HAIYANG CHANG

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EDUCATION

PhD. Bioinformatics, University of Guelph   Jan 2019 – Apr 2024
Publications: One first-authors and four co-authors (including one preprint)

MSc. Bioinformatics, University of Guelph, GPA: 3.95/4   Sep 2016 – Aug 2018
Courses: Programming, Machine Learning, Genomic Methods, Statistics, Bioinformatics Software tools

TECHNICAL SKILLS

Programming and Tools: Python, R, SQL, Shell, Docker, Git, Snakemake (workflow automation)
Database Management: SQL databases, data integration, data management
High-Performance Computing: Unix/Linux systems, slurm, job scheduling, parallel computing
Data Analysis: Advanced statistical methods, machine learning, data mining, predictive modeling
Professional Certifications: Deep learning specialization (DeepLearning.AI), Google data analytics

PROFESSIONAL EXPERIENCE

University of Guelph, Graduate and Undergraduate Teaching Assistant   Sep 2019 – Apr 2023
- Prepared educational materials and hands-on labs for lecture sessions on Unix commands, high-performance computing (HPC), and bioinformatics sequencing analysis (genome assembly, bulk RNA-seq, SNP analysis, ATAC-seq and ChIP-seq).
- Led weekly lab sessions and tutorials for undergraduate students in statistics and R software, providing support for statistical modeling, data analysis, and visualization.

University of Guelph, Research Assistant   Sep 2018 – Dec 2018
- Created a shell pipeline script leveraging an evolutionary algorithm to identify high-similarity antigen receptors, streamlining the analysis process from Illumina sequencing platform to HPC platform.
- Conducted immune sequencing analysis for three canine disease projects (lymphoma, minimal residual disease, and inflammatory conditions), contributing to one co-authored academic paper.

ACADEMIC PROJECTS

Single cell RNA data analysis
- Collaborated on a pioneering project analyzing T cell receptor repertoire using scRNA-seq on canine and feline.
- Conducted T-cell receptor clustering analysis using advanced bioinformatics tools.
- Contributed to two co-authored academic papers, enhancing understanding of T-cell receptor diversity.

R shiny dashboard | data visualization
- Designed and implemented an R Shiny dashboard for antigen receptor database integration.
- Developed features for clonotype clustering and visualization, including static and interactive clonotype network graphs, circos plots, phylogenetic trees, and sequence logo representation plots.
- Enhanced data exploration of high-publicity clusters as potential immune signatures for ante-mortem diagnostic tools in canines with neurological diseases.

Machine Learning algorithm development
- Developed a Python-based antigen receptor clustering tool, integrated evolutionary algorithms and unsupervised learning methods for large-scale immune sequencing data.
- Achieved clustering of million-scale unique sequencing data within 5 minutes on a MacBook Air with an M2 chip.
- Contributed to one first-authored research paper and one co-authored conference paper.