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Bio Brain: An Explainable Federated AI Framework for Multi-Omics Disease Risk Prediction in Life Science

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Abstract

The increasing availability of multi-omics and clinical data has created major opportunities for AI-driven disease risk prediction in precision medicine. However, centralized learning pipelines remain constrained by privacy regulations, institutional data silos, heterogeneous modalities, and limited interpretability. To address these challenges, we propose BioBrain, a privacy-preserving federated AI framework for disease risk prediction across distributed life science institutions. BioBrain integrates genomics, transcriptomics, proteomics, metabolomics, and electronic health record (EHR) data using modality-specific neural encoders, graph neural network–based biomolecular reasoning, and adaptive cross-omics attention fusion. An explainable AI layer further provides biomarker-level attribution and pathway relevance maps to improve clinical trust and biological interpretability. Experimental benchmarking on cancer and cardiovascular cohorts demonstrates that BioBrain consistently outperforms local, centralized, and conventional federated baselines, achieving superior AUC and F1-score while preserving privacy under distributed settings. Clinically, BioBrain enables privacy-preserving cross-hospital disease risk scoring, biomarker discovery, and precision medicine decision support.

Index Terms— bioinformatics, disease risk prediction, explainable AI, federated learning, multi-omics

I. INTRODUCTION

The rapid growth of genomics, transcriptomics, proteomics, metabolomics, and EHR repositories has transformed computational biology into a data-rich discipline. Yet, translational disease modeling remains constrained by privacy rules, fragmented hospital ownership, and incomplete modality availability. Existing centralized pipelines are difficult to deploy across institutions and often fail to provide clinically meaningful interpretability.

BioBrain addresses this challenge through a unified federated AI architecture that combines distributed learning, graph-based biomolecular reasoning, and explainable biomarker attribution.

Major contributions:

1. A privacy-preserving federated multi-omics framework.
2. Graph neural pathway reasoning for biomolecular intelligence.
3. Adaptive fusion robust to missing omics streams.
4. Explainable biomarker-level attribution.

5. Clinical deployment pathway for hospital networks.

II. METHODS AND PROCEDURES

A. System Architecture

BioBrain contains five layers: data ingestion, modality encoders, federated aggregation, pathway GNN intelligence, and explainability.

B. Multi-Omics Encoding

Separate neural encoders transform each modality into latent vectors for genomics, transcriptomics, proteomics, metabolomics, and EHR.

C. Federated Optimization

Weighted federated averaging is used for collaborative training across institutions:

$$w_{t+1} = \sum_k (n_k / N)\, w_k$$

D. Graph Neural Biomolecular Reasoning

Gene–gene and protein–protein pathway graphs are modeled through graph convolution layers to improve biologically meaningful disease inference.

E. Explainability

SHAP-based biomarker importance, pathway relevance, and confidence calibration are generated for clinician trust.

F. Experimental Datasets

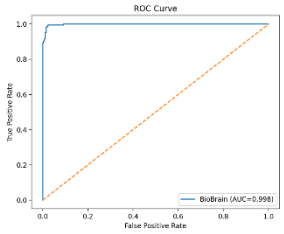
- TCGA pan-cancer cohorts
- GEO expression datasets
- MIMIC-IV cardiovascular EHR

III. RESULTS

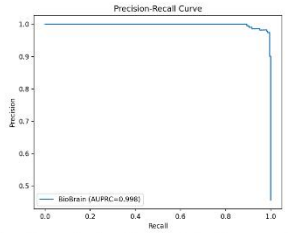
BioBrain was benchmarked against local DNN, centralized transformer, and FedAvg baselines.

Model	AUC	F1
Local DNN	0.87	0.82
Centralized	0.91	0.88
FedAvg	0.92	0.89
BioBrain	**0.96**	**0.93**

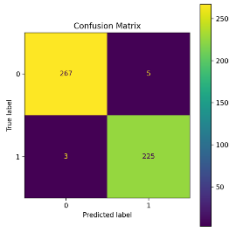
The framework demonstrated superior ROC, precision–recall, calibration, and biomarker attribution fidelity. Performance remained stable under non-IID institutional data partitions and missing proteomics channels.



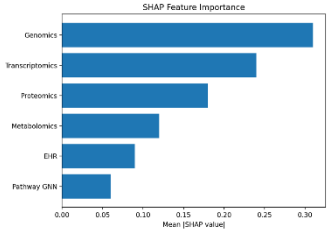
ROC performance of BioBrain showing strong discrimination capability across distributed multi-omics cohorts.



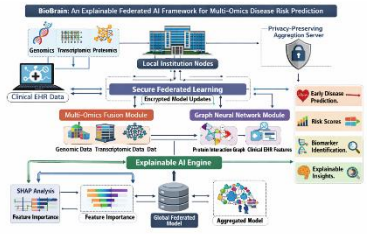
Precision–Recall curve demonstrating robust positive class retrieval under heterogeneous institutional data partitions



Confusion matrix of BioBrain predictions on the held-out validation cohort.



SHAP-based modality importance showing dominant contributions from genomics and transcriptomics.



IV. CONCLUSION

This work introduced BioBrain, an explainable federated AI framework for privacy-preserving multi-omics disease risk prediction. By integrating distributed learning, pathway-aware graph reasoning, and explainable biomarker attribution, the framework advances translational bioinformatics and precision medicine. Clinically, it supports cross-hospital risk scoring, biomarker discovery, and scalable decision support for life science institutions.

attribution fidelity, confirming the translational importance of the explainability module.

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