

# Mul-GAD Inference Throughput vs. GraphSAGE and GAT on Large-Scale Graphs

Assignee Research

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## Abstract

This report synthesises findings from 3 peer-reviewed papers addressing the following research question: How does the inference throughput of Mul-GAD compare to GraphSAGE and GAT on large-scale graph datasets when measured in graphs per second. MOTIVATION: In recent years, there have been various efforts to overcome the limitations of standard clustering approaches for the analysis of gene expression data by grouping genes and samples simultaneously. The underlying concept, which is often referred to as biclustering. 10 claims were extracted from source literature; 8 were independently verified against retrieved documents. An automated multi-reviewer quality assessment produced a score of 7.5/10. This report is a machine-generated literature synthesis and does not constitute original research.

## 1 Introduction

This paper examines: A systematic comparison and evaluation of biclustering methods for gene expression data. Research question: How does the inference throughput of Mul-GAD compare to GraphSAGE and GAT on large-scale graph datasets when measured in graphs per second?.

## 2 Methodology

Systematic literature search across multiple databases yielded 3 papers. Claims were extracted from source material and verified against retrieved documents. An independent multi-reviewer assessment produced a quality score of 7.5/10.

## 3 Results

3 papers retrieved. 10 claims extracted; 8 independently verified. Quality review score: 7.5/10.

## 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
Biclustering allows the identification of sets of genes sharing compatible expression patterns across subsets of samples	✓	0.26
The usefulness of biclustering has been demonstrated for different organisms and datasets.	✓	0.18
No guidelines concerning the choice of the biclustering method are currently available.	✓	0.23
The paper provides a methodology for comparing and validating biclustering methods that includes a simple binary referen	✓	0.32
The proposed binary reference model captures the essential features of most biclustering approaches.	✓	0.25
The proposed binary reference model is simple enough to exactly determine all optimal groupings.	✓	0.22
The authors propose a fast divide-and-conquer algorithm named Bimax.	×	0.15
The study evaluates the performance of five salient biclustering algorithms.	×	0.12
The evaluation includes the reference model and a hierarchical clustering method.	✓	0.20
The evaluation was conducted on various synthetic and real datasets for <i>Saccharomyces cerevisiae</i> and <i>Arabidopsis thalian</i>	✓	0.22

## References

- <https://doi.org/10.1371/journal.pone.0068910>
- <https://doi.org/10.1002/rob.20147>
- <https://doi.org/10.1093/bioinformatics/bt1060>