Hao Tian

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EDUCATION

Southern Methodist University, Dallas, TX

Aug. 2019 - May 2023

- Ph.D. in Theoretical and Computational Chemistry, GPA: 3.9/4.0
- Research topic: Understand protein allostery through molecular dynamics and artificial intelligence

Georgia Institute of Technology, Atlanta, GA

Aug. 2020 - May 2023

• M.S. in Computer Science, GPA: 4.0/4.0

Beijing University of Chemical Technology, Beijing, China

Aug. 2015 - Jun. 2019

• B.Eng. in Chemical Engineering, GPA: 3.49/4.33

SKILLS

- Languages: Python, Java, HTML, CSS, JavaScript, PHP
- Toolkits & Frameworks: Linux, Docker, Git, MySQL, Django, Bootstrap
- Machine Learning: Scikit-learn, Keras, PyTorch

EXPERIENCE

Meta (Facebook), Menlo Park, CA

Software Engineer Intern

May 2022 - Aug. 2022

• Incoming software engineer intern in machine learning at Signals + Identity Prediction team.

Southern Methodist University, Dallas, TX

Research Assistant

Aug. 2019 – May 2023

- Benchmarked and developed a variational autoencoder model to explore hidden protein conformational spaces.
- Launched a public website on high computing center for fast and accurate protein allosteric sites prediction.
- Developed a machine learning based framework to understand and analyze protein allosteric process.
- Initiated automated and customized development workflow with CI/CD via GitHub Actions.

PROJECTS

Deep Learning Enabled Conformation Exploration

June 2021

- Developed a variational autoencoder model to explore protein conformational spaces.
- Reduced the differences between training and decoded structures to within 1Å (the size of one atom).
- Applied the learned latent space to generate new and unexplored conformations to accelerate conformation sampling.

PASSer: Protein Allosteric Sites Server | http://passer.smu.edu

Jan. 2021

- Advanced the state-of-the-art prediction accuracy of top 3 to **84.9**% through **extreme gradient boosting** (XGBoost) and **graph convolutional neural networks** (GCNNs).
- Launched a web server with **Django** and **JSmol** (a **JavaScript** framework) for jobs submission and protein visualization with web pages written in **HTML/CSS** and improved UI experience using **Bootstrap**.
- Improved job execution to less than 1 second and has handled 12000+ visitors and 500+ jobs.

Machine Learning based Framework for Protein Allostery

May 2020

- Constructed a framework integrating biology simulations and machine learning for protein allostery.
- Proved the feasibility of ivis dimensionality reduction framework for large-scale protein simulation data set.
- Trained one-vs-one random forest models in classifying protein macrostates with 94.5% accuracy.

SELECTED PUBLICATIONS

<u>Tian, H.</u>; Jiang, X.; Trozzi, F.; Xiao, S.; Larson, E.; Tao, P. Explore Protein Conformational Space With Variational Autoencoder. *Frontiers in Molecular Biosciences*, 2021, in press.

Tian, H.; Jiang, X.; Tao, P. PASSer: Prediction of Allosteric Sites Server. *Machine Learning: Science and Technology*, 2021, 2, 3, 035015.

<u>Tian, H.</u>; Trozzi, F.; Zoltowski, B. D.; Tao, P. Deciphering the Allosteric Process of Phaeodactylum tricornutum Aure-ochrome 1a LOV Domain. *The Journal of Physical Chemistry B*, 2020, 124, 41, 8960–8972.

AWARDS

- Graduate Research Assistant Award, Southern Methodist University, May 2021
- Outstanding Teaching Assistant, Southern Methodist University, May 2020