Tianyu Chen

(+1) 773-431-6690 tianyuchen@utexas.edu Google Scholar TianyuCodings

EDUCATION

University of Texas at Austin — Austin, TX
Ph.D in Statistics (GPA:4.0) — *Oct. 2023 – July 2028(expected)*

University of Chicago — Chicago, USA
Master of Science in Statistics(GPA: 3.97) — *Oct. 2021 – July 2023*

Fudan University — Shanghai, China
Bachelor of Science in Statistics (GPA:3.7) — *Sept. 2017 – July 2021*
Bachelor of Science in Data Science — *Sept. 2018 – July 2021*

PUBLICATIONS & PREPRAINTS

- **Tianyu Chen**, Vansh Bansal, and James G. Scott."Conditional diffusions for neural posterior estimation." Submitted to: *AISTATS 2025.* [arXiv]. 2024.
- **Tianyu Chen**, Zhendong Wang, Mingyuan Zhou."Diffusion Policies creating a Trust Region for Offline Reinforcement Learning." Published in: *Neurips 2024.* [arXiv]. 2024.
- **Tianyu Chen**, Kevin Bello, Francesco Locatello, Bryon Aragam, Pradeep Ravikumar."Identifying General Mechanism Shifts in Linear Causal Representations." Published in: *Neurips 2024.* 2024.
- **Tianyu Chen***, Jin-Hong Du*, Ming Gao, Jingshu Wang."Model-based trajectory inference for single-cell rna sequencing using deep learning with a mixture prior." Published in: *Proceedings of the National Academy of Sciences* [PNAS]. 2024.
- **Tianyu Chen**, Kevin Bello, Bryon Aragam, Pradeep Ravikumar."iSCAN: Identifying Causal Mechanism Shifts among Nonlinear Additive Noise Models." Published in: *Neurips 2023.* [arXiv]. 2023.
- Jingshu Wang, **Tianyu Chen**. "Deep Learning Methods for Single-Cell Omics Data". Published in: *Handbook of Statistical Bioinformatics.* [Chapter]. 2023.

DOMAIN KNOWLEDGE & SKILLS

Domain Knowledge: Diffusion Models, Reinforcement Learning, Inverse Problems, Causal Inference, Graphical, Bioinformatics
Technical Skills: PyTorch, Git, SQL, Bash, Linux, Maven, Gradle, Conda, Java, MySQL, Spark, ZooKeeper, Hadoop

SELECTED RESEARCH PROJECTS

Diffusion Policies creating a Trust Region for Offline Reinforcement Learning — Austin, TX
Published in Neurips 2024. Supervised by Prof. Mingyuan Zhou — *March. 2024 – May. 2024*

- We introduced a dual policy approach, Diffusion Trusted Q-Learning (DTQL), which comprises a diffusion policy for pure behavior cloning and a practical **one-step policy**. We bridged the two policies with a new diffusion trust region loss.
- It **eliminates the need for iterative denoising sampling** during both training and inference, making it remarkably computationally efficient. Our method exceeded the SOTA in 3 out of 4 D4RL benchmarks, marked by a significant improvement in Average Normalized Reward, and is faster in training and inference time.

Identifying General Mechanism Shifts in Linear Causal Representations — Austin, TX
Published in Neurips 2024. Supervised by Prof. Bryon Aragam — *January. 2024 – March. 2024*

- Mathematically proved the **first identifiability result** for detecting general mechanism shifts within latent causal graphs, leveraging an approach that is based on the **Independent Component Analysis (ICA)** solution. In simulations, the method achieved an F1 Score of **1** in 20-node observation space and **0.7** in 60-node observation space.
- Our methodology extends beyond identifying diverse types of mechanism shifts; it also **relaxes some important conventional assumptions** in previous causal representation learning literature, including consistent topological order across environment assumption and every latent node needs to be intervened at least once assumption.

iSCAN: Identifying Causal Mechanism Shifts among Non-linear Additive Noise Models — Chicago, IL
Published in NeurIPS 2023. Supervised by Prof. Bryon Aragam — *January. 2023 – May. 2023*

- Established a linkage between the **Score Matching** method, extensively utilized in **diffusion-based models**, and the domain of **Causal Discovery**. Under the Gaussian noise assumption, the applicability of the Score Matching method for causal discovery by **simply eliminating data** from leaf nodes.
- For identifying **mechanism shifts** across environments, our approach involves the concatenation of datasets followed by joint and separate score calculations. Mathematically proved this efficient data manipulation combined with a single score estimation function can provide a comprehensive insight into causal discovery.

Trajectory Inference for Single-Cell RNA Sequencing Using Deep Learning with a Mixture Prior — Chicago, IL
Published in Proceedings of the National Academy of Sciences (PNAS). Supervised by Jingshu Wang — *Oct. 2021 – Oct. 2023*

- Innovated a **Variational AutoEncoder(VAE)** based model with **mixed prior** and did single cell trajectory analysis, differential test on the latent space which gives more network structure flexibility.