 | E-mail: xjzhao777@163.com Hometown: Shandong, China | Personal Homepage: https://cadenzhao.github.io Current Residence: Beijing | Job Objective: Bioinformatics, Data Analysis



Education

University of Chinese Academy of Sciences

Fuzhou University

Ph.D. in Bioinformatics Bachelor in Bioengineering Sep 2017 - Jun 2024 Sep 2013 - Jun 2017

Research Experience

Bioinformatic Integration Analysis of Human Hormone Receptors (Project Leader)

Feb 2023 – Present

- Responsibilities: Project design, data collection including hormone receptor list curation, multi-omics data, disease data, drug target data, etc. Integrative bioinformatics analysis for human hormone receptors.
- Main Achievements: Zhao X, Wang XJ. Integrated analysis of human hormone receptors. 2024. (In submission) Interactive website for human tissue hormone communication analysis (https://hthc-123456789.shinyapps.io/HTHC)

Development of a Bioprinting System (Project Participant)

Jul 2022 – Oct 2022

- Responsibilities: Assisted in the calibration and testing of the bio-3D printing robotic arm.
- Main Achievements: Zhang Z, Wu C, Dai C, Shi Q, Fang G, Xie D, Zhao X, Liu YJ, Wang CCL, Wang XJ. A multi-axis robot-based bioprinting system supporting natural cell function preservation and cardiac tissue fabrication. Bioact Mater. 2022:18:138-150.

Studying the Function of GCGR in Cerebellum using Bioinformatics and Experiment (Project Leader) Nov 2020 – Present

- Responsibilities: Participated in the design of the project, completed mouse behavior experiments, brain morphology and neuron morphology analysis, bulk RNA-seq and scRNA-seq data analysis of the cerebellum, manuscript writing.
- Main Achievements: Zhao X, Zhang Z, Xie D, Wang XJ. Glucagon receptor in cerebellar neurons regulates body weight and locomotor activity. 2024. (In preparation)

Analyzing Microenvironment and Drug Resistance of Myeloma Using scRNA-seq (Project Leader). Feb 2020 - Jun 2021

- Responsibilities: Designed and executed scRNA-seq data analysis, including cell clustering, cell annotation, cell cycle analysis, cell-cell communication analysis, trajectory inference, gene regulatory network analysis, visualization, etc.
- Main Achievements: Zhao X, Liu Z, Wang XJ. Cancer stem cells induced by mesenchymal stem cells promote drug resistance in multiple myeloma. 2024. (In preparation)

Clinical Big Data Analysis of Hypertension Patients (Project Leader)

May 2019 - Nov 2019

- Responsibilities: Processed and analyzed large hypertension datasets using Python and parallel computing, focusing on data cleaning and visualization.
- Main Achievements: Authored the report "Epidemiological Analysis of Hypertension Patients in Changzhou City" for the Health Commission of Changzhou City.

Personal Strengths

- **Project Management:** Led multiple projects, adept in problem-solving, planning, and leadership, with a track record in scholarly writing.
- **Programming:** Expertise in Python, R, Shell for data analytics, algorithm development, and web development; proficient with Linux OS.
- AI & Data Analysis: Knowledgeable in machine learning/deep learning algorithms, adept at model construction and optimization with scikit-learn, PyTorch.
- > Omics Analytics: Skilled in high-throughput sequencing analysis, including bulk RNA-seq, single-cell omics, spatial transcriptomics, CUT&Tag-seq, ChIP-seq, with strong visualization capabilities.
- **Biology:** Understanding of animal behavior, CNS, related diseases, metabolism, and cancer.
- **Communication:** Effectively presented at international conferences in both English and Chinese, with materials available on personal homepage.