

FinGeneAI: An Explainable Artificial Intelligence Framework for Predicting Genomic Healthcare Costs Using Multi-Omics Data

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HOW TO CITE:

Bhagyashree Shendkar,
Sandhya Sandeep Waghere,
Komal Sunil Munde, Jyoti Yogesh
Deshmukh, Mandar K Mokashi,
Balasaheb Baburao Gite (2026).
FinGeneAI: An Explainable
Artificial Intelligence Framework
for Predicting Genomic Healthcare
Costs Using Multi-Omics Data.
International Journal of Special
Education, 41(8s), 220-233

ABSTRACT:

The multi-omics analysis and utilization of artificial intelligence have become common tools in biomedical research, aiding in the understanding of complex diseases and precision healthcare. To date, most of the clinical studies on genomics have centered on cancer diagnosis, prognosis, prediction, or discovery of biomarkers, but the link between genomic patterns and the burden of health care costs has not been well studied. In this research, we present an explainable machine learning framework, FinGeneAI, for the prediction of categories of cost-burden in healthcare for genomic data related to diseases. The framework involves data preprocessing, feature selection, supervised modeling, model performance analysis, and finally, interpretability of influential biomedical features using Explainable AI. The transcriptomic models are developed and evaluated using computational data sources which are publicly available, such as TCGA/UCI data derived from RNA-seq. Results show that molecular features offer informative predictive signals to classify the level of healthcare burden, and explainability methods facilitate transparent interpretation of important molecular features contributing to the burden. The study also finds the potential to go beyond disease prediction, to estimate a healthcare burden assessment using genomic and transcriptomic information. This work introduces a computational connection between molecular data analysis,

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predictive modeling and cost-burden explainable decision support for future precision medicine planning..

Keywords: Multi-omics, FinGeneAI, Explainable AI, Healthcare cost prediction, Precision medicine

1. Introduction

Biomedical studies have been moving towards integrated molecular methods that study genomics, transcriptomics, proteomics, epigenomics, metabolomics, and other biological layers as a single entity to comprehend multifaceted diseases. This type of approach is significant since many diseases, including cancer, cannot be well described by a single molecular feature; rather, they are a result of interactions between several biological systems (Hasin et al., 2017). Integration of multi-omics data has thus emerged as a valuable tool in the identification of disease subtypes, identification of biomarkers, as well as patient level prediction by the joint analysis of heterogeneous biomedical data (Wang et al., 2014). Various integration techniques, such as early, intermediate, and late integration, were also devised to analyse machine learning, based on the data structure, the prediction task, and the sample size at hand (Picard et al., 2021).

The growing access to bulk and single-cell omics data has empowered the use of computational techniques in systems biology and precision medicine. These data sets facilitate individual disease-related knowledge by connecting molecular patterns to diagnosis, prognosis, and response to treatment (Li et al., 2021). Extensive cancer resources have also made it possible to perform pan-cancer analysis by offering genomic, transcriptomic and clinical data capable of being utilized to examine common and cancer-specific molecular signatures across tumor types (The Cancer Genome Atlas Research Network et al., 2013). Large-scale molecular profiling of cancers has also demonstrated the utility of large-scale molecular datasets in terms of comprehending

cancer complexity at scale and building computational models that can uncover clinically significant patterns in high-dimensional biomedical data (ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium, 2020).

The use of artificial intelligence in healthcare has gained prominence due to the capacity to process complicated biomedical information and aid in prediction, risk stratification, and decision support. The AI-based systems can also be a part of the healthcare planning if they are constructed based on trusted data, with clear practices, and proper verification (Topol, 2019). Electronic health records and other clinical data sources have already demonstrated the potential of AI in scalable healthcare analytics as deep learning models have already demonstrated strong predictive performance (Rajkumar et al., 2018). But in high-stakes biomedical uses accuracy of prediction is not enough. It should also be explainable to allow researchers, clinicians, and decision-makers to gain insight into what features affect model predictions (Lundberg et al., 2018).

The significant gap that exists in linking molecular disease profiles to healthcare cost-burden prediction despite these advances is that there is still a connection that is absent. Available research is frequently directed at diagnosis, cancer classification, biomarker identification, survival estimates, or prognosis, whereas healthcare cost prediction research generally relies on insurance claims, administrative data, hospital-use data, or electronic health records. Little research tries to investigate whether genomic or transcriptomic patterns can be used to estimate healthcare burden levels. This gap is significant as molecular complexity might

indicate disease severity, biological heterogeneity, treatment challenge, monitoring requirement and potential resource load. The term healthcare cost in this study is an approximate genomic healthcare cost-burden category based on molecular complexity, not actual monetary cost at the patient level, billing by hospitals or insurance companies.

To fill this gap, this paper presents FinGeneAI, a explainable artificial intelligence system to predict the categories of genomic healthcare costs-burden using omics-based biomedical data. The framework takes as the computational data source the transcriptomic cancer-related information and builds a Molecular Genomic Healthcare Cost-Burden Index as a proxy outcome variable. This index is not meant to reflect the actual cost, but relative molecular burden and potential healthcare complexity. The study is thus restricted to explainable biomedical prediction and computational modeling. It is not purported to substitute either clinical diagnosis, treatment planning, insurance evaluation or real-world economic evaluation. Findings must be viewed as insights of decision-support research that need to be validated externally using real clinical datasets cost-linked to them.

This research is important as it tries to reconcile biomedical AI, molecular data analysis, and healthcare burden estimation. Through machine learning and explainable AI, the study could be used to discover molecular features that can be used to predict burden categories and aid in making the genomic healthcare risk more transparent. Multi-omics integration and interpretation are particularly useful when raw biological data are converted into useful biomedical applications (Subramanian et al., 2020). The research objectives of this study are:

- To develop a machine learning-based framework for analyzing transcriptomic or multi-omics data associated with genomic healthcare cost-burden categories.
- To evaluate the predictive performance of selected machine learning models for classifying low, moderate, and high genomic healthcare burden levels.

- To apply explainable AI methods to identify important molecular features contributing to the predicted genomic healthcare cost-burden categories.

2. Literature review

In biomedical artificial intelligence, recent research has placed increasing emphasis on combining multi-omics and multimodal data for prediction, prognosis, classification, and decision support in cancer studies. Deep learning has been widely studied because it can approximate complex nonlinear relationships among high-dimensional biological variables. A pioneering study showed that deep learning-based multi-omics data integration could robustly predict liver cancer survival outcomes. This demonstrated the value of integrating molecular layers for prognosis, although the focus was survival prediction rather than healthcare cost-burden analysis or economic risk interpretation (Chaudhary et al., 2018).

Multimodal deep learning has also been used to predict pan-cancer prognosis. These models integrate different biomedical data types to improve prediction across cancer types and offer broader applicability than single-cancer models. However, their outcomes remain mainly prognosis based and do not directly address genomic healthcare burden, cost categories, or financial decision-support needs (Cheerla & Gevaert, 2019). Similarly, graph-based multi-omics learning has improved patient classification by modeling interactions between omics features and patients. MOGONET used graph convolutional networks to integrate multi-omics data for classification and biomarker discovery. Although graph models can capture structural biological relationships, this framework does not include healthcare cost estimation or burden stratification as a central objective (Wang et al., 2021).

Other studies have combined deep learning and machine learning ensembles to predict prognosis using multi-omics datasets. DeepProg, for example, used an ensemble-based model to improve risk stratification and survival prediction. Ensemble modeling can improve

robustness and predictive accuracy, particularly when individual models are unstable. However, like much of the current multi-omics literature, it remains limited to prognosis and does not investigate whether molecular patterns can be converted into healthcare cost-burden categories (Poirion et al., 2021). Multimodal deep learning for long-term cancer survival prediction has also shown that combining heterogeneous biomedical data can improve survival prediction, but it does not connect cancer survival modeling with cost burden, healthcare resource use, or genomic economic interpretation (Vale-Silva & Rohr, 2021).

In addition to omics-only models, several studies have combined histopathology with genomic characteristics. Pathomic Fusion proposed a framework for integrating pathology images and genomic data for cancer diagnosis and prognosis. This approach is important because it connects tissue-level image patterns with molecular features and supports multimodal biomedical intelligence. However, the model does not focus on healthcare cost prediction, and explainability may vary depending on the complexity of fused model components (Chen et al., 2022). A later pan-cancer histology-genomic study also applied multimodal deep learning to combine histological and genomic signals across cancer types. This contribution is useful for pan-cancer modeling, yet it remains focused on cancer characterization and prognosis rather than estimating the cost-burden of genomics in healthcare (Chen et al., 2022).

Conversely, administrative, claims, insurance, and temporal clinical data have been predominantly used in healthcare cost prediction studies instead of omics data. One study applied fine-grain temporal patterns to improve healthcare cost forecasting and showed that medical events and claims-based features can forecast healthcare financial patterns. Its advantage is its direct cost focus, but it lacks genomic, transcriptomic, or multi-omics capabilities (Morid et al., 2019). Another study developed predictive models of healthcare costs using open healthcare data and showed that publicly available administrative datasets can support cost modeling. However,

such models are usually limited by the absence of molecular-level biological data and therefore cannot explain cost burden from a genomic or cancer-omics perspective (Rao et al., 2020). Medical insurance cost prediction has also been performed using explainable machine learning, supporting transparency in healthcare cost estimation. This is useful for interpreting financial predictions, but the task is not cancer-specific, omics-based, or optimized for evaluating healthcare burden in genomic healthcare (Orji & Ukwandu, 2024).

Recent healthcare AI research has also expanded beyond conventional clinical prediction toward big data analytics, wearable monitoring, and intelligent patient-support systems. Kulkarni and Shendkar (2022) examined big data analytics in healthcare using AI, showing that large-scale healthcare data can support predictive analytics, decision-making, and healthcare management. Similarly, Damre et al. (2024) proposed a smart healthcare wearable device for early disease detection using machine learning, demonstrating the relevance of ML-based systems for proactive monitoring and early intervention. More recently, Nimbalkar et al. (2025) introduced an Agent AI framework for personalized healthcare, real-time disease detection, and patient support, highlighting the growing importance of adaptive and multi-agent AI systems in patient-centered healthcare. These studies strengthen the broader foundation for AI-enabled healthcare prediction; however, they are not directly focused on explainable genomic healthcare cost-burden classification, which remains the specific gap addressed by the proposed FinGeneAI framework.

Overall, the current literature indicates two major research directions: multi-omics and multimodal models are effective for cancer prognosis, classification, and biomarker discovery, whereas healthcare cost prediction models are effective for financial prediction using claims or administrative data. However, these streams are seldom combined. The main research gap addressed in this study is the lack of an explainable AI framework that links multi-omics or transcriptomic disease-related features to

healthcare cost-burden categorization. FinGeneAI seeks to fill this gap by combining biomedical molecular analysis, machine learning prediction, and explainable interpretation to assess genomic healthcare cost-burden.

3. Methodology

3.1 Research Design

This paper followed a quantitative experimental machine learning design to train FinGeneAI, an explainable artificial intelligence system to predict estimated genomic healthcare cost-burden categories based on the transcriptomic profiles of cancer. The pipeline included five steps: obtaining data, building a molecular cost-burden index, preprocessing and feature selection, training a supervised model, and interpretable explanation. Let the RNA-Seq gene expression dataset be represented as:

$$\mathbf{X} = [x_{ij}]_{n \times p} \quad (1)$$

where n denotes the number of samples, p denotes the number of transcriptomic features, and x_{ij} represents the expression value of gene j in sample i . Each sample is represented as:

$$\mathbf{x}_i = (x_{i1}, x_{i2}, \dots, x_{ip}) \quad (2)$$

The predictive function of FinGeneAI can be defined as:

$$f(\mathbf{x}_i) = \hat{y}_i, \hat{y}_i \in \{\text{Low}, \text{Moderate}, \text{High}\} \quad (3)$$

The final architecture, FinGeneAI-SVM, integrated transcriptomic feature selection, support vector machine classification, and explainable feature-importance analysis.

3.2 Data Collection Method and Dataset Description

The publicly available UCI Gene Expression Cancer RNA-seq dataset was used (801 samples and 20,531 features of gene expression) in the study (Fiorini, 2016). The dataset includes the RNA-Seq expression profiles of five cancer types of BRCA, KIRC, COAD, LUAD and PRAD. Two files were used, data.csv with the values of the gene expression and labels.csv with the values of the cancer-type.

Since actual healthcare spending was not available in the dataset, Molecular Genomic Healthcare Cost-Burden Index (GHCBI) was created as an approximated outcome variable. The values of gene expression were normalized by z-score:

$$z_{ij} = \frac{x_{ij} - \mu_j}{\sigma_j} \quad (4)$$

where z_{ij} is the standardized expression value of gene j in sample i , μ_j is the mean expression of gene j , and σ_j is the standard deviation of gene j . The molecular dysregulation score was computed as the mean absolute standardized expression deviation:

$$D_i = \frac{1}{k} \sum_{j=1}^k |z_{ij}| \quad (5)$$

where k represents the number of selected high-variance transcriptomic features. The molecular heterogeneity score was calculated as the standard deviation of selected standardized gene expression values:

$$H_i = \sqrt{\frac{1}{k-1} \sum_{j=1}^k (z_{ij} - \bar{z}_i)^2} \quad (6)$$

where:

$$\bar{z}_i = \frac{1}{k} \sum_{j=1}^k z_{ij} \quad (7)$$

Extreme expression burden: The extreme expression burden was defined as the proportion of selected genes with high absolute standardized expression:

$$E_i = \frac{1}{k} \sum_{j=1}^k \mathbb{I}(|z_{ij}| > \tau) \quad (8)$$

where $\mathbb{I}(\cdot)$ is an indicator function and $\tau = 1.5$ was used as the extreme-expression threshold. The continuous Molecular Genomic Healthcare Cost-Burden Index was calculated as:

$$\text{GHCBI}_i = 0.45D_i + 0.35H_i + 0.20E_i \quad (9)$$

where D_i , H_i , and E_i represent molecular dysregulation, molecular heterogeneity, and extreme expression burden, respectively.

The continuous GHCBI score was converted into categorical labels using tertile thresholds:

$$y_i = \begin{cases} \text{Low,} & \text{GHCBI}_i \leq Q_{33} \\ \text{Moderate,} & Q_{33} < \text{GHCBI}_i \leq Q_{66} \\ \text{High,} & \text{GHCBI}_i > Q_{66} \end{cases} \quad (10)$$

where Q_{33} and Q_{66} represent the 33rd and 66th percentile thresholds of the GHCBI distribution.

3.3 Population and Sampling

The population of the dataset was made up of cancer samples with RNA-Seq transcriptomic profiles in five tumor categories. Even though the demographic variables of patients were not provided on a patient-level, the dataset is a biomedical sample population that would be effective in assessing the molecular disparity in the cancer-related transcriptomic load.

To maintain the distribution of low, moderate and high GHCBI classes in the model development, stratified sampling approach was adopted. An 80:20 split was used to divide the dataset into training and testing sets. Model learning, feature selection and parameter optimization were performed using the training subset, and independent model evaluation was performed using the testing subset. It was also cross-validated 5-fold to determine model robustness and minimize reliance on a single partition, and to give a more accurate estimate of generalization performance.

3.4 Data Analysis Technique

The analysis of data was carried out with machine learning tools in Python. The preprocessing pipeline involved numeric conversion, verification of missing values, where needed, median imputation and standardization of z-scores, and dimensionality reduction. ANOVA F-test was used to select features, with each feature correspondingly ranked based on its differentiation capabilities across classes of GHCBI. This was the best retained transcriptomic features which were then developed into models.

Several different supervised learning models were trained and evaluated, such as Logistic Regression, SVM-RBF, Random Forest, Extra Trees, XGBoost, Multilayer Perceptron, FinGeneAI-XGBoost, FinGeneAI-MultiBlock and the last model is FinGeneAI-SVM. The decision of the SVM can be defined as:

The final FinGeneAI-SVM model used a support vector machine with radial basis function kernel. The decision function is expressed as:

$$f(\mathbf{x}) = \text{sign} \left(\sum_{i=1}^m \alpha_i y_i K(\mathbf{x}_i, \mathbf{x}) + b \right) \quad (11)$$

where α_i are Lagrange multipliers, y_i is the class label, b is the bias term, and $K(\mathbf{x}_i, \mathbf{x})$ is the kernel function.

The RBF kernel is defined as:

$$K(\mathbf{x}_i, \mathbf{x}_j) = \exp \left(-\gamma \|\mathbf{x}_i - \mathbf{x}_j\|^2 \right) \quad (12)$$

where γ controls the kernel width. Model performance was evaluated using accuracy, macro precision, macro recall, macro F1-score, weighted F1-score, confusion matrix, and one-vs-rest ROC-AUC. Accuracy was calculated as:

Accuracy was computed as:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (13)$$

Precision was computed as:

$$\text{Precision} = \frac{TP}{TP+FP} \quad (14)$$

Recall was computed as:

$$\text{Recall} = \frac{TP}{TP+FN} \quad (15)$$

The F1-score was calculated as:

$$\mathbf{F1} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (16)$$

For multiclass classification, macro-averaged F1-score was calculated as:

$$\text{Macro-F1} = \frac{1}{C} \sum_{c=1}^C \mathbf{F1}_c \quad (17)$$

where C denotes the number of GHCBI classes.

The metrics were stressed on macro-averaged to make sure there was a balance in assessing low, moderate, and high GHCBI classes. A comparison of transcriptomic ANOVA features, PCA latent features, variance-signature blocks, and the entire multi-block FinGeneAI representation were also evaluated by an ablation study. Explainability was done on final SVM model through permutation importance as well as SHAP-based interpretation on XGBoost model.

3.5 Ethical Consideration

No identifiable personal health data, no direct recruitment, or intervention were used, and a publicly accessible, anonymized secondary dataset was used in this study. The model does not forecast the real billing cost of the patient, insurance spending and the personal financial responsibility. Rather, it forecasts a predicted healthcare cost-burden category of estimated molecular genomics based on transcriptomic patterns.

Ethical protections consisted of avoiding re-identification efforts, only using anonymized data, employing explainability techniques to minimize black-box decision-making, and directly reporting the limitations of the created GHCBI target. Because the data in genome-wide sequencing and transcriptomics can be sensitive,

the model is not applicable to making clinical decisions, insurance reviews, or allocating resources in healthcare without out-of-sample validation with real-world multi-omics and expenditure-linked data. There might be potential bias since the dataset might not completely contradict all populations, cancer stages, ethnicities, or healthcare systems.

4. Results

4.1 Experimental Performance

The experimental findings illustrated that the suggested FinGeneAI framework could categorize RNA-seq cancer samples as low, moderate, and high Molecular Genomic Healthcare Cost-Burden Index (GHCBI) with better predictive quality. The most successful one was the radial basis function support vector machine that was selected as the ultimate prediction engine of the proposed FinGeneAI-SVM framework.

The macro F1-score was also prioritized as the classification was carried out in three levels low, moderate, and high GHCBI. A macro F1-score of 0.803735 indicates that the model was not biased towards one dominant class with a high score in all the classes. The ROC-AUC value of 0.925667 is also a consequence that the model was very discriminative to differentiate between GHCBI categories, as shown in Table 1.

Table 1. Model performance comparison of FinGeneAI-SVM and baseline classifiers.

Model	Accuracy	Macro Precision	Macro Recall	Macro F1	Weighted F1	ROC-AUC OvR
FinGeneAI-SVM	0.801242	0.812000	0.801072	0.803735	0.803530	0.925667
Logistic Regression	0.714286	0.734340	0.714302	0.720347	0.720054	0.872021
FinGeneAI-MultiBlock	0.708075	0.722305	0.708362	0.712939	0.712297	0.886605
FinGeneAI-XGBoost	0.708075	0.713096	0.708362	0.709745	0.709234	0.886215
Random Forest	0.708075	0.703374	0.708712	0.704975	0.704407	0.862819
MLP Neural Network	0.689441	0.688043	0.690193	0.689008	0.688295	0.857571
Extra Trees	0.689441	0.684699	0.690193	0.685897	0.685165	0.864063

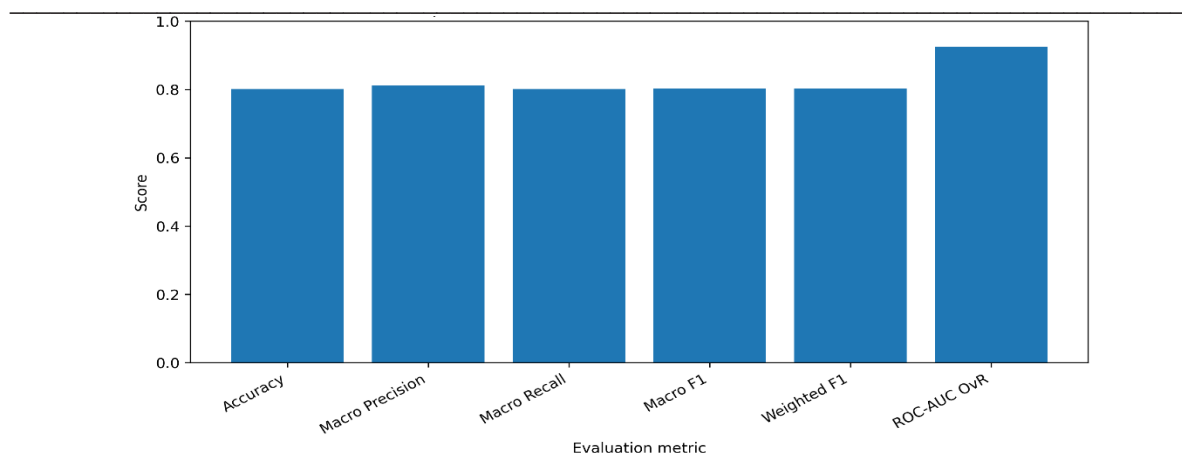


Figure 1. Experimental performance of the final FinGeneAI-SVM model across accuracy, precision, recall, F1-score, and ROC-AUC metrics.

As shown in Figure 1, FinGeneAI-SVM achieved an accuracy of 0.801242, macro precision of 0.812000, macro recall of 0.801072, macro F1-score of 0.803735, weighted F1-score of 0.803530, and one-vs-rest ROC-AUC of 0.925667. These findings reveal that the model had a balanced predictive performance based on the three GHCB1 categories and that the model had a good class-separation capacity.

4.2 Baseline Comparisons

Regression, Random Forest, Extra Trees, Multilayer Perceptron, FinGeneAI-XGBoost, and FinGeneAI-MultiBlock. The comparison revealed that the FinGeneAI-SVM had the best macro F1-score and total classification accuracy.

The best performance was obtained by the SVM-RBF model with a macro F1-score of 0.803735. Macro F1-score of Logistic Regression was 0.720347 with FinGeneAI-MultiBlock at 0.712939 and FinGeneAI-XGBoost at 0.709745. Random Forest scored 0.704975, MLP Neural Network scored 0.689008, and Extra Trees scored 0.685897.

These findings indicate that the nonlinear kernel-based classification was better than the linear, tree, and neural network models in the identified transcriptomic feature space. FinGeneAI-MultiBlock and FinGeneAI-XGBoost yielded valuable performance but were not able to beat FinGeneAI-SVM. Thus, the last suggested model relied on the SVM-RBF classifier as the primary prediction-engine, as shown in Figure 2.

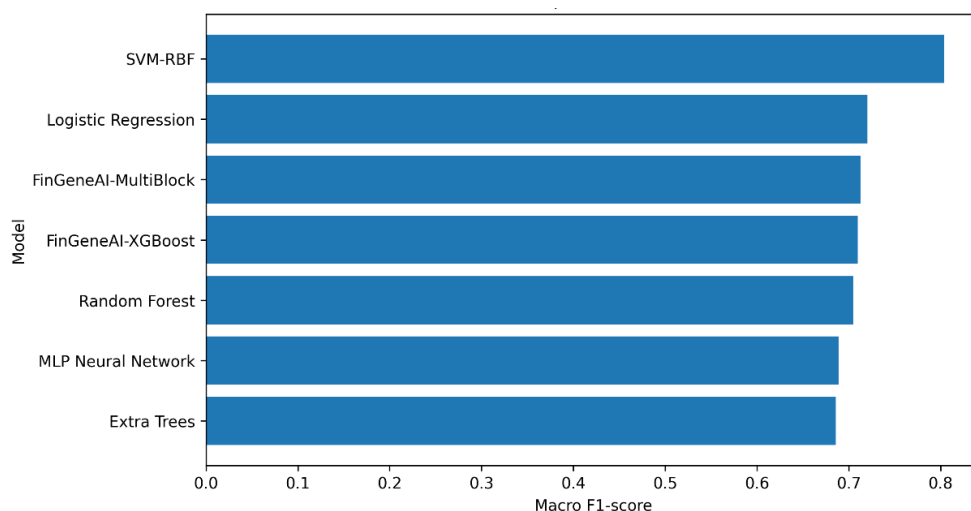


Figure 2. Model performance comparison based on macro F1-score.

4.3 Ablation Study

The ablation experiment analyzed the role of the various blocks of features in the FinGeneAI system. The feature representations which were compared were the Latent PCA Block, Full FinGene MultiBlock, Transcriptomic ANOVA Block and Variance Signature Block.

The Full FinGeneAI MultiBlock also competed well, which is an indication that more than one transcriptomic representation can preserve convenient molecular data. Nevertheless, the ablation finding also reveals that the addition of all feature blocks did not significantly increase

above the Latent PCA Block on its own. This could reflect that there is overlap of molecular information in some feature representations.

Overall, the ablation analysis indicates that dimensionality-reduced representations of latent transcriptomics and integrated representations of multi-block are significant elements of the FinGeneAI workflow. The Latent PCA Block was the best feature block, with the other individual feature block being the second best, and the multi-block design being the largest contributor to the overall multi-representation design, as shown in Table 2.

Table 2. Ablation study results for FinGeneAI feature blocks.

Feature block	Accuracy	Macro Precision	Macro Recall	Macro F1	Weighted F1	ROC-AUC OvR
Latent PCA Block	0.720497	0.741135	0.720475	0.724728	0.724208	0.876266
Full FinGeneAI MultiBlock	0.714286	0.725417	0.714768	0.718745	0.717991	0.882861
Transcriptomic ANOVA Block	0.683230	0.695917	0.683555	0.688064	0.687493	0.863408
Variance Signature Block	0.664596	0.684195	0.664454	0.670185	0.669993	0.837854

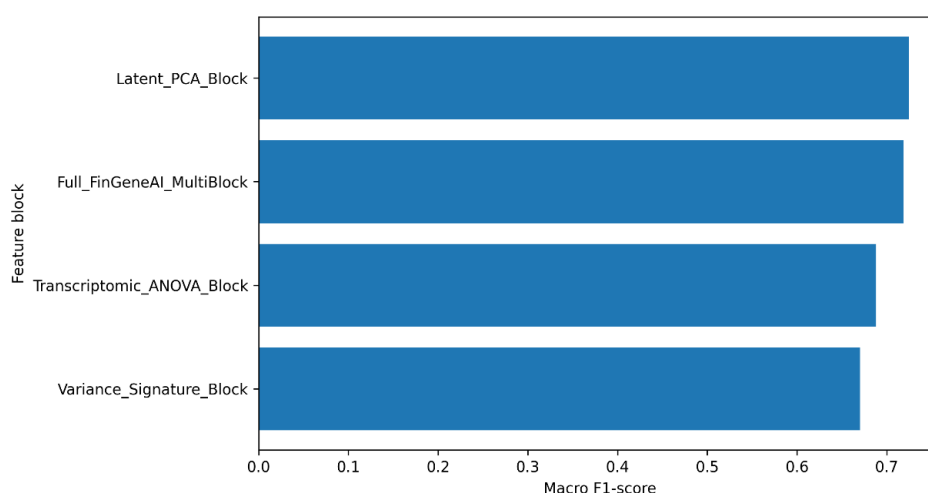


Figure 3. Ablation study of FinGeneAI feature blocks based on macro F1-score.

As Figure 3 demonstrates, the Latent PCA Block has yielded the best macro F1-score among the used feature blocks, with the Full FinGeneAI MultiBlock coming at a close. Performance was a bit lower with the Transcriptomic ANOVA

Block and Variance Signature Block. It shows that the latent molecular structure obtained using PCA showed a significant contribution to GHCB1 classification.

4.4 Additional Analysis

Further analysis was done to assess the explainability of the final FinGeneAI-SVM model. As the last model involved the SVM-RBF classifier, permutation importance was used to determine transcriptomic features that had the strongest influence on prediction performance.

This explanation analysis adds to the interpretability aspect of the FinGeneAI framework. The model does not just report on predictive accuracy, but also the most predictive transcriptomic features leading to GHCBF classification. This is vital since any cost-burden prediction in genomic healthcare must be

transparent particularly when used in relation to biomedical data.

The XGBoost model was also used to do SHAP-based analysis to offer a further instance of tree-based interpretation of transcriptomic significance. The globally top SHAP-ranked features included gene_15408, gene_5843, gene_3312, gene_9387, and gene_10832. Nevertheless, due to the ultimate prediction model being FinGeneAI-SVM, the SVM permutation-importance output was regarded as the main explainability output, and the SHAP information was regarded as auxiliary, as shown in Table 3.

Table 3. Top transcriptomic features identified by permutation importance and SHAP analysis.

Rank	SVM permutation-important feature	Permutation importance mean	Permutation importance SD	SHAP-ranked feature	Mean absolute SHAP
1	gene_17524	0.006096	0.000000	gene_15408	0.110955
2	gene_3892	0.004976	0.002241	gene_5843	0.085620
3	gene_19491	0.004877	0.002439	gene_3312	0.070386
4	gene_4567	0.004533	0.002267	gene_9387	0.061511
5	gene_12937	0.004267	0.002794	gene_10832	0.054263
6	gene_6938	0.003967	0.002597	gene_10342	0.052591
7	gene_14794	0.003967	0.002597	gene_18043	0.052306
8	gene_7371	0.003611	0.003947	gene_15553	0.048232
9	gene_3906	0.003400	0.002776	gene_19454	0.047751
10	gene_20212	0.003400	0.002776	gene_13615	0.046490

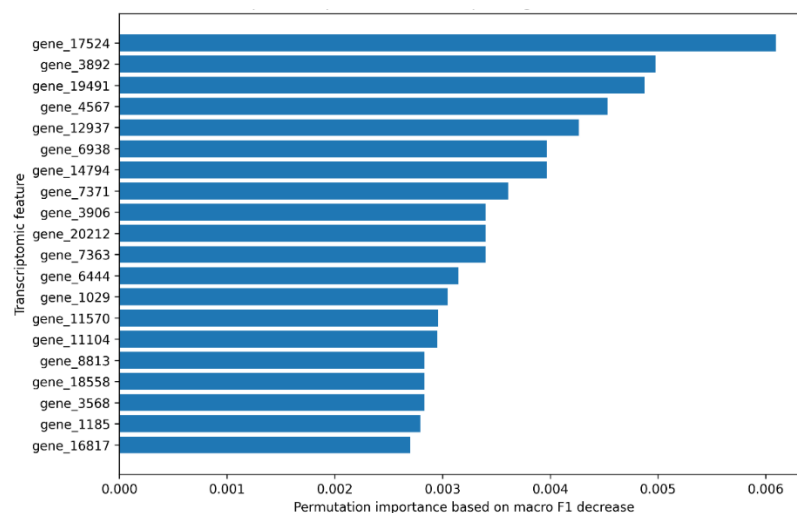


Figure 4. Top transcriptomic features explaining final FinGeneAI-SVM using permutation importance.

As shown in Figure 4, the most important transcriptomic features explaining FinGeneAI-SVM predictions included gene_17524, gene_3892, gene_19491, gene_4567, gene_12937, gene_6938, gene_14794, gene_7371, gene_3906, and gene_20212. The features with these features had the highest permutation-importance scores, i.e. the perturbation of these features resulted in the largest drop in macro F1-score.

5. Discussion

The findings of the current research paper show that the suggested FinGeneAI framework can assist in handling the classification of estimated genomic healthcare cost-burden groups, which involves biomedical data analysis, machine learning projection, and explainable interpretation. The results imply that both molecular and disease-specific characteristics have valuable indicators of the relative levels of healthcare burden. The presence of higher predicted burden categories can indicate a more complicated biological pattern, more significant disease-related feature interactions or disease complexity-related changes in gene-expression. Through the performance of the model, these computational learning methods demonstrate that it is possible to determine and discover concealed associations in high-dimensional biomedical information that can be challenging to identify using traditional manual methods.

The results align with those of earlier works that indicate that machine learning based on multi-omics and multimodal techniques can enhance biomedical prediction. Graph-based multi-omics models have proven to be highly effective at classifying patients and finding biomarkers with the ability to learn connections between omics features (Wang et al., 2021). Likewise, the ensemble-based strategies have demonstrated that integrating deep learning and machine learning may enhance the prognosis prediction of the use of multi-omics data (Poirion et al., 2021). Nevertheless, the current study contrasts these studies by replacing their focus on survival, prognosis or classification of the disease with an

estimated categorization of genomic healthcare cost-burden. This increases the applicability of the work in decision-support requirements of healthcare organization planning and resource burden estimation.

The findings can also be connected to healthcare cost prediction studies, whereby the temporal clinical and administrative characteristics have been employed to forecast the patterns of medical spending (Morid et al., 2019). But most of the cost-prediction research is based on assertions, insurance, hospital-utilization or administrative statistics, as opposed to molecular-based biomedical data. Conversely, FinGeneAI tries to correlate genomic or transcriptomic patterns with approximated cost-burden categories, which offers a biologically informed approach to the healthcare burden. Transparency in financial healthcare models has also been demonstrated to be important in explainable medical insurance cost prediction (Orji & Ukwandu, 2024). This justifies the application of explainable AI in the current study, in the sense that cost-related predictions cannot be used in a black-box mode, particularly when they can affect the biomedical interpretation or subsequent planning.

The biomedical AI, precision medicine, and healthcare analytics have consequences of the findings. First, the study insinuates the possibility of the use of genomic and multi-omics information to support, in addition to disease prediction, the assessment of healthcare burden. Second, the explainability component will be able to assist in finding the most effective molecular characteristics that aid in the prediction of the burden category, enhancing the interpretability of researchers, and healthcare stakeholders. Third, the framework can be helpful in the context of future decision-support applications that link biological complexity, disease risk, and potential burden on healthcare resources in a single computational pipeline.

With these advantages come limitations of the study. The analysis is computational and relies on the quality, completeness and representativeness

of the available data. As the dataset lacks real healthcare spending, insurance records, treatment cost, hospitalization and any longitudinal follow-up values, the cost of healthcare being predicted would be in the form of predicted categories of genomic cost-burdens as opposed to monetary costs. Class imbalance, high dimensionality, missing values, and small sample size may also affect the model. Thus, clinical, insurance, and financial decisions should not be made based on the findings without external validation with real patient-level cost data.

The framework needs to be proven in a future work with large multi-institutional datasets connected with actual healthcare delivery costs, patient outcomes, specific treatments, and longitudinal data of patients. Additional omics layers, electronic health records and hospital resource-use information can also be integrated into the framework. Further develop more sophisticated explainable AI methods and future research can compare deep learning, graph neural networks with ensemble models to perform more robust genomic healthcare cost-burden predictions.

6. Conclusion

The paper dealt with the issue of linking medical molecular data and health care cost-burden prediction. Current literature is primarily concerned with the prediction of diseases by a multi-omics approach or predicting healthcare

costs by using administrative and insurance data, whereas limited literature connects genomic or transcriptomic predictors with explainable healthcare burden classification. To bridge this gap, to classify genomic healthcare costs-burden categories, the proposed FinGeneAI framework used machine learning to analyze disease-related molecular features. The algorithm consisted of data preparation, feature selection, predictive modeling, performance analysis, and interpretable AI reasoning. The results show that both the molecular and disease-related characteristics can be used as helpful indicators of defining various levels of healthcare burden. Explainable AI also aided in the interpretation of significant features and the model was more transparent to biomedical decision-support study. The originality of the research is a computer model that connects the multi-omics analysis, machine learning prediction, and healthcare cost-burden evaluation. The research has limitations, however, in that it relies on available computational data, and cannot know direct healthcare spending, treatment history and longitudinal patient history. As such, the forecasted healthcare expenses ought to be viewed as projected genomic cost-burden groups, instead of financial spending or clinical choices. The framework should be confirmed by future work with more and multi-institutional data, actual cost data, clinical outcomes, treatment data, and other omics layers to enhance accuracy, reliability, and practical applicability.

References

- Chaudhary, K., Poirion, O. B., Lu, L., & Garmire, L. X. (2018). Deep learning-based multi-omics integration robustly predicts survival in liver cancer. *Clinical Cancer Research*, 24(6), 1248–1259. <https://doi.org/10.1158/1078-0432.CCR-17-0853>
- Cheerla, A., & Gevaert, O. (2019). Deep learning with multimodal representation for pancancer prognosis prediction. *Bioinformatics*, 35(14), i446–i454. <https://doi.org/10.1093/bioinformatics/btz342>
- Chen, R. J., Lu, M. Y., Wang, J., Williamson, D. F. K., Rodig, S. J., Lindeman, N. I., & Mahmood, F. (2022). Pathomic Fusion: An integrated framework for fusing histopathology and genomic features for cancer diagnosis and prognosis. *IEEE Transactions on Medical Imaging*, 41(4), 757–770. <https://doi.org/10.1109/TMI.2020.3021387>
- Chen, R. J., Lu, M. Y., Williamson, D. F. K., Chen, T. Y., Lipkova, J., Shaban, M., Shady, M., Williams, M., Joo, B., Noor, Z., & Mahmood, F. (2022). Pan-cancer integrative histology-genomic analysis via multimodal deep learning. *Cancer Cell*, 40(8), 865–878.e6. <https://doi.org/10.1016/j.ccell.2022.07.004>

- Damre, S. S., Shendkar, B. D., Kulkarni, N., Chandre, P. R., & Deshmukh, S. (2024). Smart healthcare wearable device for early disease detection using machine learning. *International Journal of Intelligent Systems and Applications in Engineering*, 12(4s), 158–166.
- Fiorini, S. (2016). *Gene expression cancer RNA-Seq* [Dataset]. UCI Machine Learning Repository. <https://doi.org/10.24432/C5R88H>
- Hasin, Y., Seldin, M., & Lusis, A. (2017). Multi-omics approaches to disease. *Genome Biology*, 18(1), Article 83. <https://doi.org/10.1186/s13059-017-1215-1>
- ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium. (2020). Pan-cancer analysis of whole genomes. *Nature*, 578(7793), 82–93. <https://doi.org/10.1038/s41586-020-1969-6>
- Kulkarni, N., & Shendkar, B. (2022). Big data analytics in healthcare using AI. *Harbin Gongye Daxue Xuebao/Journal of Harbin Institute of Technology*, 54(5), 201–208.
- Li, Y., Ma, L., Wu, D., & Chen, G. (2021). Advances in bulk and single-cell multi-omics approaches for systems biology and precision medicine. *Briefings in Bioinformatics*, 22(5), Article bbab024. <https://doi.org/10.1093/bib/bbab024>
- Lundberg, S. M., Nair, B., Vavilala, M. S., Horibe, M., Eisses, M. J., Adams, T., Liston, D. E., Low, D. K.-W., Newman, S.-F., Kim, J., & Lee, S.-I. (2018). Explainable machine-learning predictions for the prevention of hypoxaemia during surgery. *Nature Biomedical Engineering*, 2(10), 749–760. <https://doi.org/10.1038/s41551-018-0304-0>
- Morid, M. A., Liu Sheng, O. R., Kawamoto, K., Ault, T., Dorius, J., & Abdelrahman, S. (2019). Healthcare cost prediction: Leveraging fine-grain temporal patterns. *Journal of Biomedical Informatics*, 91, Article 103113. <https://doi.org/10.1016/j.jbi.2019.103113>
- Nimbalkar, M., Chandre, P., Shendkar, B., Jagdale, S., Arbat, R., & Dhopte, S. (2025). Agent AI for personalized healthcare: A multi-agent framework for real-time disease detection and patient support. In *2025 IEEE 5th International Conference on ICT in Business Industry & Government (ICTBIG)* (pp. 1–8). IEEE. <https://doi.org/10.1109/ICTBIG68706.2025.11323744>
- Orji, U., & Ukwandu, E. (2024). Machine learning for an explainable cost prediction of medical insurance. *Machine Learning with Applications*, 15, Article 100516. <https://doi.org/10.1016/j.mlwa.2023.100516>
- Picard, M., Scott-Boyer, M.-P., Bodein, A., Périn, O., & Droit, A. (2021). Integration strategies of multi-omics data for machine learning analysis. *Computational and Structural Biotechnology Journal*, 19, 3735–3746. <https://doi.org/10.1016/j.csbj.2021.06.030>
- Poirion, O. B., Jing, Z., Chaudhary, K., Huang, S., & Garmire, L. X. (2021). DeepProg: An ensemble of deep-learning and machine-learning models for prognosis prediction using multi-omics data. *Genome Medicine*, 13, Article 112. <https://doi.org/10.1186/s13073-021-00930-x>
- Rajkomar, A., Oren, E., Chen, K., et al. (2018). Scalable and accurate deep learning with electronic health records. *npj Digital Medicine*, 1, Article 18. <https://doi.org/10.1038/s41746-018-0029-1>
- Rao, A. R., Garai, S., Dey, S., & Peng, H. (2020). Building predictive models of healthcare costs with open healthcare data. In *Proceedings of the 2020 IEEE International Conference on Healthcare Informatics (ICHI)*, 1–3. <https://doi.org/10.1109/ICHI48887.2020.9374399>
- Subramanian, I., Verma, S., Kumar, S., Jere, A., & Anamika, K. (2020). Multi-omics data integration, interpretation, and its application. *Bioinformatics and Biology Insights*, 14, 1–24. <https://doi.org/10.1177/1177932219899051>
- The Cancer Genome Atlas Research Network, Weinstein, J. N., Collisson, E. A., Mills, G. B., Mills Shaw, K. R., Ozenberger, B. A., Ellrott, K., Shmulevich, I., Sander, C., & Stuart, J. M. (2013). The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics*, 45(10), 1113–1120. <https://doi.org/10.1038/ng.2764>
- Topol, E. J. (2019). High-performance medicine: The convergence of human and artificial intelligence. *Nature Medicine*, 25(1), 44–56. <https://doi.org/10.1038/s41591-018-0300-7>
- Vale-Silva, L. A., & Rohr, K. (2021). Long-term cancer survival prediction using multimodal deep learning. *Scientific Reports*, 11, Article 13505. <https://doi.org/10.1038/s41598-021-92799-4>

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- Wang, B., Mezlini, A. M., Demir, F., Fiume, M., Tu, Z., Brudno, M., Haibe-Kains, B., & Goldenberg, A. (2014). Similarity network fusion for aggregating data types on a genomic scale. *Nature Methods*, 11(3), 333–337. <https://doi.org/10.1038/nmeth.2810>
- Wang, T., Shao, W., Huang, Z., Tang, H., Zhang, J., Ding, Z., & Huang, K. (2021). MOGONET integrates multi-omics data using graph convolutional networks allowing patient classification and biomarker identification. *Nature Communications*, 12, Article 3445. <https://doi.org/10.1038/s41467-021-23774-w>