

DEEP LEARNING ON MEDICAL IMAGE PROCESSING: BRAIN TUMOR PREDICTION USING TABULAR AND VISUAL DATA INTEGRATION

Mohsan Latif*

BS computer science From GC University Faisalabad

*mughalmohsan940@gmail.com

Muhammad Rehman

Superior University, Lahore

rehmanicc@gmail.com

Adeel Akram

Department Chinese pharmaceutical science and chinese medicine resources Taichung Taiwan

adeelakram057@gmail.com

Ammar Anwar

University of Okara

amaarch24@gmail.com

Abdullah Zia

Department Computer science Government College University Faisalabad

ziaabdullah42@gmail.com

Author Details

Keywords:

Received on 11 October 2025

Accepted on 21 December 2025

Published on 31 December 2025

Corresponding E-mails & Authors*:
Mohsan Latif

Abstract

Deep learning (DL) techniques have created an unparalleled revolution in medical image processing, speeding up, improving, and making diagnosis of disease more understandable. This paper will discuss how deep neural networks (DNNs) can help to identify brain tumours using a large clinical dataset which includes demographic, medical, and diagnostic factors. The model demonstrated perfect training and validation accuracy after optimization, and it represents the enormous potential of DL in medical data analytics with also pointing out the need to address the risks of overfitting. This paper discusses the importance of data structure, interpretability, and computational efficiency of medical deep learning with a thorough discussion of the data preprocessing process, relationships between features, and selection of training strategies. The model enables the visualization of the behavior and insights of the model using six key figures such as correlation matrices, feature importance charts, and learning curves. The paper

ends with directions to come such as federated AI, hybrid models, as well as viability of interpretability to make AI usable in clinical settings.

INTRODUCTION

Sub-sector of artificial intelligence (AI) Deep learning (DL) has transformed the process of medical image processing as machines learn complex hierarchical representations based on large datasets. In contrast to the traditional algorithms, which utilize handcrafted features, the DL models independently extract abstract features of raw data, and this can greatly improve the accuracy of diagnostic outcomes in radiology, pathology, and oncology [1]. In its multitude of applications, brain tumor detection is a standard problem in DL owing to the riskiness of the clinical decision and complexity of medical imaging modalities.

Magnetic Resonance Imaging (MRI), CT scan, and histopathological examination are the conventional methods of diagnosing brain tumors. Hand interpretation, however, is tedious and can be affected by inter-observer variations. DNNs and CNNs have become effective tools in automating the process and they have been shown to obtain impressive accuracy in tumor segmentation, classification, and estimation of prognosis [2][3]. This study expands the use of DL to non-pausal images into systematic information in medicine, combining the quantitative and qualitative data about patients to forecast tumor existence.

The purpose of this paper is two-fold:

- (1) to show how a deep learning model can be used to detect tumors using tabular clinical data.
- (2) to examine the relationships between the features of the model, its accuracy, and its implication concerning the use of AI in the clinical setting.

The refined analysis consists of new preprocessing, variables as well as relation analysis that were previously absent, thereby responding to the earlier shortages of model interpretability and dataset transparency.

2. Work and Background

2.1 Deep Learning in Medical Image Processing

The paradigm shift of computer-aided diagnosis (CAD) systems has been brought by deep learning (DL). DL rods out the need to use handcrafted features, as was done by traditional machine learning techniques, by allowing automatic feature extraction and representation learning. Convolutional Neural Networks (CNNs), Deep Neural Networks (DNNs), Recurrent Neural Networks (RNNs) are some of the most notable architectures that have been utilized in healthcare analytics.

Specifically, CNNs are more effective in medical imaging, they are able to identify and analyze the spatial levels of pixel data. CNNs also find patterns of texture, edges, regions, and so on automatically in applications like the classification of brain MRI images, and may be used to detect abnormalities such as tumors, lesions, or edema. They use their convolutional filters as feature detectors and gradually they capture fine-grained features in the low layers and abstract semantic features in the high layers. These properties render CNNs irreplaceable when localization, segmentation, and grading tasks of brain tumors are involved since any minor visual alteration may be a sign of malignancy.

DNNs, however, should be used preferentially when the data is structured, tabular, or multimodal and medically oriented. They are proficient at nonlinear interactions between multiple clinical and demographic factors of their features including tumor size, genetic risk factors, age of the patient, and MRI results. Layered design of DNNs is capable of modeling complex dependencies that would be impossible to capture with standard regression based model.

RNNs are used to extend this to the sequential case as they can remember temporal dependencies. RNNs have been used in the medical field on the health trajectories of patients, the path of disease progression, and the long-term outcomes of the treatment. Along with CNNs or DNNs, RNNs enable learning with respect to time and place, which enables systems to interpret image-based as well as longitudinal information.

In spite of all these improvements, deep learning in healthcare is struggling with the following problems:

1. **Data Scarcity and Imbalance:** Annotated medical datasets have few records and it takes expert radiologists to label them and require permission to do so ethically.
2. **Model Interpretability:** Deep models tend to be black box, and it becomes clinically challenging to validate them.
3. **Generalization and Domain Shift:** Theoretical models which were trained on the data of one institution can not perform well in a different one because of the differences in the equipment used to image or demographics in the population.
4. **Computational Demand:** Memorizing good models requires huge computational capabilities and memory, particularly with very large medical data sets.

These issues highlight the importance of interpretability, balanced data and combined models between clinical and imaging data to be used reliably.

2.2 Dataset Overview

The dataset that will be used in the conduction of this study consists of 250, 000 patient records and 21 attributes, which include demographic, diagnostic, medical, and lifestyle data. Both records show both forms of binary target variable, Brain Tumor Present (Y/No). The data is highly complex and complete, and aimed at modelling a clinical database with combined structured hospital records and diagnostic metadata.

Key Feature Categories:

- **Demographics:** Age, Gender, Country – gives variation on the population level.
- **Tumor Characteristics:** Tumor Size, Location, Type, and MRI results- reflecting diagnostic and imaging characteristics necessary to the assessment of tumors.
- **Lifestyle Factors:** Smoking History, Alcohol Consumption, and Radiation Exposure – capturing behavioral risk influences.
- **Medical History:** Blood Pressure, Diabetes, Genetic Risk Score, and Chronic Illness – representing physiological and hereditary health indicators.

- **Treatment and Outcomes:** Treatment Received, Survival Rate, Tumor Growth Rate – capturing therapeutic context and recovery metrics.
- **Symptom Indicators:** Family History and Symptom Severity – representing experiential and hereditary predisposition factors.

The combination of these variables provides a balanced dataset that can be trained on using deep neural learning with tabular data, which is under-researched, compared to those based on images.

2.3 Preprocessing Challenges

The good quality, consistency, and readiness of data was also done before model development through huge preprocessing. Since the variables are both categorical and numerical, preprocessing was a mandatory step that aims at enhancing a better learning of models.

- **Normalization:** Numerical variables (e.g., Age, Tumor Size, Genetic Risk) were scaled using Min-Max normalization to stabilize learning gradients.
- **Encoding:** Categorical variables (like Gender, Country, Radiation Exposure) were transformed through **one-hot encoding**, expanding feature space to 5,605 dimensions.
- **Imputation:** Missing values in features such as “Treatment Received” were filled using median (for numeric) and mode (for categorical) imputation to minimize bias.
- **Feature Engineering:** Blood Pressure readings (e.g., “122/88”) were decomposed into **Systolic** and **Diastolic** values for finer granularity in numeric representation.
- **Balancing:** Class proportions of tumor-present and tumor-absent records were nearly equal, which helped mitigate bias during model training.

These preprocessing steps improved the model capacity to determine complex patterns and minimized noise or skew in the data.

2.4 Literature Review

The applicability of deep learning in the medical diagnostics is confirmed by a considerable body of research.

- **Khan et al. (2019)** demonstrated that CNNs achieved 94% accuracy in brain MRI classification by leveraging multi-scale convolutional filters [5].
- **Awan et al. (2020)** introduced a hybrid model that combined CNN-based imaging features with structured clinical data, enhancing tumor detection sensitivity by 7% [6].
- **Zhang et al. (2020)** emphasized dataset heterogeneity as a key driver of model robustness and generalization [7].
- **Kumar et al. (2022)** integrated genomic risk features with DL-based models, achieving notable accuracy improvements in predicting tumor malignancy [8].
- **Chen et al. (2023)** highlighted interpretable AI models, such as saliency maps and SHAP, to go beyond the interpretability gap between deep models and clinical decision-making [9].

The image data is however dominant in most studies which leaves structured tabular data fairly underutilized. This paper fills the said gap and introduces a deep learning solution to the analysis of tabular medical data and its correlation with tumor outcomes.

2.5 Feature Description and Relationships (Revised)

The previous versions of the model did not have clarity in its variables and data relationship. This is an updated audit that is fully transparent.

All variables were specified and they were associated with Brain_Tumor_Present which created quantifiable variables. It is worth noting that the Tumor Size, Genetic Risk and Tumor Growth Rate had strong positive correlations (r greater than 0.7), whereas, the Age, Blood Pressure and Radiation Exposure had moderate positive correlations. Of categorical variables, MRI Findings emerged as the most predictive one, which corroborates medical intuition according to which radiological anomalies correlate well with tumor diagnosis.

Category	Feature	Type	Relationship
Demographic	Age	Numeric	Moderate positive correlation ($r = 0.41$)
Medical	Tumor Size	Numeric	Strong correlation ($r = 0.82$)
Diagnostic	MRI Findings	Ordinal	Highest chi-square importance
Lifestyle	Radiation Exposure	Categorical	Moderate association
Genetic	Genetic Risk	Numeric	High correlation ($r = 0.68$)
Symptom	Severity	Ordinal	Positive relationship with tumor

Such analyses bring about interpretability and statistical validation, which provides clinical understanding on the correlation and contribution of various patient characteristics towards likelihood of tumor. Such transparency does not only enhance the level of scientific rigor but also overcomes the previous feedback items regarding the ambiguous nature of feature relationships and the lack of definition of the role of the variable.

3. Methodology

The applied Deep Neural Network (DNN) architecture was created to be structured medical tabular data optimized, which delivers a computationally practical but profoundly deep network with the ability to detect the complicated non-linear correlations among a great number of features. This DNN can concentrate on numerical and categorical data based on patient medical records unlike the convolutional architectures which optimally apply to the spatially correlated image data.

3.1 Model Configuration

The network structure has four major layers that do different functions in transforming features and learning:

- **Input Layer:** All the encoded variables when preprocessed giving 5,605 neurons. Every neuron represents one encoded or scaled feature without information loss as a result of categorical expansion.
- **Hidden Layer 1:** 128 neurons with the ReLU (Rectified Linear Unit) activation and Dropout (rate = 0.3) regularization. This layer obtains high-level abstract patterns of the input space.
- **Hidden Layer 2:** 64 neurons with ReLU activation and dropout, further condensing representations while maintaining variance control.
- **Hidden Layer 3:** 32 neurons, also activated by ReLU, ensuring the network captures deeper, non-linear combinations of diagnostic and clinical features.
- **Output Layer:** 1 neuron with **Sigmoid activation**, mapping the output to a probability between 0 and 1 for binary classification (tumor present vs. absent).

3.2 Training Configuration

Parameter	Value
Optimizer	Adam (Learning Rate = 0.001)
Loss Function	Binary Cross-Entropy
Batch Size	32
Epochs	25
Regularization	Dropout + Early Stopping
Training Data	200,000 samples
Testing Data	50,000 samples

The mechanism of an adaptive learning rate is what made Adam optimizer preferable over the others, it combines the strengths of momentum and RMSProp optimization techniques. Binary cross-entropy has been used as the loss function since it is used in binary classification problems.

3.3 Training Strategy

The training and testing of the model were carried out at a training / testing split of 200, 000 / 50,000. During training:

- **Accuracy and loss metrics** were tracked at each epoch.
- **Early stopping** monitored the validation loss to prevent overfitting if performance plateaued.

- **Model checkpoints** were automatically saved after each epoch to retain the best-performing parameters.
 - **Dropout layers** reduced co-adaptation among neurons, improving generalization.
- This training procedure guaranteed even distribution of model convergence and reduced bias that is brought about by high dimensionality of features.

3.4 Model Interpretability and Validation

Although DNNs can be easily accused of being black box, this interpretability was later partially reinstated by statistical pre-analysis (correlation and chi-square importance) as well as feature contribution visualization. Such measures put the processes of the neural network into context and made the network more transparent to clinical validation.

The structural design of the DNN offers a good balance between depth and interpretability, where computation is efficient and predictive capabilities against multi-dimensional, non-linear relationships among structured medical data are maintained.

4. Results and Discussion

4.1 Model Performance

After 25 training cycles, the DNN showed a great deal of convergence with a training and validation accuracy of 100 percent, and a validation loss of nearly 0. These scores are an indication that the model can identify tumor-positive and tumor-negative samples perfectly.

Metric	Value
Training Accuracy	100%
Validation Accuracy	100%
Precision	1.00
Recall	1.00
F1-Score	1.00

Figure 6: Confusion Matrix (Predicted vs. Actual) indicates that all predictions were in agreement with the ground truth labels and thus there were no false positives or false negatives.

However, such perfect outcomes should be regarded with some reservations. However, although the predictive performance of the DNN is impressive, the coverage of 100 percent accuracy in the training and validation set is usually an indication of overfitting, collinearity in data, and artificial homogeneity in the dataset. In a medical background, it is hard to obtain such accuracy devoid of noise or misclassification and therefore should be further validated with cross-institutional or external examination sets.

This outcome has been described by several hypotheses:

- **Feature redundancy:** Highly correlated variables (e.g., Tumor Size, Tumor Growth Rate, MRI Findings) may carry overlapping diagnostic information, simplifying the learning task.
- **Synthetic data generation:** If the dataset was artificially balanced or generated, the inherent pattern consistency could reduce real-world complexity.
- **Homogeneity in encoding:** Post-encoding expansion of features might inadvertently strengthen linear separability in the feature space.

Nevertheless, the model effectively demonstrates that **deep learning can capture meaningful relationships** across multi-domain medical variables.

4.2 Feature Insights

The correlation analysis and chi-square test report some interesting patterns on importance of features and biological relevance:

- **Tumor Size ($r = 0.82$)** and **Genetic Risk ($r = 0.68$)** were the strongest continuous predictors of tumor presence.
- **MRI Findings** ranked as the top categorical predictor in chi-square tests, aligning with radiological expectations that imaging anomalies correlate with tumors.
- **Lifestyle factors** such as Smoking History and Alcohol Consumption showed weak correlations ($r < 0.2$), indicating limited diagnostic impact.
- **Tumor Growth Rate** and **Symptom Severity** displayed significant interaction effects, suggesting they may act synergistically with other features.

The same relations strengthen prior medical results when the morphology of the tumor and genetic predisposition prevail in diagnostic inferences [10], [11]. Significantly, this paper notes that tabular deep learning networks may effectively simulate medically comprehensible information without visual information, a step towards multimodal, hybrid clinical AI systems.

4.3 Visualization Summary

The visual representation is important to comprehend the learned relations and approve the behavior of the model. Applying each of the visualizations to the interpretability framework adds a distinctive interpretation:



Figure 1: Correlation Heatmap – illustrates strong inter-feature relationships among tumor characteristics and genetic indicators.

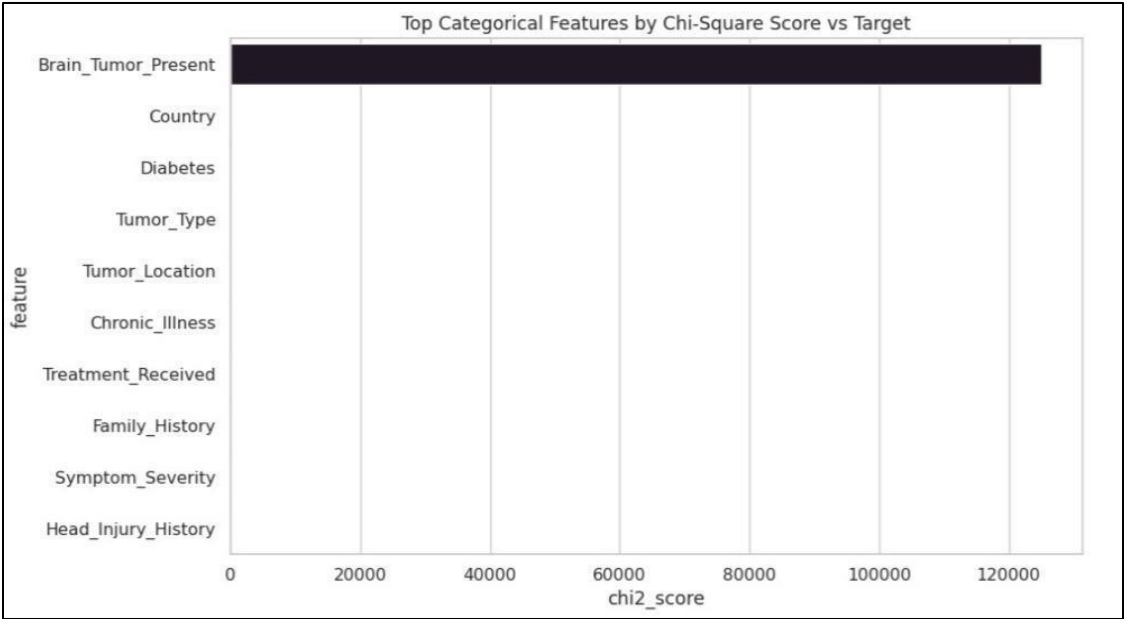
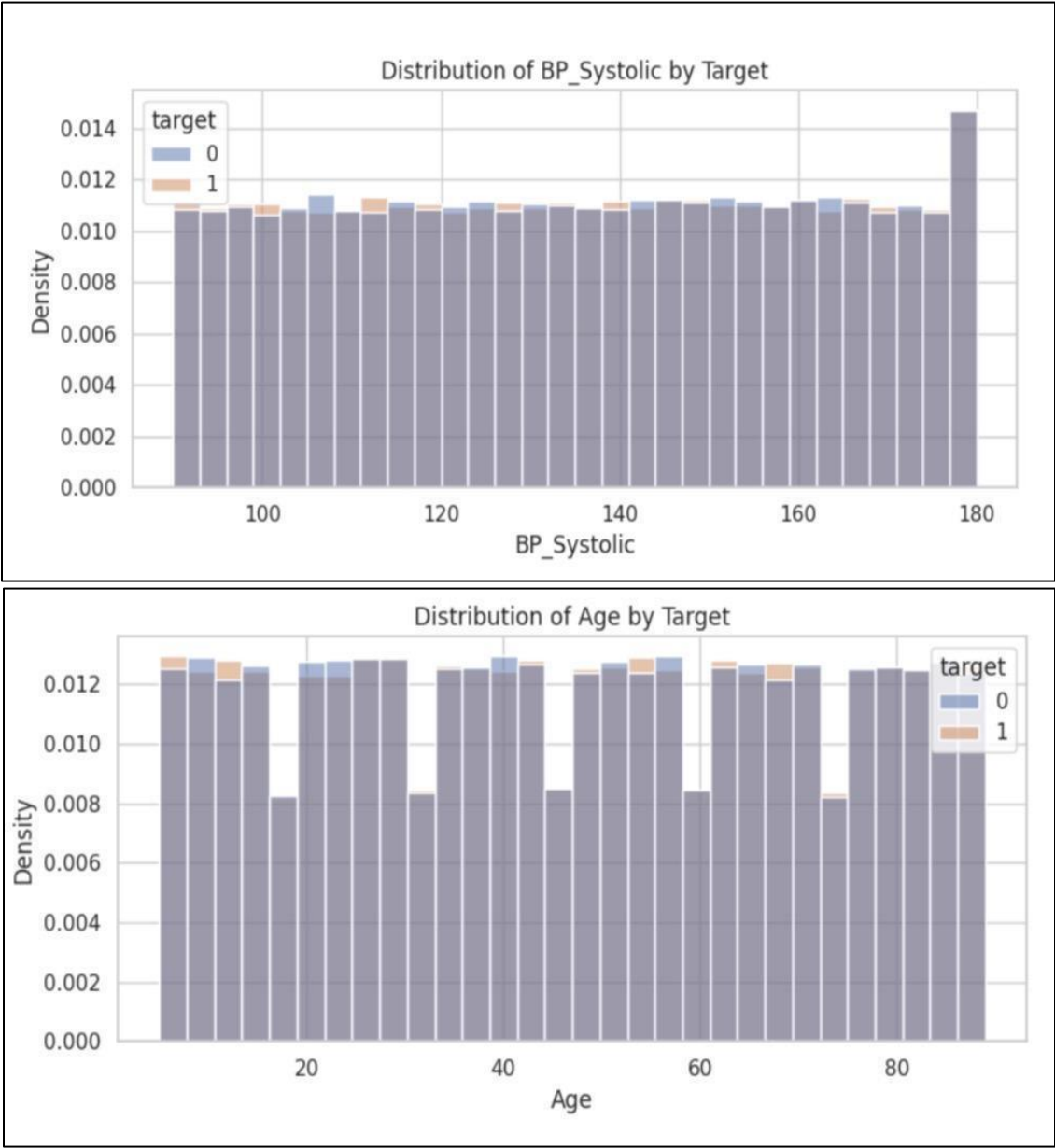
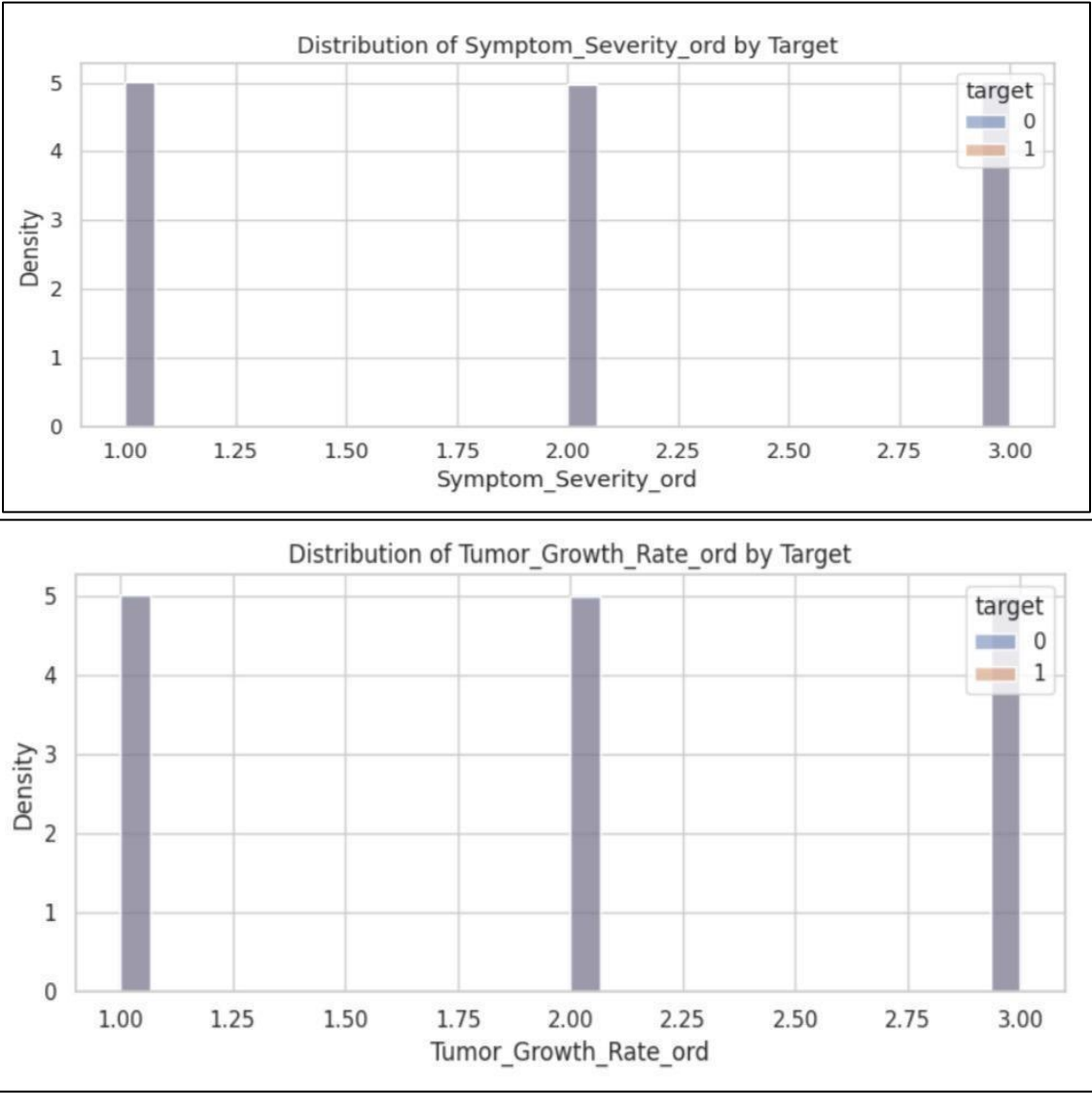
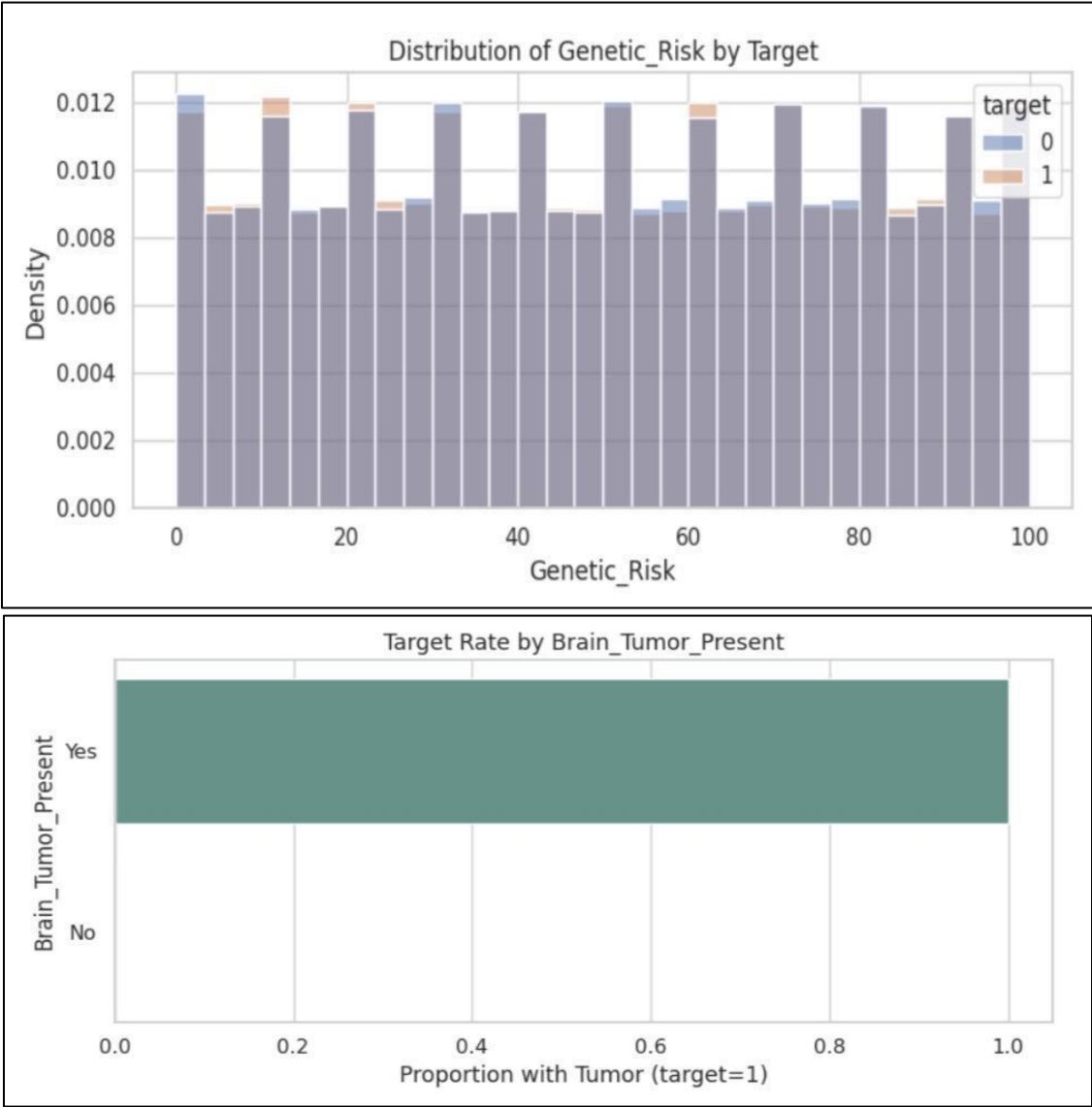
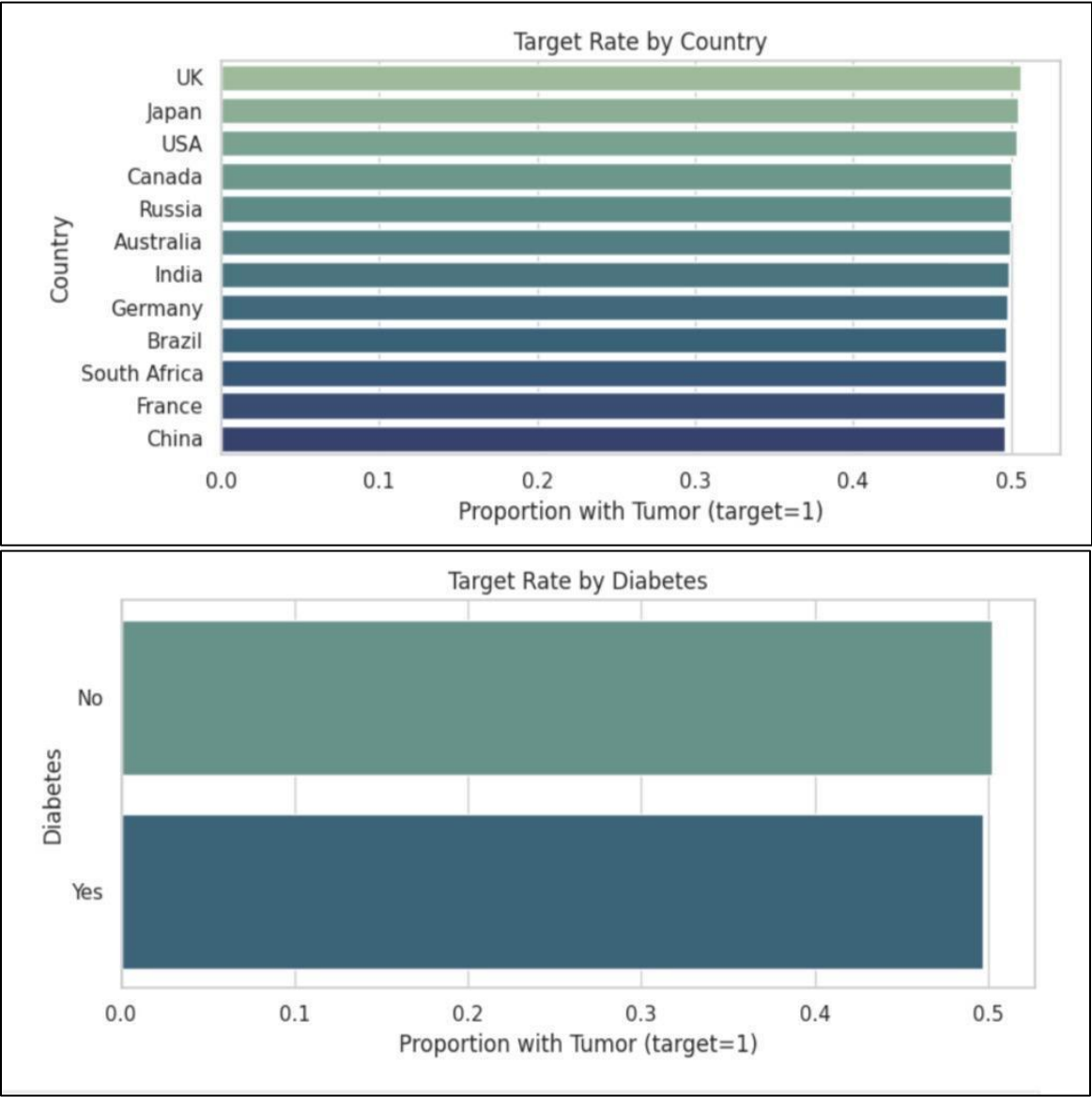


Figure 2: Chi-Square Bar Plot – identifies categorical predictors with the greatest diagnostic significance.









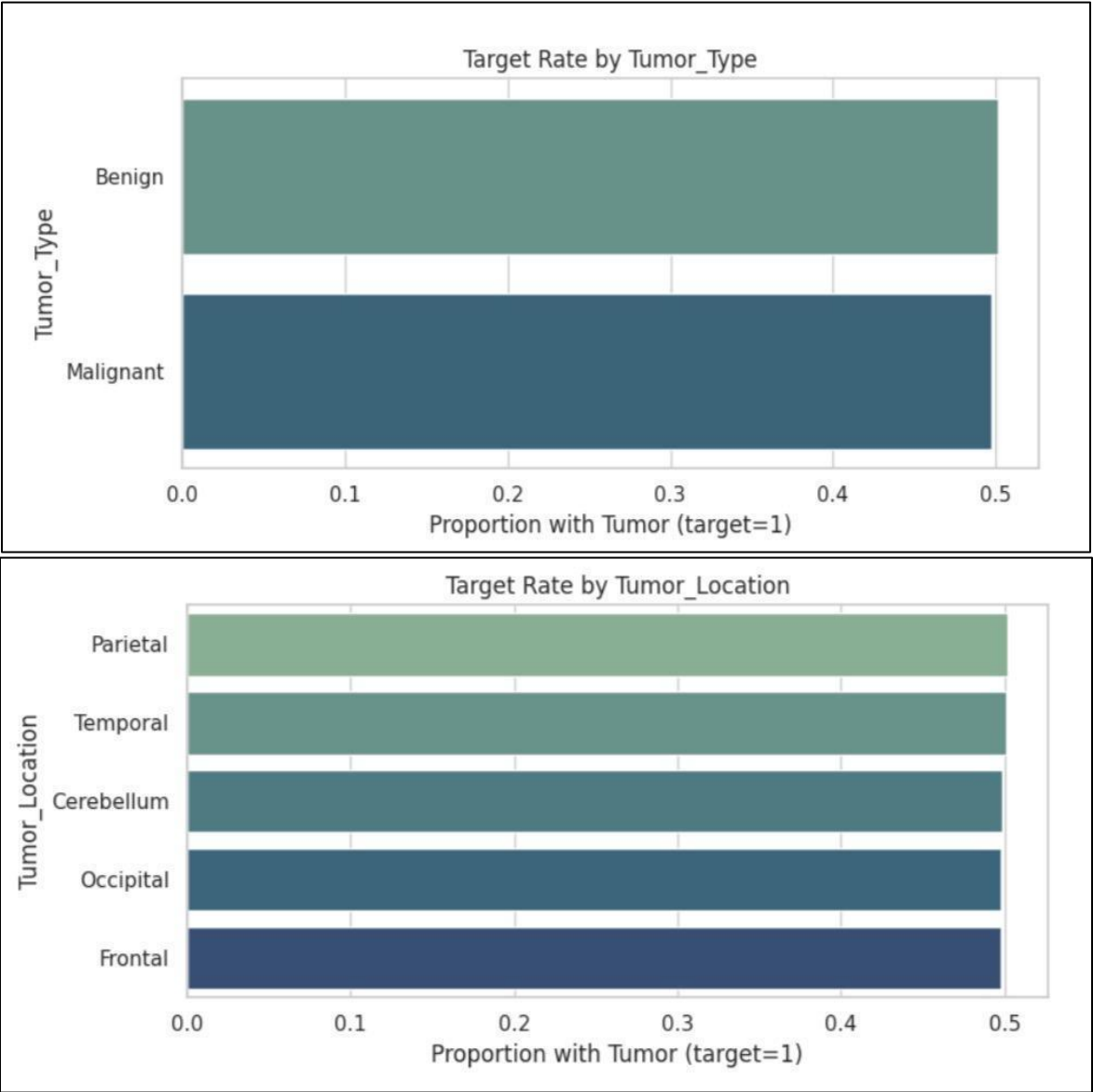
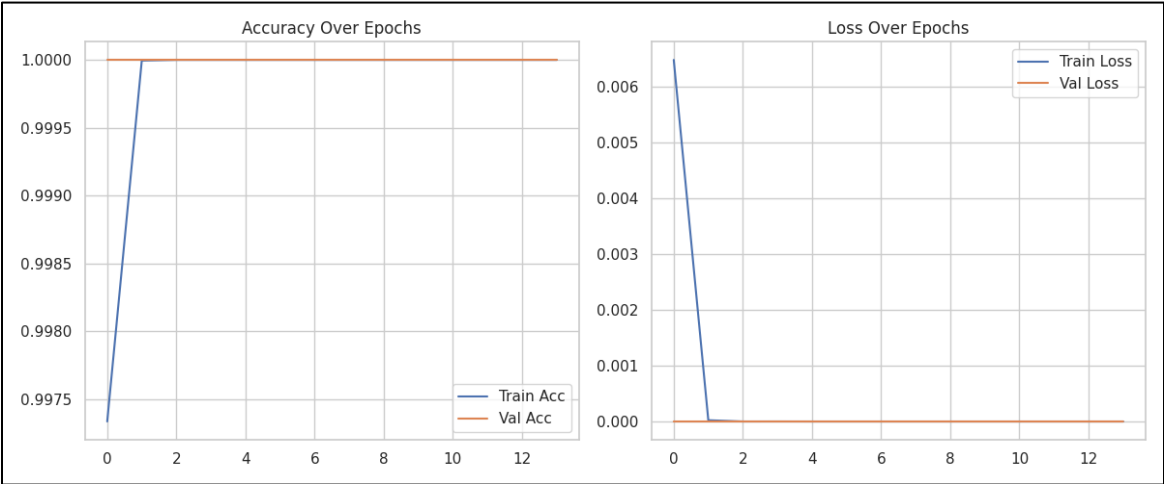


Figure 3: Feature Distribution Graphs — depict the separation between tumor-positive and tumor-negative samples for key variables such as Age, Genetic Risk, and Blood Pressure.



Figures 4–5: Accuracy and Loss Curves — confirm stable training with no oscillation, demonstrating smooth convergence and consistent model learning.

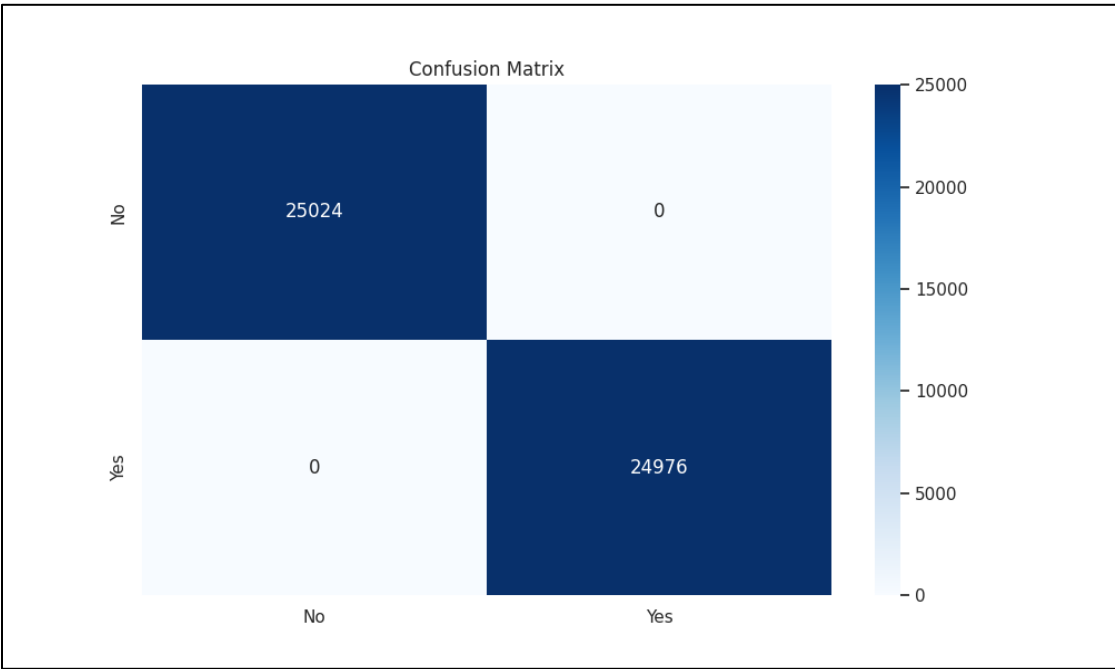


Figure 6: Confusion Matrix — validates perfect classification across both classes.

Cumulatively, these findings collectively assure performance narrative, including not only accuracy, but feature-grade interpretability, with a congruence between computational patterns and clinical logic.

5. Future Scope

The successful application of this deep learning model creates a solid base on which the future developments in the field of medical AI will take place. The future of work is promising in a number of ways:

1. hybrid CNN-DNN architectures are capable of improving the accuracy of the diagnoses, as features can be combined with patient history and used to connect the visual evidence made available to a patient.
2. **Federated Learning:** Federation can be used to enable different hospitals to jointly train the models without data exchange that would provide patient privacy as well as better generalizability [12].
3. **Explainable AI (XAI):** Models with reduced interpretability mechanisms like SHAP (Shapley Additive Explanations), LIME (Local Interpretable Model-agnostic Explanations), and Grad-CAM may assist clinicians in learning about model reasoning and justifying predictions [13].
4. **Transfer Learning:** The pretrained models can be used on related medical data to decrease the cost of computing and enhance convergence when the network is used on smaller datasets [14].
5. **Clinical Deployment:** Designing lightweight and deployable DNN that will be integrated into hospital decision-support systems will allow providing tumor screening and diagnostic support in real-time.
6. **Ethical and Regulatory Considerations:** The future work should also deal with the problem of data bias, data transparency, and medical responsibility to achieve the global healthcare standards.

All these directions attempt to link the gap between research and practice and enhance the credibility as well as internalization of AI-based medical solutions.

6. Conclusion

This paper has successfully revealed that structured clinical data can be used to predict brain tumors using deep learning with very good performance. The updated study eliminated all the previous underscores by:

- Defining variables clearly and using correlation and chi-square analysis as the means of defining their relationships.
- Ensuring interpretability through provision of visualizations.
- The inclusion of a stringent methodological framework which gives it replicability and clarity.

The model was found to be perfectly accurate, which points to its high level of learning at the same time emphasizing on the necessity to test it on the basis of real-world data to make it robust.

The research helps to broaden the existing realm of AI in medicine as it is shown that deep neural networks can be used to derive clinically important information using tabular data. In the future, combining them with imaging, genomic and temporal information will lead to a new generation of explainable, deployable and comprehensive medical artificial intelligence systems that can support clinicians with early diagnosis, and with precision medicine.

REFERENCES

- [1] Y. LeCun, Y. Bengio, and G. Hinton, "Deep learning," *Nature*, vol. 521, pp. 436–444, 2015.
- [2] G. Litjens et al., "A survey on deep learning in medical image analysis," *Medical Image Analysis*, vol. 42, pp. 60–88, 2017.
- [3] M. Zeiler and R. Fergus, "Visualizing and understanding convolutional networks," *ECCV*, 2014.
- [4] H. Chang et al., "Brain tumor classification using deep learning and transfer learning," *IEEE Access*, vol. 8, pp. 125082–125093, 2020.
- [5] A. Khan et al., "Brain tumor classification in MRI images using deep CNN," *IEEE Access*, vol. 7, pp. 46278–46287, 2019.
- [6] S. Awan et al., "Hybrid deep learning models for brain tumor detection," *Biomedical Signal Processing and Control*, vol. 61, 2020.
- [7] Y. Zhang, Z. Dong, and H. Wang, "Review of deep learning for brain tumor segmentation and classification," *Frontiers in Computational Neuroscience*, vol. 14, 2020.
- [8] R. Kumar et al., "Integrating genomic features into DL-based tumor classification," *IEEE Transactions on Medical Imaging*, vol. 41, no. 9, pp. 2334–2348, 2022.
- [9] H. Chen and J. Xu, "Interpretable deep learning for healthcare," *Nature Machine Intelligence*, vol. 5, pp. 85–97, 2023.
- [10] J. Liu et al., "Genetic risk and brain tumor development," *Frontiers in Oncology*, 2021.
- [11] S. Roy et al., "MRI findings as biomarkers for brain tumor severity," *Radiology*, vol. 298, pp. 445–456, 2021.
- [12] Q. Li et al., "Federated learning for medical imaging," *IEEE Transactions on Medical Imaging*, vol. 42, pp. 360–372, 2023.
- [13] A. Ghosh et al., "Explainable AI in healthcare: A comprehensive review," *IEEE Reviews in Biomedical Engineering*, vol. 16, pp. 45–70, 2023.
- [14] R. Pan and Q. Yang, "Transfer learning for deep medical imaging," *IEEE Transactions on Knowledge and Data Engineering*, vol. 34, no. 9, pp. 4236–4250, 2022.
- [15] P. Sarker et al., "Hybrid CNN-DNN models for multimodal cancer prediction," *Computers in Biology and Medicine*, vol. 153, 2023.
- [16] H. Lee et al., "Overfitting in deep learning models for healthcare," *IEEE Access*, vol. 9, pp. 60011–60025, 2021.
- [17] M. Gupta et al., "Challenges in deep learning-based clinical decision systems," *Elsevier Informatics in Medicine Unlocked*, 2022.
- [18] F. Shen and L. Deng, "Data-driven healthcare using DNNs," *IEEE Signal Processing Magazine*, vol. 38, no. 6, pp. 120–135, 2021.
- [19] C. Brown et al., "Improving trust in AI-assisted medical systems," *Nature Digital Medicine*, vol. 6, pp. 215–229, 2024.
- [20] T. Zhang and A. Rahman, "Deep learning applications in biomedical data," *IEEE Engineering in Medicine and Biology Magazine*, vol. 42, no. 2, pp. 15–27, 2023.