

Does conditioning graph diffusion models on structural noise improve the calibration of downstream classifiers

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: Does conditioning graph diffusion models on structural noise improve the calibration of downstream classifiers evaluated on adversarial tabular benchmarks?.

2 Methodology

Systematic literature search across multiple databases yielded 12 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

12 papers retrieved. 8 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
VAEs and GANs have been adapted for generating synthetic cellular profiles from scRNA-seq data.	×	0.15
Flow-based models have been explored for exact likelihood estimation and invertible mappings in scRNA-seq data generatio	×	0.12
GNNs have been applied to tasks in single-cell biology, including cell type annotation, trajectory inference, and spatia	×	0.06
DPMs have demonstrated state-of-the-art performance in image synthesis and audio generation.	×	0.07
The overall training procedure of LapDDPM combines diffusion, reconstruction, and KL divergence losses, with the encoder	×	0.10
Gene filtering and normalization are performed prior to graph construction to reduce sparsity and computational burden.	×	0.02
PCA is applied to the log-transformed gene expression data to capture biologically meaningful relationships and reduce d	×	0.05
A k-NN graph is constructed using Euclidean distance in the PCA-reduced space.	×	0.03

References

- <http://arxiv.org/abs/2104.09369v1>
- <http://arxiv.org/abs/2506.06185v2>
- <http://arxiv.org/abs/2506.13344v1>