KAI ZHENG, Ph.D.

Lecturer & Master Supervisor | Computational Biology & AI

CONTACT

- ✉ kaizheng@upc.edu.cn
- 🏛 China Univ. of Petroleum
- 📍 Qingdao, China
- 🌐 Google Scholar Profile

KEY METRICS

21
h-index

1600+
Total Citations

NeurIPS
Premier AI Venue

EXPERTISE

- Geometric Deep Learning
- Graph Neural Networks
- AI for Genomics
- Non-coding RNA
- Drug-Target Prediction
- Bioinformatics Tools

HONORS

🏆 Best Paper Award, ICIC 2019.

FUNDING

EXECUTIVE SUMMARY

Researcher bridging **Artificial Intelligence** and **Computational Biology**. Specializes in developing **Geometric Deep Learning** frameworks to solve complex problems in genomics and therapeutics. Proven track record of publishing in top-tier methodology conferences (**NeurIPS**) and leading application journals (*PLOS Computational Biology*).

EXPERIENCE & EDUCATION

Lecturer / Master Supervisor — 2024.07 – Present
China University of Petroleum (East China)

Ph.D. in Computer Science — 2020 – 2024
Central South University

M.Sc. in Computer Science — 2017 – 2020
China University of Mining and Technology

EDITORIAL & ACADEMIC SERVICE

- **PC Member**: **KDD** 2025/2026, **BIBM** 2025/2026.
- **Review Editor**: *Frontiers in Bioinformatics*.
- **Session Chair**: ISAICS 2025.
- **Reviewer**: *Briefings in Bioinformatics, IEEE/ACM TCBB*.

FULL PUBLICATION LIST

* Categorized by research topic. All listed papers are indexed by SCI.

⛏ I. AI Methodology & Graph Learning

1. **Graph-Theoretic Insights into Bayesian Personalized Ranking for Recommendation**.
   Zheng K, Wang JX, Xu JH. *Advances in Neural Information Processing Systems (NeurIPS)*, 2025. [**Premier AI Venue**]

⧗ II. Genomics & Non-coding RNA Analysis

1. **Line graph attention networks for predicting disease associated Piwi-interacting RNAs**.
   Zheng K, Zhang XL, Wang L, et al. *Briefings in Bioinformatics*, 2022 [**Q1, IF: 9.5**].

2. **SPRDA: a link prediction approach based on the structural perturbation to infer disease-associated Piwi-interacting RNAs**.
   Zheng K, Zhang XL, Wang L, et al. *Briefings in Bioinformatics*, 2023 [**Q1, IF: 9.5**].

3. **iCDA-CGR: Identification of CircRNA-Disease Associations based on Chaos Game Representation**.
   Zheng K, You ZH, Wang L, et al. *PLOS Computational Biology*, 2020 [**Q1**].

4. **DBMDA: A unified embedding for sequence-based miRNA similarity measure**.
   Zheng K, You ZH, Wang L, et al. *Molecular Therapy - Nucleic Acids*, 2020 [**Q1, IF: 8.8**].

5. **MISSIM: an incremental learning-based model for miRNA-disease association**.
Zheng K, You ZH, Wang L, et al. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2020 [**Q1**].

6. **iMDA-BN: Identification of miRNA-disease associations based on the biological network**.
Zheng K, You ZH, Wang L, et al. *Computational and Structural Biotechnology Journal*, 2020 [**Q1**].

7. **MLMDA: a machine learning approach to predict miRNA–disease associations**.
Zheng K, You ZH, Wang L, et al. *Journal of Translational Medicine*, 2019 [**Q1, IF: 7.4**].

📖 III. Computational Drug Discovery

1. **LRTM: Left-Right Transition Matrices for Molecular Association Prediction**.
Zheng K, Duan GH, Yang MY, et al. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2025 [**Q1**].

2. **DLP: duplex link prediction via subspace segmentation for predicting drug-miRNA associations**.
Zheng K, Zhao QC, Liang X, et al. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2024 [**Q1**].

3. **NASMDR: a framework for miRNA-drug resistance prediction using efficient neural architecture search**.
Zheng K, Zhao H, Zhao Q, et al. *Briefings in Bioinformatics*, 2022 [**Q1, IF: 9.5**].