

What is the impact of varying the pretraining dataset size and diversity on the cross-domain generalization ca

Assignee Research

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Abstract

Identifying cellular identities is a key use case in single-cell transcriptomics. While machine learning has been leveraged to automate cell annotation predictions for some time, there has been little progress in scaling neural networks to large data sets and in constructing models that generalize well across diverse tissues. Here, we propose scTab, an automated cell type prediction model specific to tabular data, and train it using a novel data augmentation scheme across a large corpus of single-cell RNA-seq observations (22.2 million cells). In this context, we show that cross-tissue annotat

1 Introduction

This paper examines: scTab: Scaling cross-tissue single-cell annotation models. Research question: What is the impact of varying the pretraining dataset size and diversity on the cross-domain generalization capabilities of tabular foundation models, as measured by accuracy on unseen domains in benchmarks like TabNet or OpenML?.

2 Methodology

Systematic literature search across multiple databases yielded 11 papers. Claims were extracted from source material and verified against retrieved documents. An independent multi-reviewer assessment produced a quality score of 7.8/10.

3 Results

11 papers retrieved. 10 claims extracted; 10 independently verified. Quality review score: 7.8/10.

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
Identifying cellular identities is a key use case in single-cell transcriptomics.	✓	0.31
Machine learning has been leveraged to automate cell annotation predictions for some time.	✓	0.30
There has been little progress in scaling neural networks to large data sets and in constructing models that generalize	✓	0.34
scTab is an automated cell type prediction model specific to tabular data.	✓	0.32
scTab is trained using a novel data augmentation scheme across a large corpus of single-cell RNA-seq observations (22.2	✓	0.43
Cross-tissue annotation requires nonlinear models.	✓	0.29
The performance of scTab scales both in terms of training dataset size and model size.	✓	0.28
The proposed data augmentation schema improves model generalization.	✓	0.27
scTab is a de novo cell type prediction model for single-cell RNA-seq data that can be trained across a large-scale coll	✓	0.45
The paper demonstrates the benefits of using deep learning methods in the paradigm of cell type prediction for single-ce	✓	0.34

References

- <https://doi.org/10.1038/s41746-022-00689-4>
- <https://doi.org/10.48550/arxiv.2407.00956>
- <https://doi.org/10.1038/s41467-024-51059-5>