BraneMF: Random Walk-based Matrix Factorization of a Multi-layer Network for Protein Function Prediction

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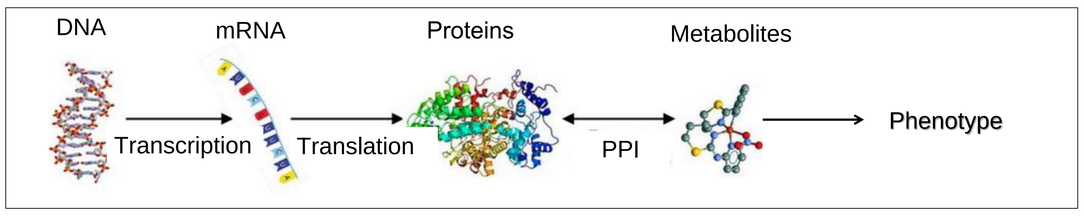
INTRODUCTION

- Interacting entities in the organism's cellular system: **Genes**, **Proteins**, **Metabolites**, etc.
- **Omics technologies**: Enable us to study the relationships of these entities.

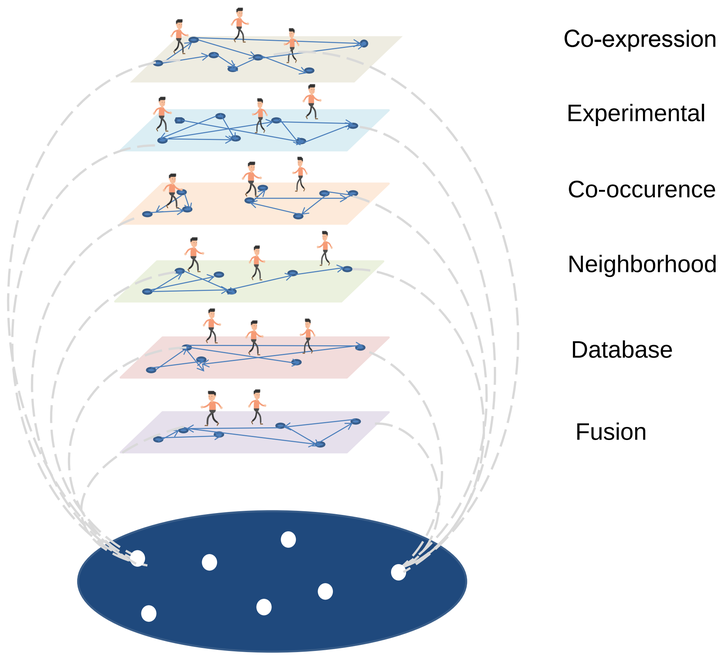


- **Biological networks**: Represent the biological relations (**edges**) between the interacting entities (**nodes**).
- Independent analysis of such networks is limited to correlations, mostly reflecting reactive processes rather than causative ones.
- **Integration** of biological networks: Can elucidate potential causative changes that can lead to a protein function prediction.
- **Graph Representation Learning (GRL)** algorithms: allow us to encode the graph structure into compact embedding vectors.

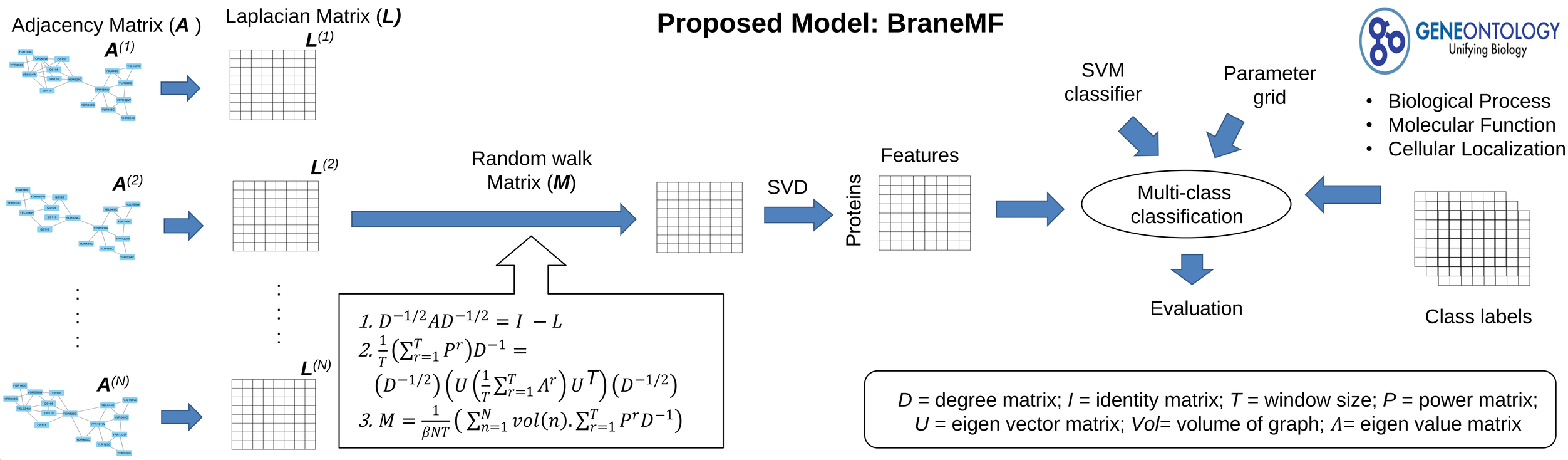
OBJECTIVE

To embed proteins of biological networks in a lower dimension latent space focusing on the application of protein function prediction

Graph Representation Learning (GRL)

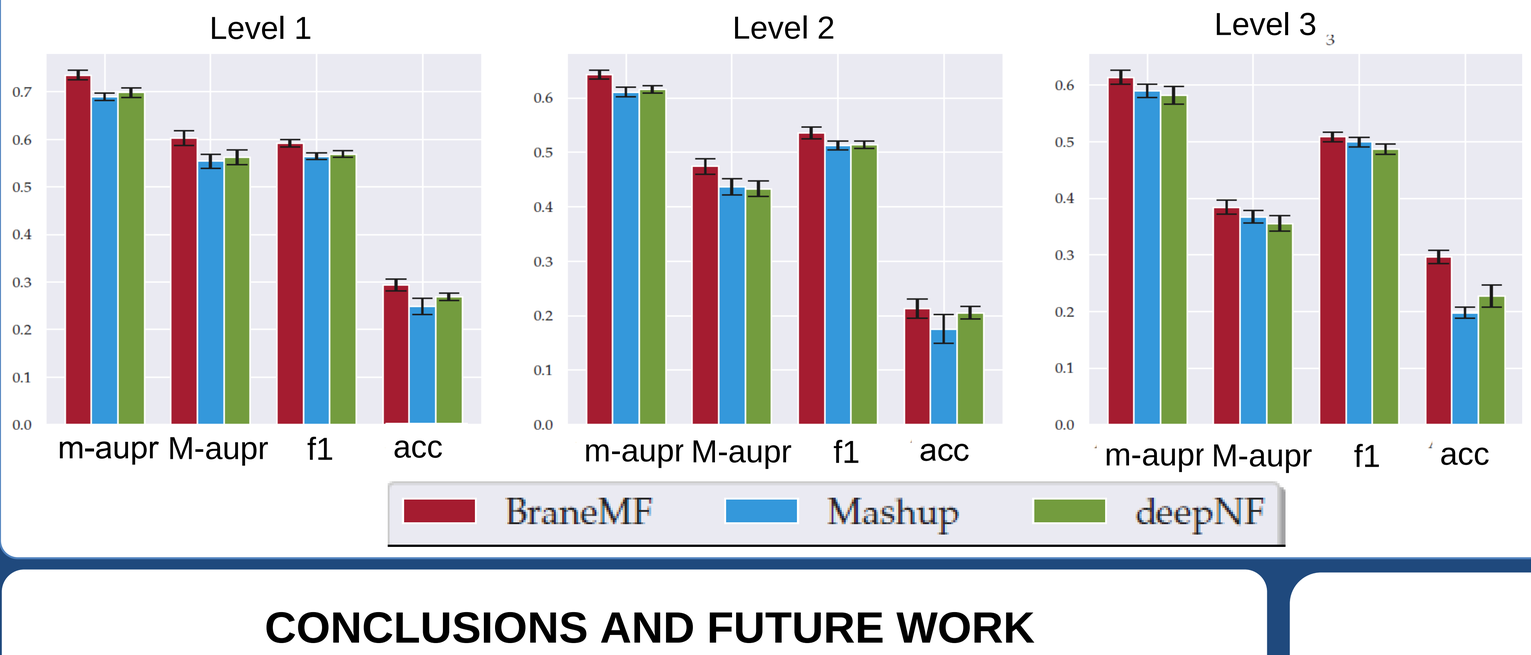


Proposed Model: BraneMF



D = degree matrix; *I* = identity matrix; *T* = window size; *P* = power matrix; *U* = eigen vector matrix; *Vol*= volume of graph; Λ= eigen value matrix

RESULTS



- Cross Validation (CV) performance of BraneMF on Gene Ontology (GO) prediction in yeast STRING networks.
- CV is compared with the performance of the state-of-the-art integration methods, Mashup and deepNF.
- Performance is measured by the area under the precision-recall curve, summarized over all GO terms both under the micro-averaging (m-aupr) and macro-averaging (M-aupr), F1 score (f1) and accuracy (acc).
- Performance shown separately for MIPS yeast annotations for Level 1, Level 2 and Level 3.
- The error bars are computed based on 10 CV trials.
- BraneMF outperforms the baseline methods in all three levels.
- The best results we can achieve is the gain of 15% in the accuracy than Mashup and 7% in deepNF.

CONCLUSIONS AND FUTURE WORK

- We have presented a graph embedding based network integration method for protein function prediction.
- We construct a compact low-dimensional protein feature representation from the selected networks. Also, we have performed an empirical analysis of the proposed approach, comparing it to state-of-art baseline methods.
- Our method is not limited to only protein function prediction tasks. There are several directions for future work with focus on extending the integration to include other data types such as protein sequences, protein structures, epigenetic marks, etc.

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Code: https://github.com/Surabhivj/BraneMF

Poster session: Representation Learning in Biology (RLB)

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