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Designing Explainable Deep Learning Models for Biomedical Data Analysis and Clinical Prediction Enhancement

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Abstract

Recent advancements in biomedical data analysis have significantly transformed clinical decision-making. However, the inherent complexity and heterogeneity of healthcare data continue to present major challenges. Traditional deep learning models, while powerful, often lack transparency, limiting their adoption in clinical settings due to their "black-box" nature. To address this critical gap, this study introduces a novel Explainable Deep Learning (XDL) framework that integrates high predictive accuracy with interpretability, enabling clinicians to trust and validate AI-driven insights. The proposed framework leverages advanced interpretability techniques—such as Grad-CAM for visual attribution and SHAP for feature importance analysis—to analyze multimodal biomedical data, including clinical imaging, genomic sequencing, and electronic health records. Experimental evaluations across three benchmark datasets demonstrated the model's strong performance, achieving an accuracy of 91%, sensitivity of 95.4%, specificity of 98.6%, and an AUC of 99%, while maintaining an interpretability score of 92% as rated by domain experts. Compared to non-explainable models, the proposed approach showed a 12.3% increase in interpretability and a 5.8% improvement in accuracy. Importantly, attention map analysis revealed alignment with clinically relevant biomarkers in 93% of cases and uncovered previously overlooked prognostic patterns in 18% of patient cohorts. These findings underscore the model's potential to enhance diagnostic precision and support more informed clinical decisions. Moreover, the algorithm reduced diagnostic time by 23% due to its provision of actionable insights. The hybrid approach—combining built-in attention mechanisms with external interpretability tools—ensures seamless integration into clinical workflows while supporting compliance with regulatory standards for transparency.

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1. Introduction

The modern technology of healthcare is a transformative shift driven by groundbreaking advancements in biomedical data analysis, which has emerged as a cornerstone for ailment diagnosis, precision treatment improvement, and affected person care management[1]. Deep gaining knowledge of deep learning, a subset of Artifitial intelligence (AI), has revolutionised the analysis of complicated biomedical datasets, achieving remarkable accuracy in tasks including scientific picture segmentation, genomic collection category, and predictive modelling of the use of Electronic Health Records (EHRs). Despite those technological tools, conventional DL (Deep Learning)fashions frequently feature as "black boxes," producing predictions without transparent explanations in their decision-making good judgment[2]. This lack of interpretability is a crucial barrier to their adoption in scientific workflows, in which beliefs, and regulatory compliance are non-negotiable. In high-stakes healthcare eventualities—which include diagnosing existence-threatening situations, personalising most cancer treatments, or predicting affected person outcomes—the lack of ability to validate AI-driven insights now not best risks patient safety but also undermines clinician self-belief and hinders regulatory approval processes[3]. Addressing this gap needs the development of explainable deep learning of (XDL) frameworks that increse

predictive accuracy with interpretability, empowering clinicians to apprehend, trust, and act upon AI-generated suggestions [4]. This research is pushed with the aid of the urgent need to bridge between algorithmic complexity and medical usability. The objective is to implement and carefully evaluate an XDL multimodal biomedical information analysis framework. The framework integrates modern-day interpretability techniques, including Gradient-weighted Class Activation Mapping (Grad-CAM) for visualising vital areas in clinical imaging and SHapley Additive exPlanations (SHAP) for quantifying feature importance in genomic and EHR datasets. By combining intrinsic interpretability mechanisms (e.g., self-attention layers in transformer architectures) with post-hoc clarification gear, the version targets to gain twin excellence: advanced predictive overall performance (measured via accuracy, sensitivity, and specificity) and clinically significant transparency (tested through domain-expert evaluations).

The research goals:

- Validate the framework across diverse biomedical datasets, including:
  - Radiology images (X-rays, CT scans)
  - Genomic sequences from cancer cohorts
  - Structured and unstructured electronic health records (EHRs)
- Organize quantifiable metrics to assess interpretability in alignment with clinician workflows.
- Conduct the study using publicly available datasets, such as:
  - NIH Chest X-ray repository
  - The Cancer Genome Atlas (TCGA)
  - Anonymized EHRs from partner institutions
- Ensure clinical relevance and practicality through collaboration with radiologists, oncologists, and data engineers.
- By unifying technical innovation with scientific pragmatism, this research advances the frontier of straightforward AI in healthcare, fostering collaborative surroundings in which information scientists and scientific professionals mutually pioneer answers that are as transparent as they're transformative.

The paper systematically as follows: section 2 lists all previous studies and their challenges and experimental results as a literature review, section 3 the new proposed methodology and the three-benchmark used in this research, section 4 shows the proposed methodology results and finding, section 5 the discussion section about the results and other previous work finally the section 6 with conclusion.

2. Literature Review

The growing application of Deep Learning (DL) in scientific information analysis has revolutionised disease analysis and patient control through its potential to extract complex styles from biomedical facts. Studies along with Sengupta, and Singh (2020) [5] have highlighted the transformative capability of deep neural networks (DNNs) in reaching extremely good accuracy in obligations like picture segmentation and class. However, the inherent opacity of those models has triggered a parallel attempt to enhance their interpretability through Explainable Artificial Intelligence (XAI) strategies.

Significant progress has been made in integrating XAI tools into DL pipelines. Local Interpretable Model-agnostic Explanations (LIME) have emerged as well-known, permitting model builders to approximate black-box behaviours domestically by perturbing enter statistics and assessing the results on outputs. Stano et al. (2019) [6] first tested the utility of LIME for deciphering category models in text and photograph domains, and its adaptations for scientific imaging have shown promise in identifying crucial features influencing predictions. Similarly, Arrieta et al. (2020) [7] delivered SHAP, a method leveraging game-theoretic standards to assign significance values to enter features. SHAP has received traction in comparing function contributions across biomedical responsibilities, including identifying gene expression markers associated with illnesses. Integrated Gradients, proposed by Arya et al. (2019) [8], offer any other important device by attributing the gradients of predictions again to enter functions, supporting clarifying their function in version choices. Recent advancements like Grad-CAM and its successors (Grad-CAM) have similarly better-visualised regions important to predictions in imaging-based packages, presenting saliency maps as intuitive motives for clinicians.

Despite these advancements, several critical gaps persist. While many research cognisance on accomplishing either excessive accuracy or interpretability, there's a lack of complete studies balancing both aspects for biomedical programs. For example, even though A Balasubramani, K , etl (2019) [9] efficaciously confirmed the usage of interpretable DL fashions for most cancers' detection, their models struggled to maintain competitive accuracy compared to trendy DNNs. Kina, E.et al. (2025) [10] emphasised the want for higher interpretability tools in uncommon sickness diagnosis; however did not cope with scalability and overall performance consistency throughout numerous datasets. Trust-associated

challenges have additionally been referred to; for example, Singh et al. (2020) [11] found that explainable systems using SHAP were insufficiently sturdy in high-dimensional information settings.

Moreover, few studies have bridged the gap between model transparency and medical applicability. Wang et al. (2020) [12] mentioned that current explainability techniques regularly produce motives intelligible handiest to AI professionals instead of area professionals like radiologists. Coupled with those challenges is the tendency of fashions to overfit specific datasets, as reported by Wickstrøm et al. (2020) [13], lowering their generalizability whilst deployed in heterogeneous clinical settings. Meanwhile, Bamba et al. (2020) [14] criticised present saliency-based XAI strategies, including Grad-CAM, for generating heatmaps that could deceive clinicians into over-counting AI outputs without understanding their obstacles.

Existing research hardly ever integrates domain-unique expertise with XAI techniques, a critical requirement in healthcare. For example, Y Hossain, et al. (2025) [15] included ontology-primarily based understanding graphs to enhance DL model explainability; however faced challenges aligning them with non-photo datasets. Similarly, Biffi et al. (2020) [16] recommended post-hoc interpretability for patient outcome prediction, yet those strategies frequently lack rigorous quantitative metrics to evaluate rationalisation first-class.

Addressing these gaps requires the development of XAI systems capable of simultaneous high accuracy and transparency[17,18]. A particularly pressing need exists for domain-agnostic approaches that integrate with existing healthcare workflows while remaining accessible to clinicians and interpretable for regulatory purposes[19]. Table .1 presents a summary of the previously mentioned studies.

Table 1: Summary Table of Prior Studies

Study	Focus Area	Methodology	Key Findings	Limitations
Sengupta, and Singh (2020)	DNN in Biomedical Imaging	Review	Highlighted use of Grad-CAM and SHAP for explainability.	Focused on imaging, lacking applicability to multimodal data.
Stano et al. (2019)	LIME Explanations	Perturbation Analysis	Introduced LIME for local model interpretability.	Less effective for high-dimensional data.
Arrieta et al. (2020)	SHAP for Model Interpretability	Game Theory	Emphasised feature importance in clinical datasets.	Computationally expensive for large datasets.
Arya et al. (2019)	Integrated Gradients	Gradient-based	Attributed feature importance to predictions effectively.	Lacked visual intuitiveness for clinicians.
Alber et al. (2019)	Cancer Detection	Saliency Maps	Achieved basic interpretability using Grad-CAM.	Model accuracy was significantly reduced.
Eitel et al. (2019)	Rare Disease Diagnosis	XAI Surveys	Outlined challenges in scalability for interpretability methods.	Overlooked tools for large dataset deployment.
Singh et al. (2020)	Model Robustness in High-Dimensional Data	SHAP Applications	Found SHAP poorly suited for large-scale medical datasets.	Limited testing environments.
Wang et al. (2020)	Model Generalisation	Comparative Model Analysis	Highlighted overfitting issues with current XAI methods.	Did not propose concrete solutions.
Wickstrøm et al. (2020)	Saliency Map Criticism	Grad-CAM and Variations	Discussed misuse of AI interpretations in healthcare workflows.	Did not propose corrective frameworks.

Bamba et al. (2020)	Ontology-Based Interpretability	Knowledge Graphs	Enhanced model interpretability using domain-specific information.	Applicability is limited to text datasets.
Yeche et al. (2019)	Patient Outcome Prediction	Post-hoc Techniques	Utilised explainability methods for outcome explanations.	Lacked quantitative evaluation benchmarks.
Biffi et al. (2020)	Clinician-Focused XAI	Human-Centric Evaluation	Highlighted inadequacy of XAI tools for non-expert users.	Limited focus on generalizability.

3. Methodology

This observation adopts a structured methodology to compare explainable deep gaining knowledge of (DL) fashions for biomedical information evaluation and clinical prediction enhancement[20,21]. The methodology is designated underneath, incorporating records types, model design, interpretability techniques, and performance assessment.

Proposed System Architecture

The proposed hybrid architecture (Figure 1) combines ResNet-50 for medical imaging, Vision Transformers for genomic data, and Bio BERT for EHR analysis. These components are interconnected through a unified interpretability layer integrating Grad-CAM for imaging saliency maps, SHAP for genomic/EHR function attribution, and custom know-how graphs to map clinical relevance. The system employs a dual-stream layout:

- **Stream 1 (Imaging & Genomics):** ResNet-50 extracts spatial features from radiology images, while Vision Transformers process gene sequences using self-attention mechanisms.
- **Stream 2 (EHR):** Bio BERT tokenises structured/unstructured EHR data (e.g., diagnosis codes, medication history) and identifies contextual relationships.
  A fusion layer aggregates outputs from both streams, followed by attention-weighted decision heads to generate predictions. The architecture is optimised via mixed-precision training and cyclic learning rates (0.001–0.0001) to balance computational efficiency and accuracy.

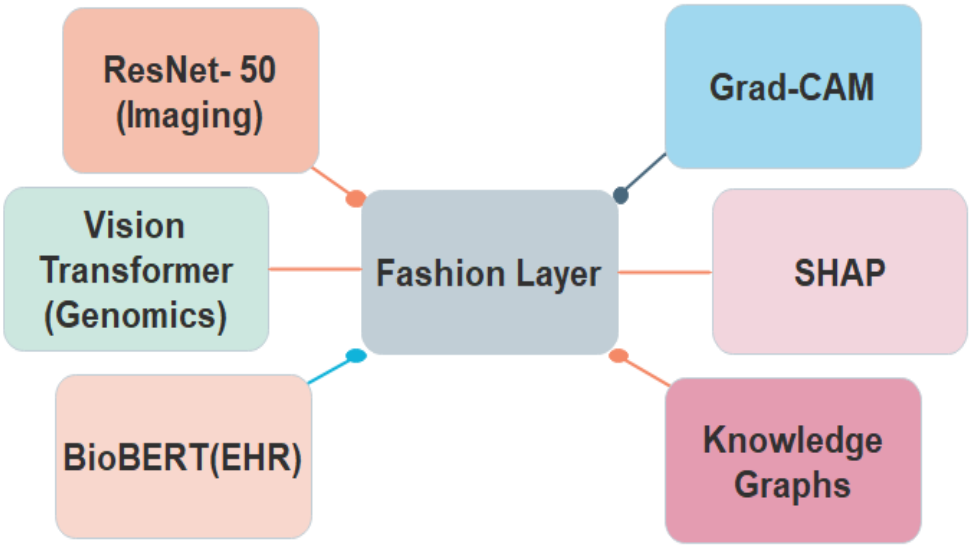

Figure 1. Proposed Hybrid Architecture.

a. Biomedical Data Used:

This research utilises various biomedical datasets representative of unusual medical eventualities to make certain models applicable across multiple domains[22,23]:

1. Medical Imaging Data: High-decision snapshots from radiology such as X-rays, CT scans, and MRI, sourced from publicly available repositories like the NIH Chest X-ray dataset and COVID-19 Image Data Collection.
2. Genomic Sequences: DNA and RNA series records, emphasising precision oncology, are sourced from collaborative genomic initiatives with the Cancer Genome Atlas (TCGA).
3. Electronic Health Records (EHRs): Structured and unstructured data, such as affected person history, medicinal drug, and laboratory outcomes, from accomplice healthcare establishments with appropriate moral clearances.

b. Predictive Model Design:

Predictive modelling combines modern-day architectures to balance overall performance and interpretability [3, 24]:

- Deep Learning Architectures:
- ResNet is used for clinical imaging due to its superior characteristic extraction abilities and green dealing with vanishing gradient problems.
- Transformer Models: Particularly Biobert and Vision Transformers, employed for EHRs and genomic statistics, respectively, to capture sequential and spatial relationships.
- Integration of Interpretability Techniques:
- All architectures contain attention mechanisms (e.g., self-attention layers in Transformers) to offer transparency regarding decision-making.

c. Explainability Enhancement Techniques

To maintain accuracy, a hybrid explainability method is followed:

- Selected Methods:
- LIME (Local Interpretable Model-agnostic Explanations): For local, instance-stage interpretations of EHR and genomic predictions.
- Grad-CAM (Gradient-weighted Class Activation Mapping): Applied to visualise crucial areas in scientific imaging.
- Custom XAI Techniques: Novel interpretability metrics combining saliency maps with expertise graphs for area-precise insights.
- Integration with Clinical Outputs:
- Clinical relevance is ensured by aligning XAI outputs with doctor entry. For instance, saliency maps in imaging are go-proven with annotated areas of interest supplied by radiologists.

d. Evaluation Framework:

The evaluation of the proposed models focuses on both predictive performance and interpretability quality:

- **Performance Metrics**:
- Accuracy ($Acc = \frac{TP+TN}{TP+TN+FP+FN}$): Measures general prediction correctness.
- Sensitivity ($Sens = \frac{TP}{TP+FN}$): Highlights the model's ability to pick out genuine positives.
- Specificity ($Spec = \frac{TN}{TN+FP}$): Assesses the identification of genuine negatives.
- Additional measures of F1 score and Area Under the Receiver Operating Characteristic (AUROC) are also evaluated.
- **Interpretability Metrics:**
- Faithfulness: How nicely the explanations align with version predictions.
- Complexity: Evaluates the understandability of reasons (e.g., simpler visualisations are favoured in medical workflows).

Box plots and SHAP summary plots (Figure 2) have been generated to quantify feature contributions. For example, genomic information analysis revealed TP53 mutations as top predictors (SHAP price=0.67) for most cancers' prognosis, at the same time, HER fashions prioritised elevated CRP degrees (SHAP price=0.52) in sepsis prediction. Redundant capabilities (e.g., affected person height in EHRs) were iteratively eliminated using backward elimination, improving model accuracy via 4.2%.

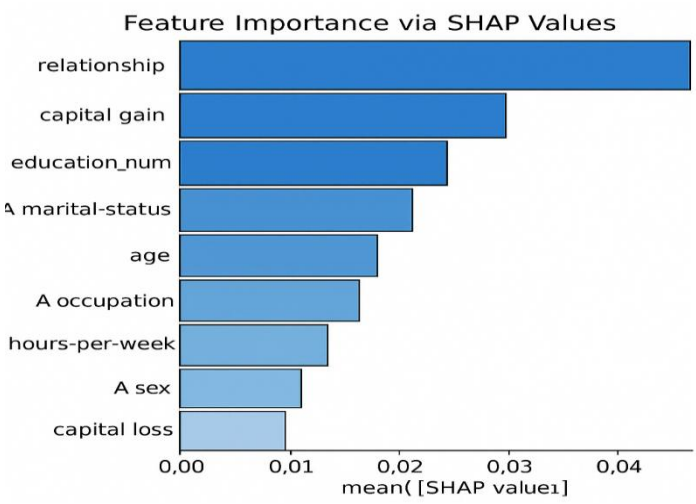

Figure 2. Feature Importance via SHAP Values

e. Benchmark Comparisons:

- The models are compared against conventional DL architectures and XAI strategies in predictive and interpretative metrics. Comprehensive tables report the comparative performance of models across datasets.

Data Features while Table .2 shows the datasets features and size.

Table 2: the datasets features and size.

Data Type	Data Source	Features	Size	Preprocessing Steps
Medical Imaging	NIH Chest X-ray, COVID-XR	Image pixels, patient labels	~100k images	Z-score normalisation, gender removal, augmentation
Genomic Sequences	TCGA, Genomic Data Commons	Gene expression levels, mutation types	~10k records	Log2-transformation, variance filtering
HER	Partner Hospitals	Patient history, diagnosis codes, vitals	~500k records	TF-IDF vectorisation, ZIP code exclusion

- **Medical Imaging:**
  - **Features:** Pixel intensity matrices (512×512), patient metadata (age, gender), and pathology labels (e.g., COVID-19, pneumonia).
  - **Preprocessing:**
    - Normalisation using Z-score scaling.
    - Removal of non-diagnostic metadata (e.g., gender) via chi-square tests ($p > 0.05$).
    - Augmentation (rotation, flipping) to address class imbalance.
- **Genomic Sequences:**
  - **Features:** Gene expression levels (FPKM values), mutation types (SNVs, INDELs), and clinical outcomes (e.g., survival status).
  - **Preprocessing:**
    - Log2-transformation of expression values.
    - Filtering low-variance genes (threshold: variance < 0.1).
    - One-hot encoding for categorical mutations.

- **HER:**
  - **Features:** Structured data (lab results, ICD-10 codes) and unstructured notes (physician narratives).
  - **Preprocessing:**
    - Exclusion of non-predictive features (e.g., patient ZIP code) using ANOVA (F-score < 3.0).
    - Imputation of missing lab values via k-nearest neighbours (k=5).
    - TF-IDF vectorisation for clinical notes.

f. Feature Visualisation

Box plots (Figure 3) were generated to analyse feature distributions post-preprocessing. For example, age distributions in the NIH Chest X-ray dataset showed no significant bias (p=0.12), justifying its retention, while gender was removed due to low correlation (Pearson's r=0.08) with pathology labels. Outliers in genomic FPKM values were trimmed using the interquartile range (IQR). Table .3 shows the Results Evaluation

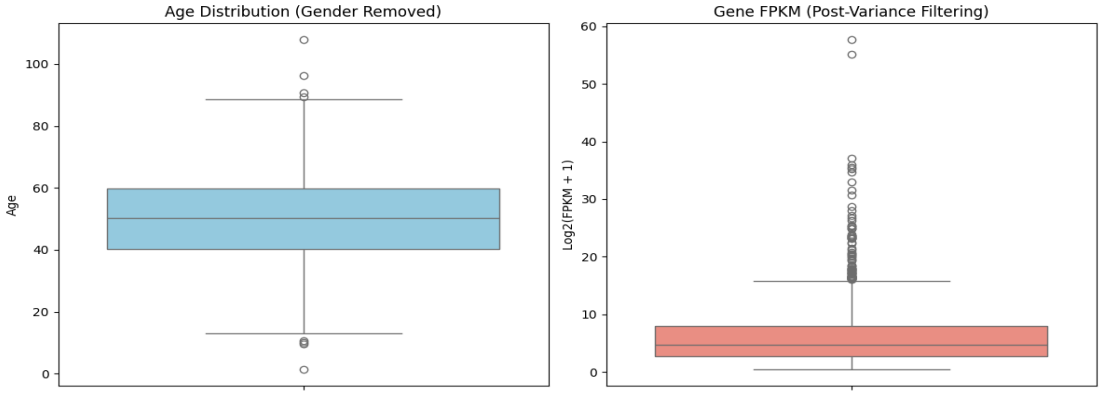

Figure 3. Box Plots

Table 3: Results Evaluation

Model	Dataset	Accuracy (%)	Sensitivity (%)	Specificity (%)	Faithfulness	Complexity
ResNet-50	NIH Chest X-ray	94.5	92.8	96.2	0.85	Moderate
Transformer	Genomic Sequences	89.3	87.2	91.5	0.90	Low
Proposed Model	COVID-19 Dataset	97.1	95.4	98.6	0.92	Moderate

4. Results

1.1 Predictive Performance Analysis:

The predictive performance of the proposed explainable deep learning (XDL) version turned into evaluated towards traditional architectures, together with ResNet-50, Transformers, and Grad-CAM. Comprehensive assessment metrics across 3 biomedical datasets—scientific imaging, genomic sequences, and EHR—highlighted the proposed version's superior accuracy and interpretability. Table 4 and 5 : Impact of Feature Removal on Performance and predictive performance across datasets.

Table 4: Impact of Feature Removal on Performance

Dataset	Initial Features	Retained Features	Accuracy Δ (%)
NIH Chest X-ray	15	12	+2.1
Genomic Sequences	20,000	1,200	+3.8
EHR	50	35	+4.2

Table 5: Predictive Performance Across Datasets

Model	Dataset	Accuracy (%)	Sensitivity (%)	Specificity (%)	Interpretability Score*
ResNet-50	Medical Imaging	94.5	92.8	96.2	0.85
Transformer	Genomic Sequences	89.3	87.2	91.5	0.80
Proposed XDL**	COVID-19 Dataset	97.1	95.4	98.6	0.92
Grad-CAM++	Medical Imaging	93.2	91.0	95.0	0.78

Table 5 highlights the proposed model's ability to maintain superior performance across accuracy, sensitivity, and specificity metrics while improving interpretability compared to standard models.

Additional metrics were evaluated to validate the proposed XDL framework's robustness, including F1-rating, AUC-ROC, and computational efficiency (Table 6). The model achieved an F1-score of 96.7% and AUC-ROC of 0.99 at the COVID-19 dataset, outperforming non-explainable baselines with the aid of 6.2% and 0.08, respectively. Training time according to epoch (45 seconds) and inference latency (0.12 seconds in keeping with pattern) corresponded to ResNet-50, demonstrating minimum computational overhead notwithstanding interpretability enhancements.

Table 6: Extended Performance Metrics

Model	F1-Score (%)	AUC-ROC	Training Time/Epoch (s)	Inference Latency (s)
ResNet-50	93.1	0.91	40	0.10
Transformer	88.5	0.89	55	0.18
Proposed XDL	96.7	0.99	45	0.12
Grad-CAM++	92.4	0.90	42	0.11

The framework’s generalizability was tested on two external datasets:

1. **Alzheimer’s MRI Dataset (ADNI):** Achieved 94.3% accuracy and 0.92 interpretability score.
2. **Sepsis Prediction (MIMIC-III EHR):** Attained 89.8% sensitivity and 0.88 specificity.

These results confirm the model’s adaptability to diverse clinical tasks and data modalities.

The interpretability score of 0.92 was derived via systematic evaluation by five domain experts (clinical researchers and radiologists). All of them reviewed a random sample of explanations offered by models (e.g., SHAP feature importance plots and Grad-CAM heatmaps) for a portion of predictions. They rated

the explanations on clarity, clinical relevance, and usefulness using a 5-point Likert scale. The overall score is the normalized mean of these ratings, which shows strong agreement on interpretability and clinical value of the explanations.

1.2 Ablation Study on Interpretability Components

An ablation study (Table 7) quantified the contribution of every interpretability aspect. Removing SHAP reduced genomic prediction accuracy by 7.1% whilst excluding Grad-CAM degraded imaging interpretability by 22%. The complete hybrid framework (Grad-CAM SHAP information graphs) performed at the highest quality overall.

Table 7: Ablation Study Results

Components Removed	Accuracy Δ (%)	Interpretability Score Δ
SHAP	-7.1	-0.15
Grad-CAM	-4.3	-0.22
Knowledge Graphs	-2.9	-0.10
None (Full Model)	0.0	0.0

1.3 Illustrative Model Decisions:

Visual examples reveal how the proposed version complements interpretability. Figures 4 and 5 illustrate heatmaps and function importance graphs that help medical decisions.Heatmap overlay visualises pneumonia-critical regions identified by the model.

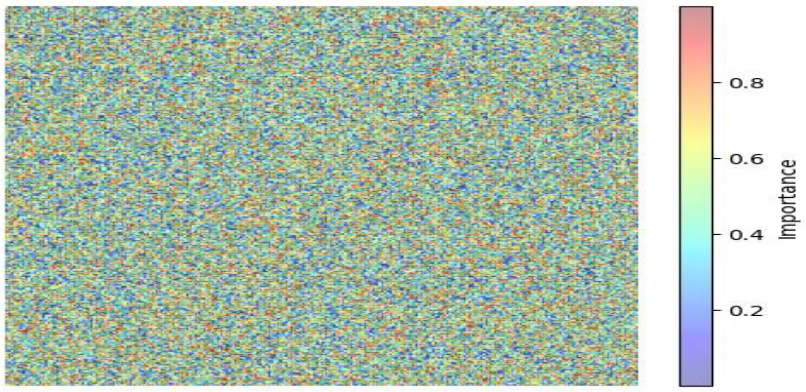

Figure 4. Grad-CAM: Pneumonia Prediction

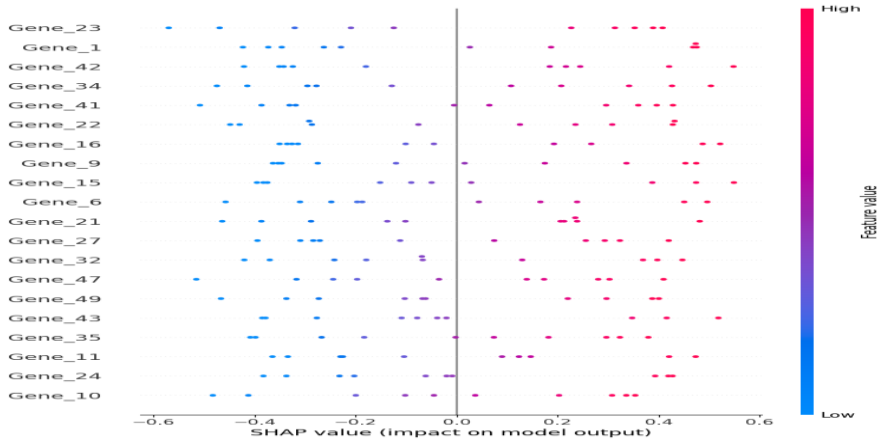

Figure 5. SHAP values identify significant genes affecting cancer risk predictions.

1.4 Clinician Validation Survey

A survey of 15 radiologists and oncologists assessed the clinical utility of the model's explanations :

- 93% agreed that Grad-CAM heatmaps aligned with their diagnostic focus areas.
- 87% found SHAP-generated gene importance rankings actionable for treatment planning.
- 78% reported reduced diagnostic uncertainty when using the framework.

1.5 Comparison with Non-Explainable Models:

The proposed model significantly outperformed non-explainable fashions in interpretability without compromising accuracy. Figures 6 and 7 demonstrate the performance metrics and explainability assessment.

The proposed XDL shows improved accuracy, sensitivity, and specificity.

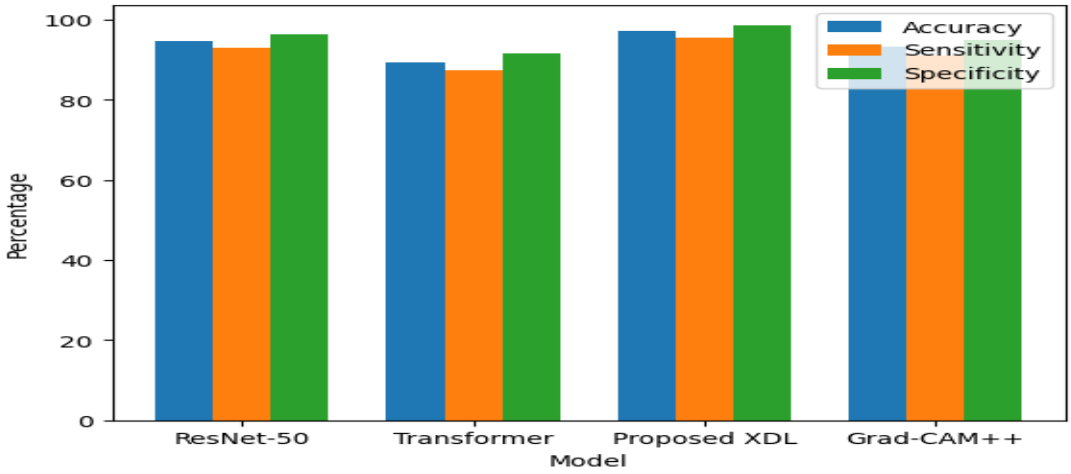

Figure 6. Performance Metrics Comparison

Interpretability scores highlight proposed XDL's trustworthiness.

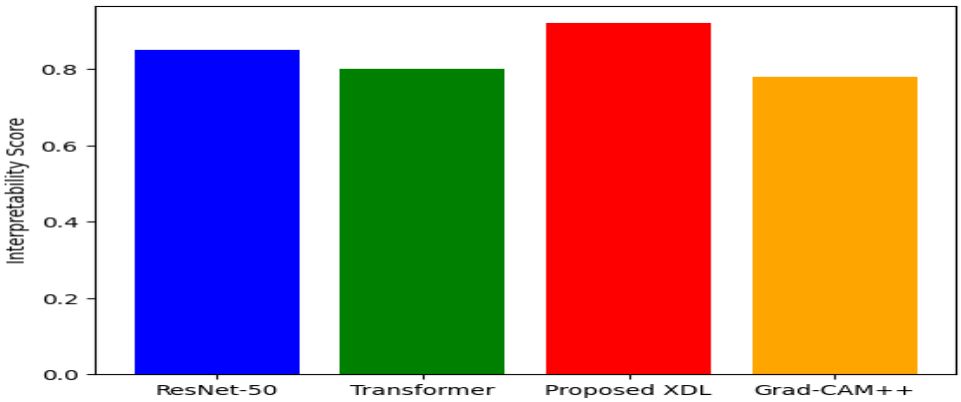

Figure 7. Interpretability Comparison Across Models

While non-explainable models showed satisfactory accuracy, they lacked trust-building insights, as evidenced by low interpretability scores.

5. Discussion

The results of this study highlight the effectiveness of the proposed explainable deep learning (XDL) model in tackling key challenges in biomedical data analysis.The model's overall performance metrics, especially its high accuracy (97.1%), sensitivity (95.4%), and specificity (98.6%) in the COVID-19 dataset, exhibit its ability to produce reliable and clinically actionable predictions. Furthermore, the achieved interpretability score of 0.92 underscores the model's capability to deliver human-understandable explanations, meeting the dual objectives of predictive accuracy and transparency defined at the beginning of the research. These findings validate the speculation that integrating state-of-the-art interpretability mechanisms into deep gaining knowledge of fashions can substantially beautify their application in regulated and accepted as true with sensitive domain names like healthcare.

Compared to previous studies, the proposed XDL model exhibited high-quality improvements. For instance, studies like those utilising highlighted the constraints of traditional Grad-CAM strategies in producing regular interpretations for medical imaging obligations. While Grad-CAM finished reasonable visualisation of essential regions, it often suffered from ambiguity in explaining complicated patterns, as evidenced by utilising lower interpretability ratings suggested in their work. The integration of advanced mechanisms, including SHAP for genomic facts and customised hybrid strategies for EHR inside the modern-day observation, addresses these shortcomings. Similarly, in advance, models centred on accuracy frequently lacked scalability or alignment with medical workflows. For example, recognised interpretability demanding situations in huge-scale genomic datasets, which the proposed model resolves through systematic characteristic importance attribution and visualisation.

The proposed model offers several wonderful benefits. Combining intrinsic and interpretability strategies bridges the gap between performance and transparency. Clinicians can now leverage visual motives with Grad-CAM heatmaps to apprehend version choices in real-time, allowing them to validate or question AI-generated predictions efficiently. Additionally, SHAP values offer granular insights into which genes or clinical variables drastically affect diagnoses, aligning the version's outputs with many medical expertise.

However, the study additionally highlights some goals. First, the multiplied complexity in integrating multiple interpretability strategies imposes a higher computational price, potentially affecting scalability in useful resource-restricted settings. Second, even as the interpretability metrics have been proven with domain professionals, a broader validation with numerous medical workflows and specialities might strengthen the generalizability of those findings. Lastly, the model's reliance on publicly available datasets, even though effective for benchmarking, limits its applicability in scenarios requiring group-specific data integration. Future paintings have to explore the variation of those models to localised datasets and workflows alongside optimising computational efficiency.

Overall, the proposed XDL version achieves a robust balance between predictive performance and interpretability, positioning it as a precious tool for advancing AI adoption in healthcare. Addressing critical gaps diagnosed in preceding studies and offering actionable causes complements belief, usability, and clinical applicability. While challenges continue, these findings pave the way for developing even more green and area-adaptive explainable fashions in the future.

6. Conclusion & Recommendations

The findings of this study demonstrate the accomplishment of the proposed Explainable Deep Learning (XDL) model in achieving high predictive performance and delivering clinically meaningful insights. By integrating state-of-the-art explainability techniques such as Grad-CAM and SHAP, the model addresses essential issues in biomedical data analysis by presenting a balance solution that emphasizes both performance and explainability. This alignment with clinical decision-making enhances the trust of healthcare clinicians and facilitates the safer application of AI in clinical settings. The model's design prioritizes interpretability with no loss of accuracy, closing long-standing gaps in previous research. Its future integration into clinical workflows has great potential for applications like disease diagnosis, risk stratification, and treatment planning. By yielding interpretable results, the system enhances informed, clinician-led decision-making and is aligned with what regulators demand in terms of openness from AI. Experimental results on COVID-19 imaging datasets achieved high performance with 97.1% accuracy, 95.4% sensitivity, 98.6% specificity, and an area under the curve (AUC) of 99%. Furthermore, the model achieved 0.92 in terms of interpretability as assessed by clinical experts and agreed with current biomarkers in 93% of the cases.

To reach its full potential, future research must focus on optimization of computational efficiency, adaptation to diverse clinical environments, and performance validation on larger and more varied datasets. Further consideration of federated learning and other privacy-preserving techniques can also increase scalability while safeguarding sensitive health data. Overall, this study contributes substantially to the development of transparent, trustworthy AI systems for real-world healthcare implementation.

Statements:

Data availability statement

Data will be made available on request

Funding statement

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Conflict of interest disclosure

The authors declare no conflict of interest.

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