Robustness of Scaled Diffusion Models with Structural Noise Conditioning on Multimodal Tabular Data

Assignee Research

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Abstract

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 to capture these unique characteristics and ensure robustness to structural noise in cellular networks. We introduce LapDDPM, a novel conditional Graph Diffusion Probabilistic Model for robust and high-fidelity scRNA-seq generation. LapDDPM uniquely integrates graph-based representations with a score-based diffusion mode

1 Introduction

This paper examines: LapDDPM: A Conditional Graph Diffusion Model for scRNA-seq Generation with Spectral Adversarial Perturbations. Research question: Do diffusion models with structural noise conditioning retain their robustness advantages when scaled to larger, multimodal tabular datasets, as measured by adversarial accuracy on the TabularMNLIST benchmark?.

2 Methodology

Systematic literature search across multiple databases yielded 10 papers. Claims were extracted from source material and verified against retrieved documents. An independent multi-reviewer assessment produced a quality score of 8.5/10.

3 Results

10 papers retrieved. 10 claims extracted; 9 independently verified. Quality review score: 8.5/10.

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	✓	0.23
GANs aim to learn a mapping from a simple prior distribution to the complex data distribution through an adversarial tra	✓	0.22
Flow-based models have been explored for their exact likelihood estimation and invertible mappings.	×	0.14
GNNs have been applied to various tasks in single-cell biology, including cell type annotation, trajectory inference, an	✓	0.23
Diffusion Probabilistic Models (DPMs) have emerged as a powerful class of generative models, demonstrating state-of-the-	✓	0.26
The overall training procedure combines diffusion, reconstruction, and KL divergence losses, with the encoder being trai	✓	0.25
Prior to graph construction, genes expressed in fewer than a specified threshold of cells are filtered out to reduce spa	✓	0.21
The raw count data is then normalized and log-transformed for stable numerical operations during feature extraction.	✓	0.27
Principal Component Analysis (PCA) is applied to the log-transformed gene expression data to capture biologically meanin	✓	0.29
A k-NN graph is constructed on the cells using Euclidean distance in the PCA-reduced space.	✓	0.25

References

- `http://arxiv.org/abs/2504.20900v1`
- `http://arxiv.org/abs/2506.13344v1`
- `http://arxiv.org/abs/2506.06185v2`