## 000MULTISCALEGRAPHREPRESENTATIONSFOR002CROSS-MODALBIOLOGICALDATAINTEGRATION

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**Meaningfulness Statement:** A meaningful representation of life should capture the hierarchical structure of biological systems, from molecules to multicellular processes. We propose a **multiscale graph representation** that learns shared embeddings across different biological modalities, ensuring cross-scale generalization and interpretability.

1 INTRODUCTION

Understanding biological systems requires integrating heterogeneous data sources (e.g., genomic sequences, protein interactions, cell imaging, and tissue-level features). Traditional methods treat these separately, losing important hierarchical relationships. We propose a graph representation learning framework that unifies biological modalities by embedding them into a multiscale latent space that preserves cross-scale interactions.

2 Methodology

**Graph Construction:** Nodes represent different biological entities (genes, proteins, cells), and edges encode known interactions, functional relationships, or inferred similarity.

027 Multiscale Hierarchy: We define coarse-to-fine graph structures (molecule  $\rightarrow$  cell  $\rightarrow$  tissue) using hierarchical graph attention.

 Representation Learning: We train a multimodal graph autoencoder that simultaneously learns embeddings across different biological scales while enforcing cross-modal alignment.

3 Results

- **Higher accuracy in downstream tasks** (disease classification, cell-type annotation) compared to single-modality methods.
- **Cross-modal alignment evaluation:** Our method finds shared embeddings across different biological domains, improving interpretability.
- Scalability: We demonstrate our approach on large-scale datasets (e.g., Human Cell Atlas, Protein Interaction Networks).

## 4 FUTURE WORK

- Extending the framework to model **long-range dependencies** in biological processes.
- Enhancing **causal reasoning** in biological systems through graph interventions.

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- 5 Conclusion
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Our work presents a novel multiscale representation of biological life that captures
the complexity of cellular and molecular systems while ensuring interpretability and generalization across modalities.

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