

# Haiyang Chang

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## Education

### University of Guelph

PhD in Bioinformatics

Jan 2019 – Apr 2024

### University of Guelph

MSc in Bioinformatics

Sep 2016 – Aug 2018

### Dalian University of Technology

MSc in Biology

Sep 2013 – Jun 2016

### Dalian Polytechnic University

BSc in Biology Technology

Sep 2009 – Jun 2013

## Research Experience

### Characterization of immune repertoires in dogs with central nervous system disease 2023 – Present

- Collaborated on a pioneering project to conduct single-cell RNA analysis of dog T cells, performing the TCR (T-cell receptor) clustering analysis.
- Executed comprehensive comparative analysis of immune repertoires in dog neurological diseases across two anatomical compartments, identifying novel ante-mortem diagnostic tools through clonotype clustering and sequence pattern similarity analysis.
- Designed and implemented an [R Shiny dashboard](#) for clonotype clustering visualization, incorporating interactive network graphs, phylogenetic trees, and logo representation plots, enhancing the exploration of high-publicity clusters as potential immune signatures.

### Clustering large-scale immune repertoire sequencing data 2020 – 2023

- Enhanced the performance of evolutionary algorithms for clustering antigen receptor sequencing data, achieving high efficiency in processing complex immune repertoire datasets.
- Developed a Python-based antigen receptor [Clustering Tool](#), processing one million unique sequences in 5 minutes on a MacBook Air with an M2 chip, maintaining high clustering quality comparable to established tools.

### Analysis immune repertoire sequencing data

2017 – 2019

- Created a shell pipeline script leveraging an evolutionary algorithm to identify high-similarity antigen receptors, streamlining the analysis process.

- Conducted immune sequencing analysis for three canine disease projects, including lymphoma, minimal residual disease, and inflammatory conditions, providing critical insights for disease diagnosis and treatment.

**Protein expression, purification and crystallization.** 2013 – 2016

- Conducted experiments involving the construction and expression of plasmid vectors of human glutamate oxaloacetate transaminases, performing protein purification and enzymatic activity assessment.
- Optimized protein expression conditions, successfully published the crystallization structures in the Protein Data Bank (PDB) with IDs: [3WZF](#) & [5AX8](#).

Teaching Experience

**Teaching Assistant, University of Guelph** 2020 – 2022

**BINF\*6110: Genomics Methods for Bioinformatics**

- Facilitated laboratory sessions on high-throughput sequencing data analysis using high-performance computing (HPC), covering genome assembly, functional genomics analysis, and population genetics.
- Guided students through practice questions and clarified doubts related to bioinformatics tools during class sessions.

**Teaching Assistant, University of Guelph** 2019 – 2021

**BIOL\*3300: Applied Bioinformatics**

- Prepared [educational materials and hands-on labs](#) for an undergraduate-level course introducing students to applied bioinformatics.
- Conducted tutorial sessions on Unix commands, HPC, and bioinformatics sequencing analysis (RNA-seq), including foundational topics like sequence alignment, database searching, and gene prediction.

**Teaching Assistant, University of Guelph** 2020 – 2023

**STAT\*2030&2040: Statistics I & R Statistical Analysis**

- Led weekly lab sessions and tutorials for undergraduate students in statistics and R software, providing support for data analysis and visualization.
- Assisted students in understanding statistical concepts and R programming for data analysis, visualization, and statistical modeling.

Skills

- **Programming Languages:** Python, R, SQL, Shell
- **Next-Generation Sequencing (NGS) Analysis:** Genome assembly, functional genomics, population genetics, sequence alignment, RNA-seq
- **High-Performance Computing:** Unix/Linux systems, HPC environments, job scheduling, parallel computing
- **Database Management:** SQL databases, data integration, data management
- **Version Control and Workflow:** Git, Snakemake, workflow automation

- **Statistical Analysis:** Advanced statistical methods, machine learning, evolutionary algorithms, data mining, predictive modeling
- **Data Visualization:** R Shiny, ggplot2, Matplotlib, interactive network graphs

## Publications

[Anchor Clustering for million-scale immune repertoire sequencing data.](#)

H Chang, DA Ashlock, SP Graether, SM Keller.

*BMC Bioinformatics*, 2024.

[Canine peripheral blood TCR \$\alpha\beta\$  T cell atlas: Identification of diverse subsets including CD8A+ MAIT-like cells by combined single-cell transcriptome and V \(D\) J repertoire analysis.](#)

M Eschke, PF Moore, H Chang, G Alber, SM Keller.

*Frontiers in Immunology*, 2023.

[Use of immune repertoire sequencing to resolve discordant microscopic and immunochemical findings in a case of T cell-rich large B cell lymphoma in a young dog.](#)

Gary Kwok Cheong Lee, Dorothee Bienzle, Stefan Matthias Keller, Mei-Hua Hwang, Nikos Darzentas, Haiyang Chang, Emily Rätsep, Rebecca Egan, Janet Beeler-Marfisi.

*BMC Veterinary Research*, 2021.

[Odd Distance Anchors for Rapid Clustering.](#)

Daniel Ashlock, Haiyang Chang, Matthew Stoodley.

*2020 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*, 2020.

[Recombinant expression, purification and crystallographic studies of the mature form of human mitochondrial aspartate aminotransferase.](#)

Xiuping Jiang, Jia Wang, Haiyang Chang, Yong Zhou

*BioScience Trends*, 2016.

[Expression, purification and preliminary crystallographic studies of human glutamate oxaloacetate transaminase 1 \(GOT1\).](#)

Xiuping Jiang, Haiyang Chang, Yong Zhou

*Protein Expression and Purification*, 2015