How do diffusion-based tabular generative models compare to GANs in preserving adversarial robustness on the T

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: How do diffusion-based tabular generative models compare to GANs in preserving adversarial robustness on the TabMNAR benchmark under spectral perturbations?.

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 3.7/10.

3 Results

13 papers retrieved. 17 claims extracted; 0 independently verified. Quality review score: 3.7/10.

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
Early approaches for generating synthetic scRNA-seq cellular profiles adapted Variational Autoencoders (VAEs) and Genera	×	0.09
VAE-based models for scRNA-seq learn a low-dimensional latent representation and reconstruct gene expression, often acco	×	0.07
GANs for scRNA-seq aim to learn a mapping from a simple prior distribution to the complex data distribution through an a	×	0.08
Flow-based models have been explored for scRNA-seq generation for their exact likelihood estimation and invertible mappi	×	0.09
Existing generative models for scRNA-seq often face challenges in capturing intricate multimodal distributions, preserv	×	0.10
In single-cell data, cells can be viewed as nodes in a graph connected by biological similarity such as gene expression	×	0.05
GNNs have been applied to single-cell biology tasks including cell type annotation, trajectory inference, and spatial tr	×	0.05
Applications of GNNs in single-cell biology typically use GNNs as feature extractors or classifiers.	×	0.04
LapDDPM utilizes GNNs within a generative framework specifically as a spectral encoder to process graph-structured scRNA	×	0.11
Diffusion Probabilistic Models (DPMs) have demonstrated state-of-the-art performance in image synthesis and audio genera	×	0.10
The LapDDPM overall training procedure combines diffusion, reconstruction, and KL divergence losses.	×	0.03
In LapDDPM, the encoder is trained on graphs perturbed by a spectral adversarial mechanism.	×	0.09
In the LapDDPM graph representation, nodes correspond to individual cells and edges represent cellular proximity.	×	0.04
Prior to graph construction in LapDDPM, genes expressed in fewer than a specified threshold of cells are filtered out.	×	0.02
Raw count data in LapDDPM is normalized and log-transformed prior to graph construction.	×	0.03
LapDDPM constructs a k-NN graph on cells using Euclidean distance in a PCA-reduced space of log-transformed gene express	×	0.03
Principal Component Analysis (PCA) is applied in LapDDPM to capture biologically meaningful relationships and reduce the	×	0.06

References

- http://arxiv.org/abs/2504.20900v1
- http://arxiv.org/abs/2104.09630v2
- http://arxiv.org/abs/2506.13344v1