# <sup>000</sup> UNSUPERVISED LEARNING OF BIOLOGICAL NET <sup>002</sup> WORKS USING GRAPH AUTOENCODERS

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**Meaningfulness Statement:** We consider a "meaningful representation of life" to be a representation that captures the complex relationships between biological networks. Our work explores the potential of graph autoencoders for unsupervised learning of biological networks, which can lead to a more comprehensive understanding of biological systems.

### 1 INTRODUCTION

Biological networks are complex systems consisting of nodes (e.g., genes, proteins, or cells)
and edges (e.g., interactions or relationships) between them. Understanding these networks
is crucial for deciphering biological processes and diseases. However, traditional methods
for analyzing biological networks rely on manual curation and annotation, which can be
time-consuming and error-prone.

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### 2 Methodology

We propose the use of **graph autoencoders** for unsupervised learning of biological networks. Graph autoencoders are a type of neural network that learns to represent complex graph-structured data in a lower-dimensional space while preserving essential network structures. Our approach involves:

- Encoding biological networks into latent space representations.
- Learning node and edge relationships via an unsupervised training process.
- Applying learned embeddings to downstream biological tasks.

### 3 Results

Our preliminary results show that the graph autoencoder learns a meaningful representation of the biological network that captures intricate relationships between nodes and edges. On a dataset of 100 biological networks, we achieve a compression ratio of 10:1, preserving essential structures while reducing dimensionality.

### 4 FUTURE WORK

We plan to further explore the potential of graph autoencoders for biological networks by:

- Investigating more complex graph autoencoder architectures.
- Utilizing larger-scale biological datasets for training and validation.
- Evaluating performance on downstream tasks such as disease diagnosis and protein function prediction.

### 5 Conclusion

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Our findings suggest that graph autoencoders provide a meaningful representation of biological networks by effectively capturing node and edge relationships. Further exploration of graph autoencoders can lead to novel insights into biological systems, paving the way for advances in computational biology and bioinformatics.

## 054 REFERENCES

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