

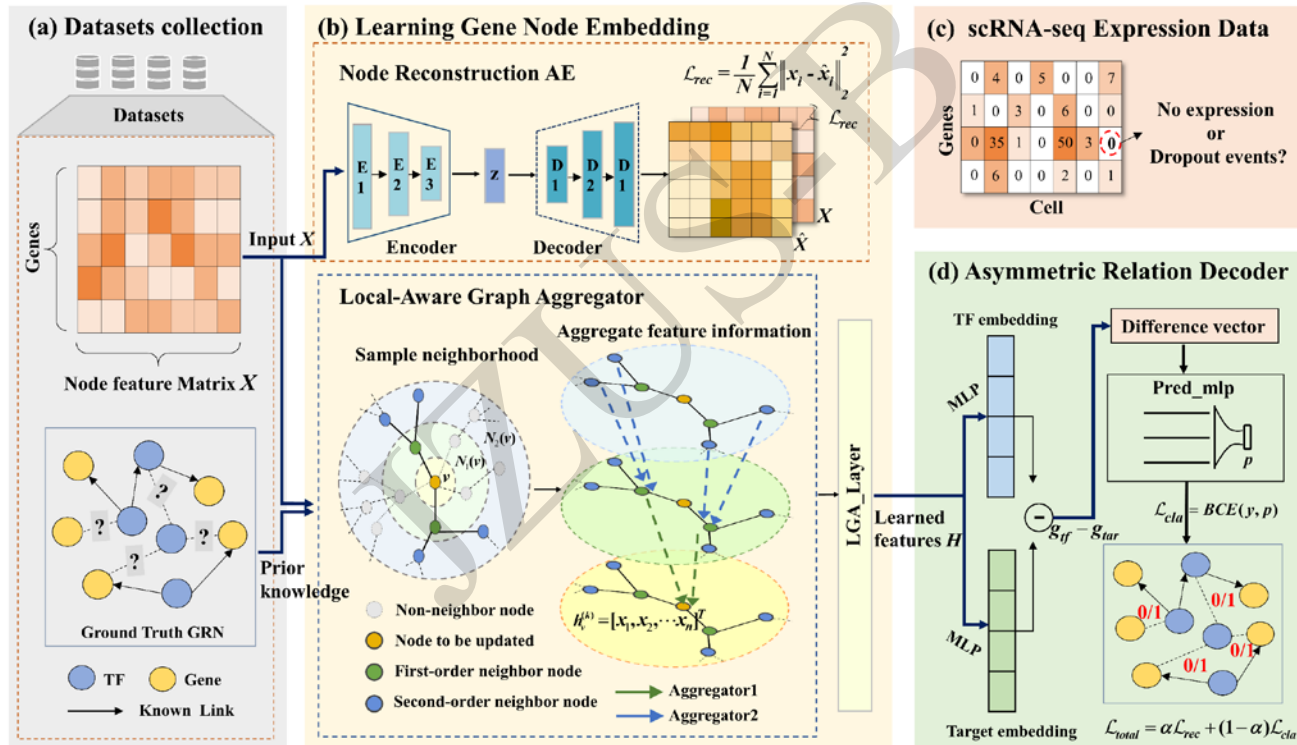
Cite this as: Binhua TANG, Yingying FENG, Xinyu GAO, Mengyao MAO, Yujia ZHANG. Integrative graph deep learning with directional decoding for robust gene regulatory network inference from single-cell transcriptomics. *Journal of Zhejiang University-SCIENCE B*, 2026, 27(10):1129-1139. <https://doi.org/10.1631/jzus.B2500424>

Integrative graph deep learning with directional decoding for robust gene regulatory network inference from single-cell transcriptomics

Key words: Single-cell RNA sequencing (scRNA-seq); Gene regulatory network (GRN) inference; Local-aware graph aggregation (LGA); Node reconstruction autoencoder; Asymmetric relation decoder

Research Summary

We propose scGRAIL, a supervised graph deep learning framework for robust gene regulatory network (GRN) inference from scRNA-seq data.



- Node reconstruction autoencoder (NAE)
- Local-aware Graph Aggregation (LGA)
- Asymmetric relation decoding module

Innovation points

- **Introduction.** We propose scGRAIL, a supervised graph deep learning framework for robust gene regulatory network (GRN) inference from scRNA-seq data. It targets three key challenges in existing methods—noise/dropout, missed long-range regulation, and weak directionality modeling—by learning transferable TF–target representations and explicitly scoring directional regulatory links.

- **Design.** scGRAIL is designed with three coupled modules: (i) LGA that performs multi-hop neighborhood aggregation on the TF–Target graph to capture long-range regulatory dependencies; (ii) NAE that reconstructs gene expression from embeddings to improve robustness and generalization; and (iii) an asymmetric relation decoder that uses ordered embedding differences to model TF→Target directionality and target specificity for accurate edge prediction.

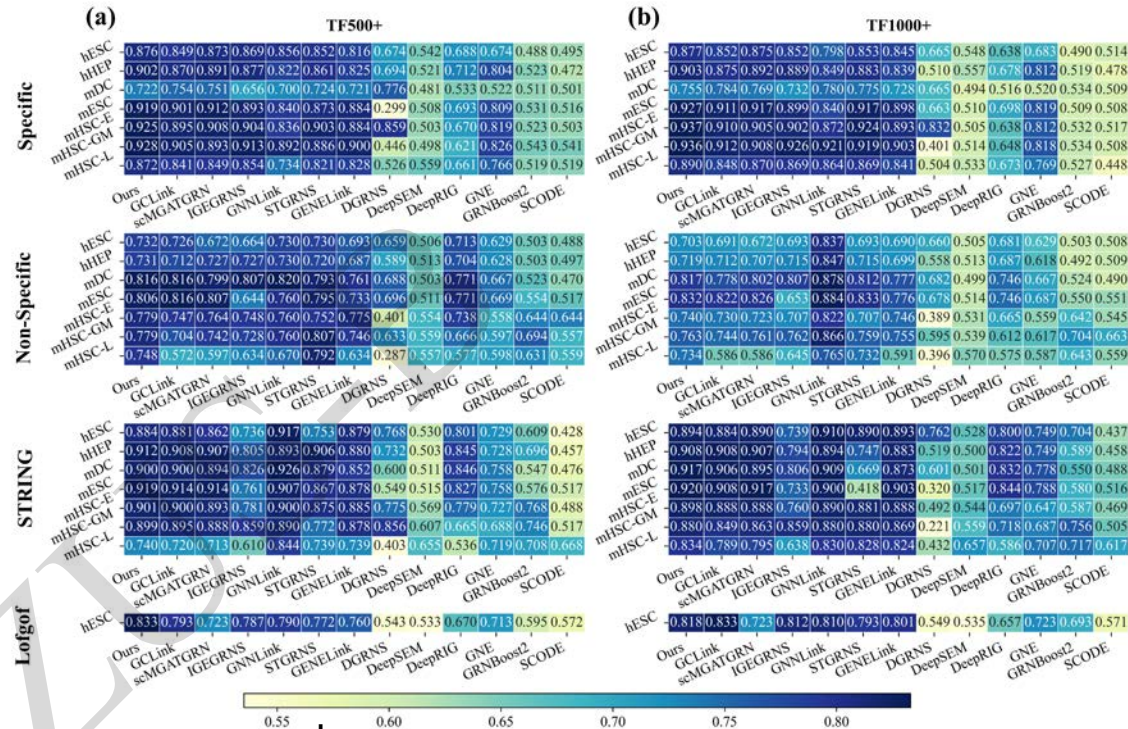


Fig. 2 | Performance comparison with other methods on benchmark datasets

Related experiments

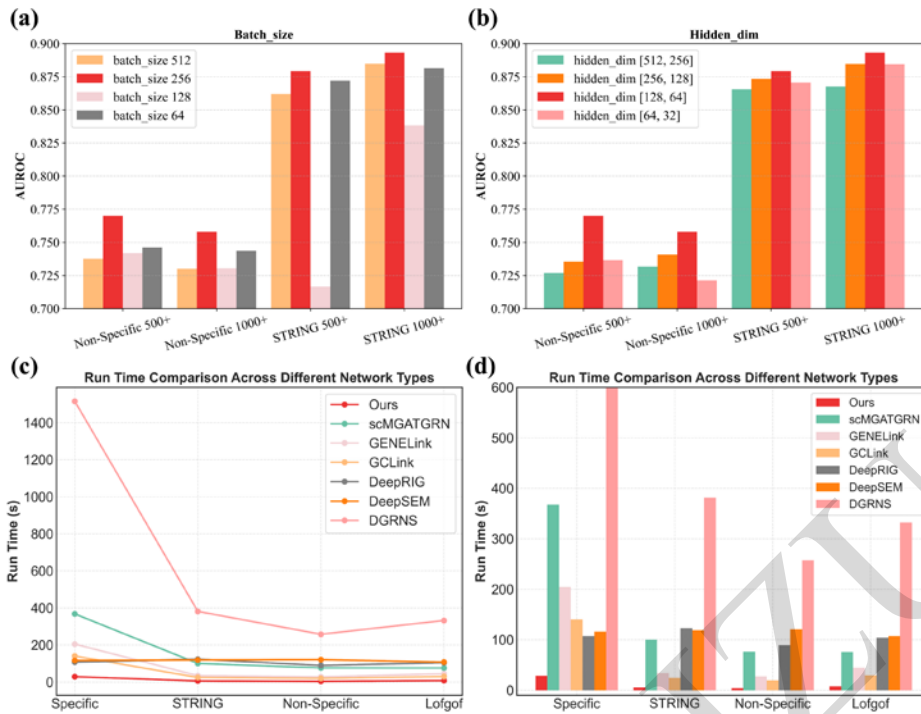


Fig 3 | (a) and (b) display its average AUROC performance under different batch_size and hidden_dim; (c) and (d) present comparative analyses of average runtime between seven existing methods

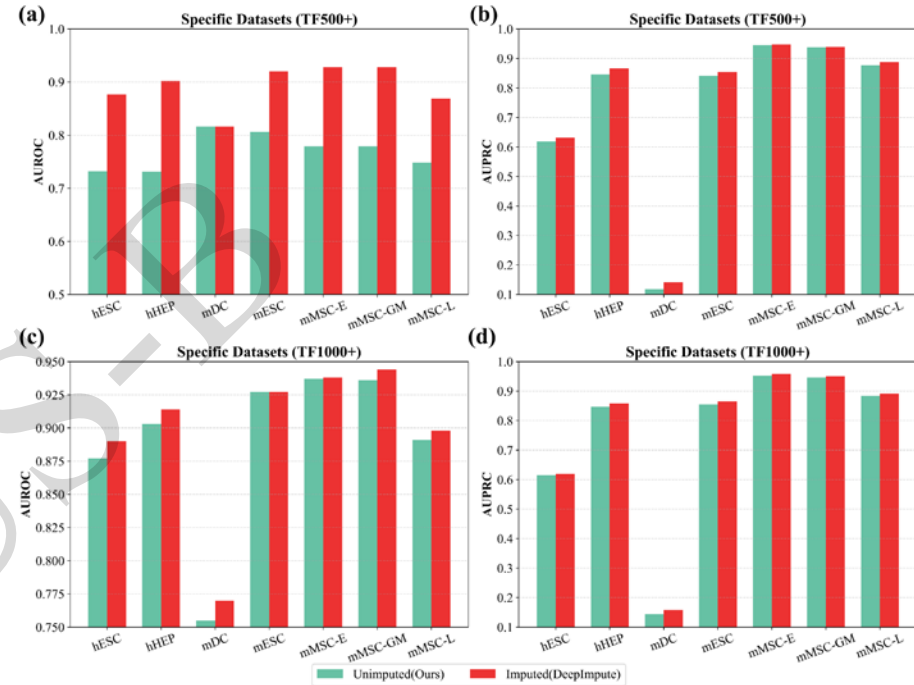


Fig 4 | Effects of single-cell data imputation. AUROC : Area Under the Receiver Operating Characteristic Curve; AUPRC : Area Under the Precision-Recall Curve.