Huilin Tai

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Education

McGill University, Montreal, QC, Canada

Bachelor of Science - Major statistics and computer science, GPA 3.85 (Sep. 2020 - present)

Mathematics: strength in Analysis, Algebra, Probability, Bayesian Inference

Computer science: Algorithm and Data Structures, Machine Learning, Deep learning, Python, Java, R language, Matlab, JavaScript, C, HTML/CSS, Bash/Shell, MIPS, OCaml

Publications

- [1] Dehai Wu, Congyi Zhang, Guanqun Liao, Kaiming Leng, Bowen Dong, Yang Yu, **Huilin Tai**, Lining Huang, Feng Luo, Bin Zhang, Tiexiang Zhan, Qiuhui Hu, Sheng Tai. Targeting uridine-cytidine kinase 2 induced cell cycle arrest through dual mechanism and could improve the immune response of hepatocellular carcinoma. Cellular & Molecular Biology Letters, 105 (2022).
- [2] Adam M.R. Groh, Nina Caporicci-Dinucci, Brianna Lu, Maxime Bigotte, Elia Afanasiev, Joshua Gertsvolf, Dale J. Hatrock, Victoria Mamane, Sienna Drake, **Huilin Tai**, Jun Ding, Alyson Fournier, Catherine Larochelle, Jo Anne Stratton. *Ependymal cells undergo an astrocyte-like gliosis in response to chronic and acute neuroinflammation*. Journal of Neurochemistry (under review)
- [3] Xiaorong Guo, **Huilin Tai**, Xiaoqing Li, Peng Liu, Jin Liu, Shan Yu SPARC is a novelty prognostic biomarker for ovarian cancer and associated with immune signatures and drug response. Clinical and Experimental Obstetrics & Gynecology (accepted)

Computer Science Research Experience

Mcgill University Department of Computer Science (Sep. 2023 - April 2024)

Research Assistant (Supervised by Professor Hamed Hatami)

Communication Complexity for Hamming Distance Estimation

- Developed a protocol based on a group testing algorithm to estimate the Hamming distance between two n-bit strings and reduced the upper bound of communication complexity from O(log n) to O(log log n).
- Adopted adaptive solutions to improve algorithm efficiency, focusing on randomized algorithms for Hamming distance estimation.

Excess-Error Dependent Replicability

- Proposed an algorithm for covering hypothesis classes with finite VC dimensions, focusing on accurately approximating real error rates using empirical data.
- Explored the concept of excess-error dependent replicability in agnostic learning, establishing a framework for generating hypothesis lists with guaranteed risk limits.

University at Buffalo (June 2023 - Feb. 2024)

Voluntary Research Assistant

- Advanced the TartanVO model by integrating a Vision Transformer, leveraging deep learning techniques to optimize visual odometry (VO) performance in real-world scenarios to increase the model's adaptability and computational efficiency.
- Employed machine learning algorithms and deep learning architectures to directly incorporate up-to-scale loss functions and camera intrinsic parameters into the TartanVO model. The revised model outperformed existing geometric-based VO methods and demonstrated robust generalization capabilities on real-world datasets.

Mcgill University Department of Computer Science (Jan. 2023 - Jan. 2024)

Research Assistant (Lab of Professor Jun Ding)

Unsupervised Learning for Cell Profiling

- Robustly performed data mining and removed batch effects with Harmony, thereby ensuring the data quality and comparability across different experiments or conditions.
- Designed and fine-tuned unsupervised models for clustering based on PCA and UMAP to determine the composition of the PBMCs , to identify potentially pathogenic cell subsets and their associated transcriptional signatures.

Computational Analysis and Website Enhancement of Cellar (Cooperating with Stratton Lab)

- Improved the data presentation layer of Cellar, a web-based platform for single-cell analysis by adding new features enabling more effective visualization and interpretation of epidermal cell data particularly in the context of neuroimmunological diseases.
- Conducted robust data preprocessing and cleansing operations and employed visualization techniques to present data in an insightful manner, aiding in the exploration and understanding of complex biological interactions.

Machine Learning Application for Sex Prediction

• Developed machine-learning classifiers for sex prediction based on gene expressions to isolate significant sex markers through advanced feature selection strategies., utilizing xgbooster, randomforest, svm, logistic models.

• Achieved a 93.5% accuracy rate in sex prediction with 12 elected features by fine-tuning a multi-layer perceptron neural network through grid search and tailored architecture.

Deep Learning Model for Spatial Gene Expression Prediction

- Designed a Variational Autoencoder integrated with Stochastic Variational Inference for scalable learning and developed a comprehensive data visualization process to graphically depict the results of a clustering algorithm on scaled tissue images to enhance the understanding of the interaction of genomic features in the physical tissue space.
- Implemented custom Evidence Lower Bound and shift sigmoid transformation functions to optimize model performance.

Applied Math Research Experience

Mcgill University Department of Mathematics and Statistics (Nov. 2022 - Dec. 2023)

Research Assistant (Lab of Professor Anmar Khadra)

NP Binding Process Quantification:

- Applying probability models to quantify nanoparticle binding dynamics, correlating IFN γ dose-response and valence of pMHC, with the resulting models exhibiting strong agreement with experimental data.
- Optimized serial engagement model with Markov chain Monte Carlo Simulation to study the effect of geometry factors on T-cell activation, underscoring the biophysical properties of the agents involved.

Quantification for Multivalent Nanoparticle T-cell Therapies

- Utilizing mathematical models that employ Poisson and Rayleigh distributions to investigate the selective binding phenomena towards the clustered surface and uniformly distributed tcr surface.
- Designing model calculating binding capacity with randomization algorithm, and perform visualization of binding probability of different surface with respect to tcr distribution.
- Utilizing Monte Carlo simulations to analyze nanoparticle and TCR binding dynamics, incorporating kinetic parameters and spatial considerations.

Biostatistics Research Experience

Mcgill University Faculty of Science (Jan. 2023 - June 2023)

Research Mentee (Mcgill DRP program)

• Applied Bayesian and Generalized Linear models for survival analysis, skillfully managing missing data and improving the detection of individual risk factors.

Harbin Medical University (May 2022 - Sep. 2023)

Research Assistant

- Developed survival analysis to estimate if targeting uridine-cytidine kinase 2 could improve the immune response of hepatocellular carcinoma. Implemented an interactive monogram with R language for 1-year, 3-year, and 5-year survival analysis.
- Launched a GSEA analysis, processed data with different tumor risk levels to elucidate the enrichment patterns within KEGG and Hallmark pathways, and identified pathways in the order of Normal-TumorLR-Tumor-HR according to the enrichment output.
- Led a pivotal study on the SPARC gene's impact on ovarian cancer prognosis, applied Kaplan-Meier survival analyses, and validated data integrity through log-rank tests.
- Extracted and analyzed data from UCSC XENA and GTEX databases, and correlated SPARC expression with key clinical parameters.

Honors and Awards

- Mackey-Glass Summer Research Bursary, Issued by McGill Faculty of Medicine, Apr. 2023
- Hugh Brock Scholarship, Issued by McGill University, Sep. 2020

Leadership and Extracurricular

McGill University (Sep. 2022 - present)

Course Assistant

• Graded assignments for Math235 Algebra, Math240 Discrete Math, and Math356 Honor Probability .

Simplify McGill (2020 - 2021)

Finance Department Member

• Managed the club budget across multiple departments and led enterprise-sponsored activities.

4-D English (2017 - 2019)

English Volunteer Teacher

• Coached middle school students to improve English speaking skills, providing personalized learning strategies.