Curriculum Vitae
Qi Guo

CONTACT INFORMATION

Email: Qi.Guo@osumc.edu; guo.2101@osu.edu
Phone: 614-634-5309
GitHub: https://github.com/1QiGuo

EDUCATION

Graduate student — **Biomedical informatics** — **2022 - present**
The Ohio State University, Columbus, OH, USA
Advisors: Prof. Qin Ma, Prof. Phillip Popovich
Training: *Bioinformatics, Computational system biology, spinal cord injury, and Neuroinflammation.*

B.E. — **Biomedical engineering** — **2018 - 2022**
Harbin Medical University, China
Advisors: Xia Li, Yingqi Xu.
Training: *Bioinformatics, Pharmaco-Informatics*

RESEARCH INTEREST

- Single-cell and spatial multi-omics analysis
- Cell-cell communication prediction
- Neurological diseases, such as spinal cord injury and Alzheimer's Disease
- Neuroinflammation

RESEARCH EXPERIENCES

Elucidation of the Dynamic Mechanism of Cardiac Hypertrophy to Heart Failure based on scRNA-seq and Precision Medication based on Network **2021-2022**
Supervisors: Prof. Xia Li and Prof. Yingqi Xu
Undergraduate thesis project

- 32 potential markers were found by comparing the expression value of data from normal to hypertrophy to heart failure. These potential markers have a decreasing expression with the development of the disease. Hence, those which are statistically significant($p<0.05$) can predict the stage of cardiac hypertrophy.
- 12 potential markers were found by extracting genes name from Heatmap drawn by Pseudo-time series analysis. These 12 potential markers have increasing expression from normal to heart failure. Heatmaps were drawn by Monocle 2.
- 4 functional cell clusters were identified by Spearman correlation analysis. The drawn landscape of cardiomyocytes from myocardial hypertrophy to heart failure and landscapes of 4 functional cell clusters in distinctive stages.
- Identified a crucial disease cell cluster that has immune-related functions by GO and a specific crucial alternative stage from myocardial hypertrophy to heart failure.
- The cell-cell interaction network of different types of heart cells was constructed by iTalk in the crucial stage of disease progression and identified decreasing interactions and increasing interactions of different types of cells after cardiac hypertrophy.
- Validated potential markers using RNA next-generation sequencing of cardiac hypertrophy from GEO and constructed prediction classification model based on logistic regression.
- Constructing the WGCNA network and finding potential drug targets by random walk algorithm.

Innovations:

- Identification of cell types of the cardiac single-cell cluster by double screening: a: classified the potential marker of each cell cluster by function FindMarkers of Seurat package and took their intersections with the paper-based marker of heart cell types in CellMarker database to classify the type of unknown cell clusters; b: employed FeaturePlot to solve the classification of cell clusters with no intersections due to the lack of sufficient data; achieved good classification accuracies, especially for the classification of myocardial cells and fibroblasts.
- Focusing on the dynamic process and constructing a prediction model to predict the stage of cardiac hypertrophy patients.

Skills & Tools: R, Seurat, monocle, iTalk, T-Test, WGCNA, GO, KEGG, Machine Learning, Random Walk, Cytoscape**.**

Searching and verifying SNV and CNV of Liver Cancer Using Second-Generation Sequencing Data **06/2021**
Supervisor: Prof. Zhaoqi Liu
Internship project at Beijing Institute of Genomics, Chinese Academy of Science

- Present the literature "Pharmacologic modulation of RNA splicing enhances anti-tumor immunity" and "Splicing factor mutation in hematologic malignancies."
- Identified and counted microvascular invasion SNV of liver cancer with SAVI2 and IGV.
- Identified and counted CNV of liver cancer samples with CNVkit; obtained CNV mutation genes with high confidence by GISTIC

filtering, segmented bin areas and made correlation analysis with prior data from cBio database to verify the accuracy, utilized BVI for further verification and got highly consistent CNV results.

Identified miRNA as a Potential Drug Target Based on a Compound Network of miRNA-DEGs-DEGs for Breast Cancer 2021
Molecular Network Pharmacology Assignment

- Constructed drug-drug, drug-target, and target-target networks using anti-cancer drugs and target information from the Drugbank database.
- Got RNA expression data of breast cancer from GEO and screened 2726 differential expressed genes using T-test; got protein interaction information from HPRD of such genes and found 39 differential expressed genes from PPI network intersected with the target gene set.
- Integrated miRNA and target gene interaction information about breast cancer from the mirTarbase, HMDD, and target scan databases. Searched 57621 interacted pairs between miRNA and target gene, which are differentially expressed genes.
- Constructed compound network of miRNA-differential expressed gene, protein-protein interaction of differential expressed genes network. Imported into Cytoscape and highlighted those 39 target genes.
- Searched 12 potential miRNA drug targets as neighbor nodes of differentially expressed target genes based on a Random walking algorithm.

A Risk Assessment Platform for Single-gene Disorders 2019-2020
College Students' Innovative Entrepreneurial Training Plan Program *Team Leader*
Supervisor: Prof. Yihan Wang

- Collated and summarized environmental factors and obtained 52 couples' variation data (vcf) by 1000 Genome.
- Annotated variation information based on the InterVar database with VarNote, screened for mutation sites according to ACMG statistics, and only kept pathogenic and likely pathogenic mutation sites.
- Annotated gene mutation site using ANNOVAR.
- Information about mutated genes and their inheritance patterns for single-gene disease statistics from OMIM.
- Prediction of risk of single-gene disorder score for infants based on mutation sites information of parents; Risk score of the infant was computed by pathogenicity of mutation sites and genetic disease pattern of parents.
- The results show which single-gene disorders babies are likely to have and their probability.
- Designed a sample platform website interface in HTML.

Design Three Ligands for Dihydrofolate Reductase 04/2021-05/2021
Computer-Aided Drug Design Assignment

- ***Preparation of Small Molecules***
  The 2D structures of these three compounds were built using Chemdraw11.0. The property and drug-likeness of compounds were predicted by Molsoft, a web server for drug design. The final drug-likeness scores of the three compounds are 1.53, 1.47, and 1.0. The 3D structures of compounds were built using Chem3D11.0, followed by MM2 energy minimization.
- ***Preparation of Drug Target***
  The co-crystal structure of Dihydrofolate reductase was obtained from the PDB database. The protein target was prepared for the molecular docking simulation by removing the water molecules and bound ligands. Hydrogen atoms and Kollman charges were added to each protein atom.
- ***Molecular Docking with Autodock (version 4.2.6)***
  The molecular docking study was performed using Auto-Dock Tools version 1.5.6. A grid box of 40 × 40 × 40 with a spacing of 0.375Å enclosed the binding site. The Lamarckian genetic (LGA) was adopted to search for the best binding poses.
- ***Molecular Docking with Vina***
  The molecular docking simulations were also carried out using the Vina program. The final, binding energies of design compounds are -8.8 kcal/mol, -7.8 kcal/mol, and -8.2 kcal/mol.

Identification of Drug Response Markers and Prediction of Individual Drug Response 2020
Pharmacogenomics Assignment

- Obtain gene expressions profile of drug response and drug response labels of samples from cMap.
- Preprocessing and preliminary screen of drug response marker by **Wilcoxon rank sum test** and **univariate logistic regression**.
- Further screen drug response markers by multivariate logistic regression.
- The drug response model was constructed based on screened markers by the **logistic regression model,** and the accuracy rate reached 86%.

Identification of Differential Metabolic Markers 2021
Pharmacokinetics Assignment

- Raw Data Processing by XCMS.
- Data pre-processing and pre-treatment. Handled missing values and filtered. Normalization and scaling.
- Univariate difference analysis was performed on the treated metabolome data by T-Test ($P<0.05$) and obtained 52 markers.
- Multivariate analysis by PLA (FDR<0.05, VIP<1.5) obtained 43 markers by intersecting with 52 from Univariate Analysis.

PUBLICATION

- Faith H Brennan, Yang Li, Cankun Wang, Anjun Ma, **Qi Guo**, Yi Li, Nicole Pukos, Warren A Campbell, Kristina G Witcher, Zhen Guan, Kristina A Kigerl, Jodie CE Hall, Jonathan P Godbout, Andy J Fischer, Dana M McTigue, Zhigang He, Qin Ma, Phillip G Popovich. Microglia coordinate cellular interactions during spinal cord repair in mice. Nat Commun 13, 4096 (2022). https://doi.org/10.1038/s41467-022-31797-0
- Shuo Chen, Yuzhou Chang, Liangping Li, Diana Acosta, Yang Li, **Qi Guo**, Cankun Wang, Emir Turkes, Cody Morrison, Dominic Julian, Mark E Hester, Douglas W Scharre, Chintda Santiskulvong, Sarah XueYing Song, Jasmine T Plummer, Geidy E Serrano, Thomas G Beach, Karen E Duff, Qin Ma, Hongjun Fu Spatially resolved transcriptomics reveals genes associated with the vulnerability of middle temporal gyrus in Alzheimer's disease. acta neuropathol commun 10, 188 (2022). https://doi.org/10.1186/s40478-022-01494-6

PREPRINT MANUSCRIPT

- Ricardo D'Oliveira Albanus, Gina M Finan, Logan Brase, Shuo Chen, **Qi Guo**, Abhirami Kannan, Mariana Acquarone, Shih-Feng You, Brenna C Novotny, Patricia M Ribeiro Pereira, John C Morris, David M Holtzman, Eric McDade, Martin Farlow, Jasmeer P Chhatwal, Dominantly Inherited Alzheimer Network (DIAN), Emily E Mace, Bruno A Benitez, Laura Piccio, Greg T Sutherland, Qin Ma, Hongjun Fu, Celeste M Karch, Oscar Harari, Tae-Wan Kim. Systematic characterization of brain cellular crosstalk signaling networks in Alzheimer's disease reveals a novel role for SEMA6D in TREM2-dependent microglial activation. bioRxiv. (2022). https://doi.org/10.1101/2022.11.11.516215.

MANUSCRIPT IN PREPARETION

- **Qi Guo**, Kristina Kigerl, Asghari Adib, Elham, Phillip Popovich, Qin Ma. An integrated microglia atlas of the mouse spinal cord in health and injury condition. In Preparation. 2023
- Kristina Kigerl, **Qi Guo**, Asghari Adib, Elham, Qin Ma, Phillip Popovich. Single-cell transcriptome analysis characterizes transcripts alteration of the spinal cord affected by gut microbiome after spinal cord injury. In Preparation. 2023

ABSTRACT & PRESENTATION

- **Qi Guo**, Kristina Kigerl, Phillip Popovich*, Qin Ma*. Gut microbiota modifies microglia transcriptome after spinal cord injury. Abstract and Oral Presentation. The 2023 OSU – NRI Summer Symposium. Columbus, OH. Presenter: Qi 06/23/2023
- **Qi Guo**, Kristina Kigerl, Elham Asghari Adib, Anjun Ma, Cankun Wang, Yi Jiang, Qin Ma*, Phillip Popovich*. An Integrated Mouse Spinal Cord Atlas Revealing Microglia Phenotypes in Health and Injury Conditions. Abstract and Oral Presentation. Advanced Computational Neuroscience Network (ACNN). Columbus, OH. Presenter: Qi 09/14/2023

CONFERENCE POSTER

- **Qi Guo**, Kristina Kigerl, Elham Asghari Adib, Anjun Ma, Cankun Wang, Yi Jiang, Qin Ma*, Phillip Popovich*. An Integrated Mouse Spinal Cord Atlas Revealing Microglia Phenotypes in Health and Injury Conditions. Advanced Computational Neuroscience Network (ACNN). Columbus, OH. 09/14/2023

LEADERSHIP ROLES and COMMUNITY SERVICE

- Volunteer, Asian Festival Member 2023
- Youth Volunteers Association 2018-2022
- Vice Leader, Vocal Group of Art Troupe 2019-2020
- Officer, Learning Department of Student Union 2018-2019

OTHER INFORMATION

- ***Patent:*** Haiping Guo, Qi Guo. An Absorbable Left Atrial Appendage Clip, Patent No.: ZL 2020 2 1164863.X, 05/25/2021, Utility Model Patent.
- ***Programming:*** **R, Python**, **HTML**, and **Linux**.
- ***Bioinformatics Methods:*** skilled in RNA-seq analysis, Metabonomic analysis; Pharmacogenomics; Computer-aided drug design; Network Analysis (Random walking), WGCNA; Multivariate analysis, Univariate difference analysis; Survival Analysis; Machine Learning; Cystoscape.