Noise Scaling Effects on Calibration of Tabular Foundation Models in TabBench Tasks

Assignee Research

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Abstract

Generative AI foundation models offer transformative potential for processing structured biological data, particularly in single-cell RNA sequencing, where datasets are rapidly scaling toward billions of cells. We propose the use of agentic foundation models with real-time web search to automate the labeling of experimental data, achieving up to 82.5% accuracy. This addresses a key bottleneck in supervised learning for structured omics data by increasing annotation throughput without manual curation and human error. Our approach enables the development of virtual cell foundation models capable

1 Introduction

This paper examines: DeepSeq: High-Throughput Single-Cell RNA Sequencing Data Labeling via Web Search-Augmented Agentic Generative AI Foundation Models. Research question: How does noise scale in synthetic tabular data generation influence the calibration of tabular foundation models as measured by expected calibration error across diverse TabBench tasks?.

2 Methodology

Systematic literature search across multiple databases yielded 9 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

9 papers retrieved. 12 claims extracted; 11 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
DeepSeq's two-stage evaluation assesses both the biological plausibility of marker gene matches and the accuracy of resu	✓	0.28
The top panel in Figure 4 confirms that marker genes extracted for each cluster match canonical gene sets for known cell	✓	0.29
The full set of results—including per-cluster marker genes, predicted labels, ground truth matches, and evaluation score	✓	0.34
Each step of the pipeline—from filtering and dimensionality reduction to LLM prompting and evaluation—outputs interpreta	✓	0.26
The DeepSeq pipeline integrates single-cell RNA-seq preprocessing with foundation model–driven cell-type annotation usin	✓	0.28
The full workflow spans filtering, clustering, marker gene extraction, prompting, and structured evaluation.	✓	0.22
All core analysis and evaluation scripts are provided in the public repository.	✓	0.17
Algorithm 1 describes the LLM-Based Cell-Type Labeling with DeepSeq.	×	0.14
Raw single-cell data is processed into gene-by-cell matrices and converted into the AnnData format.	✓	0.18
Filtering is performed using three strategies: (1) standard thresholding (e.g., $\geq$200 genes per cell), (2) automated knee	✓	0.27
Dimensionality reduction is performed using PCA, and cells are clustered using the Leiden algorithm based on neighborhoo	✓	0.21
UMAP is used to embed cells in 2D for visualization.	✓	0.18

References

- http://arxiv.org/abs/2501.19047v5
- http://arxiv.org/abs/2506.13817v1
- http://arxiv.org/abs/2504.20900v1