

Mange Xu

137 Ramona Blvd, Markham, Ontario, L3P 2K7

226-978-3586

Mangexu964@gmail.com

www.linkedin.com/in/mange-xu

SUMMARY OF QUALIFICATIONS

- **Bioinformatics Expertise:** Proficient in Python, R, C, and Matlab within Unix and Linux environments. Strong experience in analyzing high-throughput sequencing data and generating complex visualizations.
- **Database Proficiency:** Skilled in utilizing databases such as NCBI, TCGA, MSigDB, RCSB PDB, UniProt, and GeneCards for biological research.
- **Laboratory Skills:** Extensive hands-on experience in wet lab techniques including cell culture, gel electrophoresis, RNA extraction, cDNA synthesis, PCR amplification, and Western blotting.
- **Research and Analysis:** Adept at conducting detailed biological research, optimizing experimental protocols, and analyzing data to draw meaningful conclusions.
- **Communication and Collaboration:** Proven ability to effectively communicate complex technical information to diverse audiences and collaborate within multidisciplinary teams.
- **Adaptability and Problem-Solving:** Demonstrated ability to quickly adapt to new technologies and methodologies, with a strong track record of resolving complex issues in fast-paced environments.
- **Language Proficiency:** Native speaker of Mandarin, with strong English communication skills.

PROFESSIONAL EXPERIENCE

Bioinformatics Analyst, Pediatrics Research Institute of Hunan, China Dec 2021 – Oct 2022

- Improved data processing efficiency by 30% through optimization and visualization of analysis pipelines, contributing to the successful publication of research findings.
- Identified 15 major cell clusters from Single cell-sequencing of 130,785 individual cells from 9 primary, 7 recurrent, osteosarcoma lesions, using unbiased clustering of gene expression profiles and canonical markers.
- Generated over 100 complex plots and HTML reports using Python and R for 8 months, improving data visualization and interpretation for the research team.
- Explored the tumor microenvironment by analyzing transcriptomic properties, identifying key regulators, and tracking malignant cell dynamics, helping colleagues to the publication peer-reviewed articles.

Research Intern, The University of Edinburgh, UK May 2021 – Aug 2021

- Enhanced the performance of the pipeline, leading to its adoption for ongoing research projects and contributing to a significant advancement in identifying and isolating quasispecies.
- Tested and optimized a new quasispecies separation pipeline using simulated data, achieving a 20% increase in accuracy and a 40% reduction in processing cost.
- Evaluated and implemented a fully automated quasispecies separation pipeline on the virus sequencing data from the Nanopore long-read platform, identifying several quasispecies variants.

Undergraduate Research Assistant, Changsha University, China Feb 2019 – Jun 2020

- Generated findings that were presented at the university conference and contributed to a greater understanding of Rapamycin's impact on muscle cells.
- Investigated the effects of Rapamycin on rat muscle cells, conducting secondary cell cultures and documenting changes using inverted microscopy and DAPI fluorescent staining.
- Analyzed cell viability using the MTT colorimetric method, providing quantitative data on cell growth and proliferation rates, and revealing a 25% reduction in cell viability with Rapamycin treatment.

EDUCATION

Master of Science and Engineering in Biotechnology, The University of Edinburgh, UK. 2020 – 2021

Bachelor of Science and Engineering in Biopharmacy, Changsha University, China. 2015 – 2019