

Multi-Modal Transformer Architecture for Genomic Data Integration: A Novel Approach to Cancer Classification

■■ PATENT PROTECTED TECHNOLOGY ■■

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Title: Systems and Methods for Cancer Classification Using Multi-Modal Transformer-Based Architectures

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Abstract

Cancer genomics research increasingly relies on multi-modal data integration to capture the complex molecular landscape of tumors. Here, we present a novel multi-modal transformer architecture specifically designed for integrating heterogeneous genomic data types in cancer classification tasks. Our approach addresses key computational challenges in applying attention mechanisms to genomic data through modality-specific encoders, cross-modal attention layers, and synthetic data generation strategies. The architecture demonstrates effective fusion of methylation patterns, fragmentomics profiles, and copy number alteration data through learned attention weights. We validate our approach using synthetic genomic datasets that preserve realistic data characteristics while enabling controlled experimentation. This work contributes to the growing field of AI-driven cancer genomics by providing a scalable framework for multi-modal genomic data analysis that can be adapted across different cancer types and genomic platforms.

Keywords: transformer networks, multi-modal learning, cancer genomics, attention mechanisms, methylation analysis, fragmentomics

1. Introduction

The integration of multiple genomic data modalities represents one of the most promising frontiers in computational cancer biology. Traditional machine learning approaches in cancer genomics have largely focused on single-modality analyses, limiting their ability to capture the complex interdependencies between different molecular layers. Recent advances in transformer architectures, originally developed for natural language processing, have shown remarkable success in biological sequence analysis, yet their application to multi-modal genomic data integration remains underexplored.

2. Methods

Our multi-modal transformer architecture consists of three main components: modality-specific encoders, cross-modal attention layers, and classification heads. The overall architecture is implemented using PyTorch Lightning to ensure reproducible training and efficient distributed computing.

3. Results

Our multi-modal transformer architecture successfully integrates three genomic modalities with effective attention-based fusion. The modality-specific encoders produce meaningful representations as evidenced by clustering analysis of the encoded features. Cross-modal attention weights reveal biologically meaningful patterns, with the model learning to focus on relevant genomic regions for classification.

4. Conclusion

We present a novel multi-modal transformer architecture specifically designed for cancer genomics applications. The architecture effectively integrates methylation, fragmentomics, and copy number alteration data through modality-specific encoders and cross-modal attention mechanisms. Our synthetic data generation framework enables controlled validation and reproducible research in multi-modal genomic analysis. The computational efficiency and modular design of our approach make it suitable for large-scale genomic applications and extensible to additional data modalities.

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