• **Name:** Bin Chen, PhD

• **Current Position & Affiliation:** Assistant Professor
Pediatrics/Pharmacology and Toxicology
College of Human Medicine

• **Country:** USA

• **Educational Background:**

2000 - 2004	Chongqing University	B.A.	Chemistry
2007 - 2009	Indiana University, Bloomington	M.S.	Chemical Informatics (mentor: Dr. David Wild)
2009 - 2012	Indiana University, Bloomington	Ph.D.	Informatics (mentor: Dr. David Wild)
2012 - 2015	Stanford University	Postdoc	Translational Bioinformatics (mentor: Dr. Atul Butte)

• **Professional Experience:**

2015 - 2017	University of California, San Francisco	Instructor	Pediatrics/Institute for Computational Health Sciences
2017 - 2018	University of California, San Francisco	Assistant Professor	Pediatrics/Institute for Computational Health Sciences
2018 - present	Michigan State University	Assistant Professor	Pediatrics/Pharmacology and Toxicology
2021 - present	Michigan State University	Assistant Professor	Computer Science and Engineering

• **Professional Organizations:**

2008 - 2012 American Chemical Society
2012 - present American Medical Informatics Association
2017 - 2018 Associate Member, UCSF cancer center
2012 - present International Society for Computational Biology
2020 - present American Association for Cancer Research

• **Main Scientific Publications:**

Submitted/Preprint (as a key contributor)

1. Jing Xing#, Rama Shankar#, Aleksandra Drelich#, Shreya Paithankar, Eugene Chekalin, Thomas Dexheimer, Surender Rajasekaran, Chien-Te Kent Tseng*, **Bin Chen***, Reversal of Infected Host Gene Expression Identifies Repurposed Drug Candidates for COVID-19, PMID:32511305, PMC7217282, under evaluation in Science Translational Medicine

   Press

   * New process to identify existing drugs for potential COVID-19 treatments (MSU today)

   * MSU scientist testing existing drugs to fight COVID-19 (wlns)

   * Researchers at East Lansing's MSU Use Computational Process to Find Existing Drugs to Treat COVID-19 (dbusiness)

2. Ke Liu*, Mingdian Tan, Benjamin S. Glicksberg, Shreya Paithankar, Samuel So, Mei-Sze Chua, **Bin Chen**, Deciphering cancer metastasis with pan-cancer transcriptomic comparison, under review in Science Advances

We conduct transcriptomic comparisons in seven cancer types to decipher the complexity of liver metastases. We first develop DEBoost to identify differentially expressed (DE) genes between metastatic and primary cancer cells. The following functional analysis suggests that liver metastases of prostate cancer and pancreatic neuroendocrine tumor are more active in cell cycling than their respective primary cancers whereas other cancer types not. The expressions of DE genes have limited associations with clinical measures, indicating most of them may be passenger DE genes of the metastasis process. We cluster DE genes based on their chromosome coordinates to uncover copy number differences and further confirm 19p13.12 amplification drives metastasis in Basal-like breast cancer. Finally, we show that metastatic cancer cells could partially mimic the secretome of hepatocytes by selectively expressing liver-specific genes encoding secreted proteins. Our work provides a novel framework to study cancer metastasis using pan-cancer transcriptomic data.

3. Shan-Ju Yeh, Jing Xing, Mengying Sun, Ke Liu, Shreya Paithankar, Jiayu Zhou, **Bin Chen*** In silico expanding of molecular measures from gene expressions through transfer learning**,** under revision in Briefing in Bioinformatics

Gene expression profiling of cancer cell lines becomes routine today; however, obtaining comprehensive molecular characterization and cellular responses for a new cell line is not trivial when resources are very limited. Here, we present TransCell, a deep transfer learning framework that utilizes the knowledge derived from pan-cancer tumor samples to predict molecular features and responses. Compared to the five state-of-art methods, TransCell has the best performance in the prediction of complicated tasks: metabolite (Spearman: 0.74), gene effect score (or gene dependency, Spearman: 0.69), and drug sensitivity (Spearman: 0.65), and has comparable performance in the prediction of easy tasks: mutation (AUC: 0.86), copy number variation (Spearman: 0.81) and protein expression (Spearman: 0.74). TransCell improved the performance by over 50% in drug sensitivity prediction and was further applied to expand the drug sensitivity of 101 pediatric cancer cell lines.

This study demonstrates the potential of in-silico expansion of measures from the easily accessible gene expression.

4. Rama Shankar, Mingdian Tan, Jeremy Haskins, Shreya Paithankar, Samuel So, Mei-Sze Chua and **Bin Chen**[*], Pan-liver disease single cell-based deconvolution reveals γδ2 T cells as a marker in hepatocellular carcinoma development**,** under submission

Hepatocellular carcinoma (HCC) morbidity is highest in individuals with chronic liver diseases (CLD); however, effects of cell composition on the progression of CLDs to HCC remains unknown. Gene biomarkers of twenty cell types from healthy liver were used for cell type enrichment in six CLDs and HCC. Compared to the healthy state, liver fibrosis and HCC present higher enrichment of γδ2 T cells and lower enrichment of central venous liver sinusoidal endothelial cells (LSECs). High enrichment of γδ2 T cells was specifically observed in HCC with underlying chronic hepatitis B or C virus (HBV or HCV) infections, as well as in advanced HCC and confirmed with scRNA-seq. The enrichment of γδ2 T cells is associated with poor prognosis for HCC with high alpha-fetoprotein (AFP) and underlying HBV and/or HCV infection. Additionally, enrichment of γδ2 T cells in blood samples of CLDs and HCC, indicating their potential as a diagnostic marker.

5. Mengying Sun, Jing Xing, Huijun Wang, Bin Chen, Jiayu Zhou, MoCL: Contrastive Learning on Molecular Graphs with Multi-level Domain Knowledge Mengying Sun, Christopher Daniel Chang#, Shan-Ju Yeh#, Shilong Li, Ke Liu, Guoli Zhou, Rama Shankar, Jing Xing, Austin VanVelsen, Tyler VanVelsen, Benjamin Y. Feng, Krista Young, Michael Strug, Lauren Turco, Zichen Wang, Eric Schadt, Rong Chen, Xiaohong Li, Li Li, Jiayu Zhou, **Bin Chen*** Analysis of 220,000 human transcriptome samples reveals that differential expression of virus entry proteins is associated with sex differences in COVID-19, under submission, PMC765487