Biologically Informed Self-Supervised Learning for Gene Expression Data

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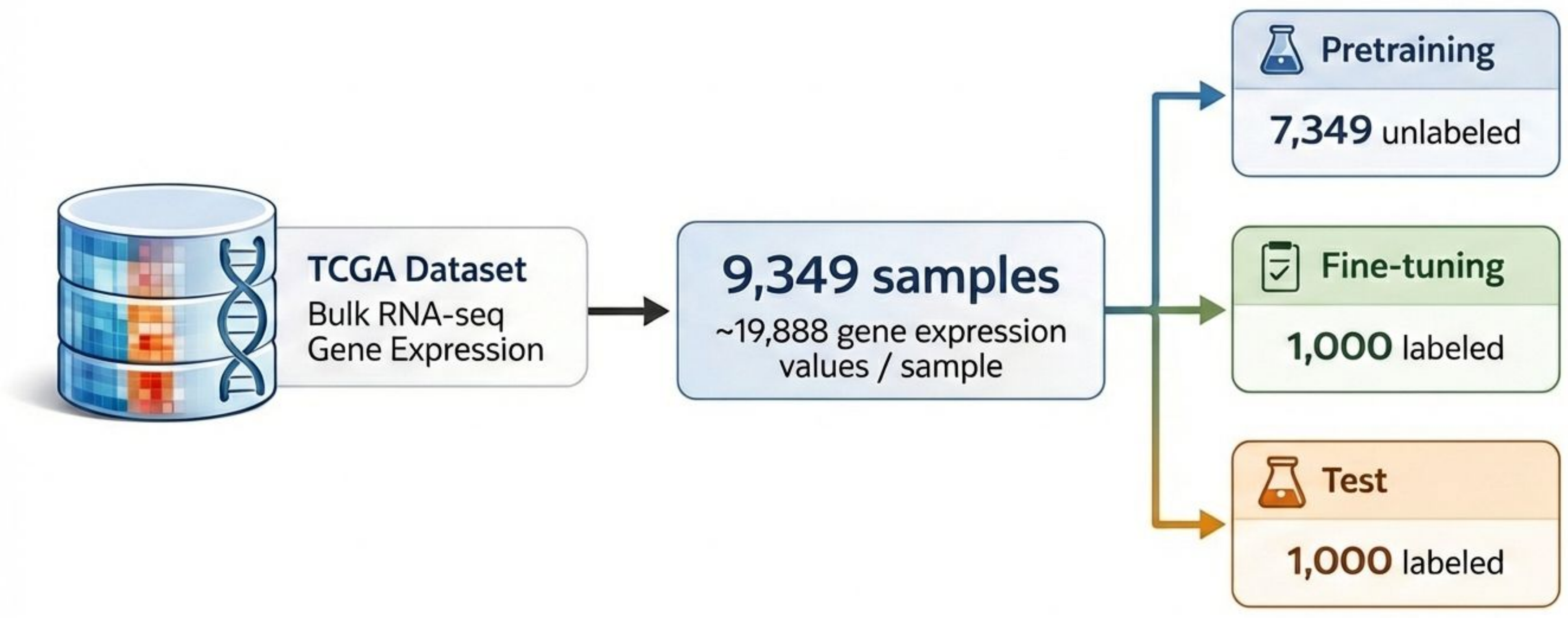
Introduction

Gene expression data are extremely high-dimensional and **weakly labeled**, making supervised learning unreliable in **low-label regimes**.Moreover, standard models ignore the **biological structure of coordinated gene pathways**.

We address this challenge using **biologically informed self-supervised learning** to learn **transferable representations** from **unlabeled transcriptomic data**.

Dataset

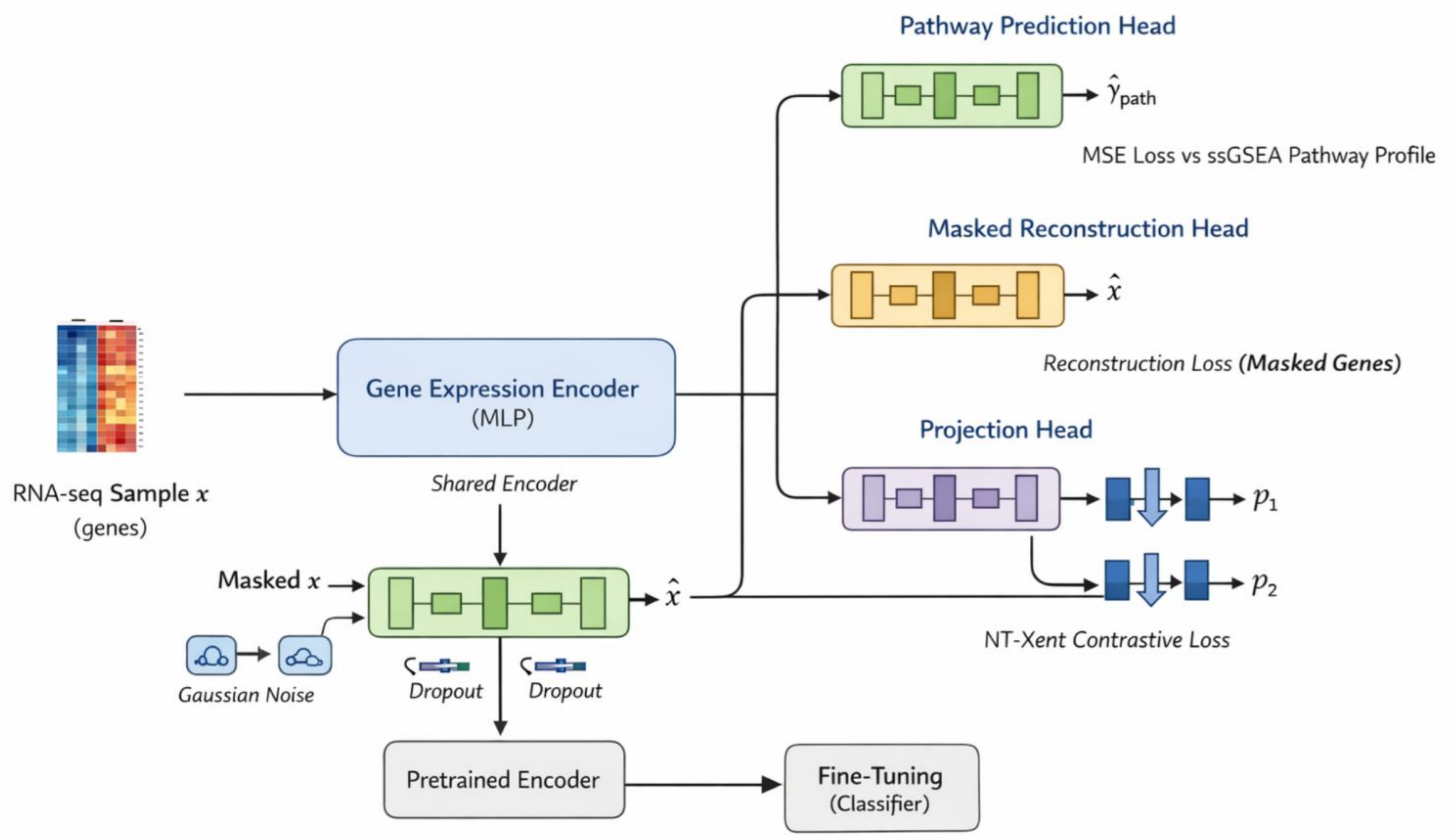


Method Overview

This work presents **self-supervised framework for transcriptomic data** based on a **shared gene expression encoder**.

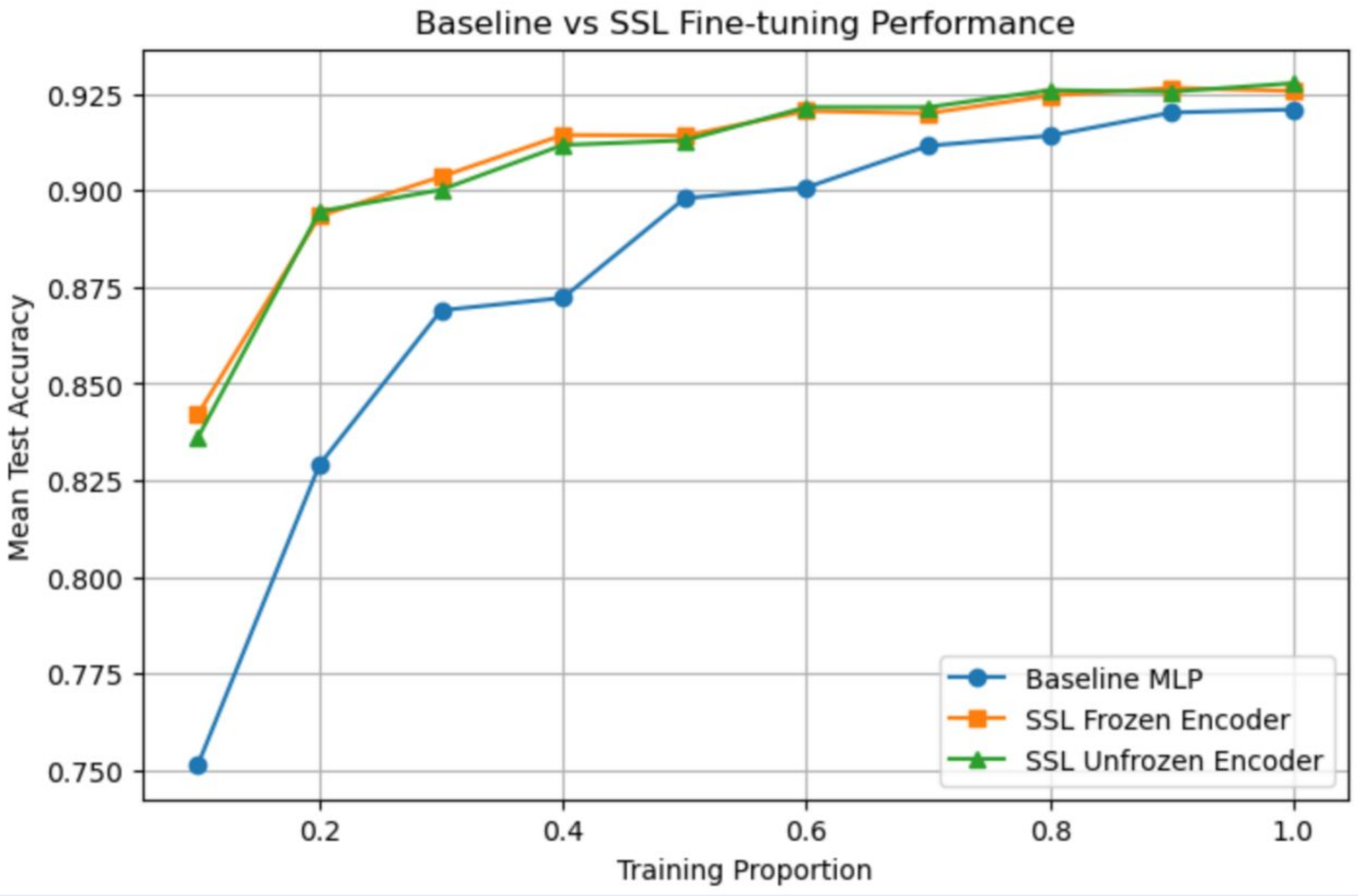
The encoder is pretrained using **pathway activity prediction**, **masked gene reconstruction**, and **contrastive learning**, enabling the model to capture **biologically meaningful and robust representations** from unlabeled RNA-seq data.

The learned representations are evaluated on cancer classification via **linear probing** and **full fine-tuning**, allowing us to assess **data efficiency and transferability in low-label regimes**.



Results

Self-supervised pretraining yields **data-efficient, transferable representation**, with the **largest performance gains in low-label regimes**.



Analysis & Interpretation

Supervised learning degrades sharply in low-label regimes, confirming the difficulty of modeling high-dimensional gene expression with limited annotations.

Pathway-based self-supervised pretraining consistently improves performance, indicating that pathway prediction provides a meaningful biological inductive bias.

Strong results with a frozen encoder show that the learned representations are **transferable** and not task-specific.

Additional gains from full fine-tuning suggest that pretrained representations can be further adapted when more labeled data are available.

Conclusion

Biologically informed self-supervised learning improves data efficiency and transferability in transcriptomic analysis. The learned representations remain effective even with limited labeled data, highlighting their potential for cancer-related applications.

References

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