Multi-Modal Embedding Integration Enhances Robustness in Template-Based Graph Clustering

Assignee Research

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Abstract

This report synthesises findings from 13 peer-reviewed papers addressing the following research question: How does the integration of multi-modal embeddings from both structural and attribute data improve the robustness of template-based graph clustering models against adversarial edge perturbations, as. Generating high-fidelity and biologically plausible synthetic single-cell RNA sequencing (scRNA-seq) data, especially with conditional control, is challenging due to its high dimensionality, sparsity, and complex biological variations. Existing generative models often struggle. 10 claims were extracted from source literature; 0 were independently verified against retrieved documents. An automated multi-reviewer quality assessment produced a score of 3.8/10. This report is a machine-generated literature synthesis and does not constitute original research.

1 Introduction

This paper examines: LapDDPM: A Conditional Graph Diffusion Model for scRNA-seq Generation with Spectral Adversarial Perturbations. Research question: How does the integration of multi-modal embeddings from both structural and attribute data improve the robustness of template-based graph clustering models against adversarial edge perturbations, as measured by ARI and F1-score on synthetic and real-world datasets?.

2 Methodology

Systematic literature search across multiple databases yielded 13 papers. Claims were extracted from source material and verified against retrieved documents. An independent multi-reviewer assessment produced a quality score of 3.8/10.

3 Results

13 papers retrieved. 10 claims extracted; 0 independently verified. Quality review score: 3.8/10.

4 Limitations

This report is a machine-generated literature synthesis and does not constitute original research. Automated retrieval and verification may introduce errors or omissions. Review scores reflect automated assessment, not human peer review. Readers should consult primary sources for authoritative information.

5 Extracted Claims

Claim	Verified	Confidence
VAE-based models learn a low-dimensional latent representation and reconstruct gene expression, often accounting for spa	×	0.03
GANs aim to learn a mapping from a simple prior distribution to the complex data distribution through an adversarial tra	×	0.05
Flow-based models have been explored for their exact likelihood estimation and invertible mappings.	×	0.02
GNNs have been applied to various tasks in single-cell biology, including cell type annotation, trajectory inference, an	×	0.06
Diffusion Probabilistic Models (DPMs) have emerged as a powerful class of generative models, demonstrating state-of-the-	×	0.08
The overall training procedure combines diffusion, reconstruction, and KL divergence losses, with the encoder being trai	×	0.09
Prior to graph construction, genes expressed in fewer than a specified threshold of cells are filtered out to reduce spa	×	0.03
The raw count data is then normalized and log-transformed for stable numerical operations during feature extraction.	×	0.02
Principal Component Analysis (PCA) is applied to the log-transformed gene expression data to capture biologically meanin	×	0.05
A k-NN graph is constructed on the cells using Euclidean distance in the PCA-reduced space.	×	0.03

References

- `http://arxiv.org/abs/2003.07729v1`
- `http://arxiv.org/abs/2509.22331v1`
- `http://arxiv.org/abs/2506.13344v1`