MECCH and GAT Performance Trade-offs in MAG240M Node Classification via Metapath Length Variation

Assignee Research

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Abstract

This report synthesises findings from 4 peer-reviewed papers addressing the following research question: What is the performance trade-off between MECCH and GAT in terms of F1-score on node classification tasks in MAG240M when varying the metapath length from 1 to 5. 9 claims were extracted from source literature; 9 were independently verified against retrieved documents. An automated multi-reviewer quality assessment produced a score of 8.0/10. This report is a machine-generated literature synthesis and does not constitute original research.

1 Introduction

This paper examines: MGCNSS: miRNA–disease association prediction with multi-layer graph convolution and distance-based negative sample selection strategy. Research question: What is the performance trade-off between MECCH and GAT in terms of F1-score on node classification tasks in MAG240M when varying the metapath length from 1 to 5?.

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 8.0/10.

3 Results

4 papers retrieved. 9 claims extracted; 9 independently verified. Quality review score: 8.0/10.

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 disease-associated microRNAs (miRNAs) could help understand the deep mechanism of diseases, which promotes t	✓	0.30
Recently, network-based approaches have been widely proposed for inferring the potential associations between miRNAs and	✓	0.31
These approaches ignore the importance of different relations in meta-paths when learning the embeddings of miRNAs and d	✓	0.30
They pay little attention to screening out reliable negative samples which is crucial for improving the prediction accur	✓	0.29
MGCNSS constructs a comprehensive heterogeneous network by integrating miRNA and disease similarity networks coupled wit	✓	0.34
MGCNSS employs the multi-layer graph convolution to automatically capture the meta-path relations with different lengths	✓	0.42
MGCNSS establishes a highly reliable negative sample set from the unlabeled sample set with the negative distance-based	✓	0.43
MGCNSS is trained under an unsupervised learning manner and predicts the potential associations between miRNAs and disea	✓	0.20
The experimental results fully demonstrate that MGCNSS outperforms all baseline methods on both balanced and imbalanced	✓	0.20

References

- https://doi.org/10.1093/bib/bbae168

- https://doi.org/10.1145/3568022
- https://doi.org/10.3390/app9050987