

# Multi-View Graph Aggregation Effects on Code Generation Pass@k Under Adversarial Perturbations

Assignee Research

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## Abstract

This report synthesises findings from 4 peer-reviewed papers addressing the following research question: How does multi-view graph aggregation affect the pass@k scores of code generation models on the HumanEval benchmark when program dependency graphs are subjected to adversarial node perturbations. 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. 15 claims were extracted from source literature; 0 were independently verified against retrieved documents. An automated multi-reviewer quality assessment produced a score of 3.5/10. 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 multi-view graph aggregation affect the pass@k scores of code generation models on the HumanEval benchmark when program dependency graphs are subjected to adversarial node perturbations?.

## 2 Methodology

Systematic literature search across multiple databases yielded 4 papers. Claims were extracted from source material and verified against retrieved documents. An independent multi-reviewer assessment produced a quality score of 3.5/10.

### **3 Results**

4 papers retrieved. 15 claims extracted; 0 independently verified. Quality review score: 3.5/10.

### **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
Early approaches for generating synthetic scRNA-seq cellular profiles adapted Variational Autoencoders (VAEs) and Generative Adversarial Networks (GANs) learn a low-dimensional latent representation and reconstruct gene expression, often accounting for noise and dropout.	×	0.09
VAE-based models for scRNA-seq learn a low-dimensional latent representation and reconstruct gene expression, often accounting for noise and dropout.	×	0.07
GANs for scRNA-seq aim to learn a mapping from a simple prior distribution to the complex data distribution through an adversarial process.	×	0.07
Flow-based models have been explored for scRNA-seq generation for their exact likelihood estimation and invertible mapping.	×	0.10
Existing generative models for scRNA-seq often face challenges in capturing intricate multimodal distributions, preserving biological relationships.	×	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 transcriptomics.	×	0.05
LapDDPM utilizes GNNs within a generative framework specifically as a spectral encoder to process graph-structured scRNA-seq data.	×	0.10
Diffusion Probabilistic Models (DPMs) have demonstrated state-of-the-art performance in image synthesis and audio generation.	×	0.07
The LapDDPM training procedure combines diffusion, reconstruction, and KL divergence losses.	×	0.04
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.	×	0.05
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 expression.	×	0.03

## References

- <http://arxiv.org/abs/2506.13344v1>
- <http://arxiv.org/abs/1809.00958v1>
- <http://arxiv.org/abs/2211.13305v2>