Yuanzhe Zhou

📞 +86 18682060091   🌐 yuanzhezhou.com   🐙 github.com/zhou0312   ✉ yuanzhezhou@gmail.com

Education

Southern University of Science and Technology (SUSTech)   **2012 - 2016**
BS in Physics   *Shenzhen, China*

University of Missouri - Columbia   **2016-2021**
PhD in Physics   *Columbia, United States*

Work Experience

Postdoctoral Fellow   **Dec 2021 - Present**
Department of Physics and Astronomy, University of Missouri - Columbia   *Columbia, United States*

Research Interests

Computational modeling of RNA interactions.

Major Publications

1. **Zhou Y**, Jiang YW, Chen SJ. SPRank - A knowledge-based Scoring Function for RNA-Ligand Pose Prediction and Virtual Screening. *Journal of Chemical Theory and Computation.* 2024.
2. **Zhou Y**, Chen SJ. Graph deep learning locates magnesium ions in RNA. *QRB discovery.* 2022.
3. **Zhou Y**, Jiang Y, Chen SJ. RNA–ligand molecular docking: Advances and challenges. *Wiley Interdisciplinary Reviews: Computational Molecular Science.* 2022.
4. **Zhou Y**, Chen SJ. Advances in machine-learning approaches to RNA-targeted drug design. *Artificial Intelligence Chemistry.* 2024.
5. **Zhou Y**, Li J, Hurst T, Chen SJ. SHAPER: A web server for fast and accurate SHAPE reactivity prediction. *Frontiers in Molecular Biosciences.* 2021.
6. **Zhou Y**, Fichman Y, Zhang S, Mittler R, Chen SJ. Modeling the Reactive Oxygen Species (ROS) wave in *Chlamydomonas reinhardtii* colonies. *Free Radical Biology and Medicine.* 2024.
7. Hurst T, Zhang D, **Zhou Y**, Chen SJ. A Bayes-inspired theory for optimally building an efficient coarse-grained folding force field. *Communications in information and systems.* 2021.
8. Sun LZ, Jiang Y, **Zhou Y**, Chen SJ. RLDOCK: a new method for predicting RNA–ligand interactions. *Journal of chemical theory and computation.* 2020.
9. Hurst T, **Zhou Y**, Chen SJ. Analytical modeling and deep learning approaches to estimating RNA SHAPE reactivity from 3D structure. *Communications in Information and Systems.* 2019.

Projects

MgNet   [Source Code]
- a convolutional neural network model for predicting Mg^{2+} binding sites in RNAs.

SPRank   [Source Code]
- a knowledge-based scoring function for RNA-ligand pose prediction.

RLDOCK-Score-V2   [Source Code]
- a physics-based scoring function for RNA-ligand pose prediction.

Skills

Programming Languages: Python, C++
MD simulation: Amber, OpenMM

Conference Presentations

SPRank - A knowledge-based scoring function for RNA-ligand docking and virtual screening, American Chemical Society National Meeting, August 18-22, 2024.