Interpretable AI for Precision Brain Tumor Prognosis: A Transparent Machine Learning Approach

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ABSTRACT

Advancements in brain tumor prognosis, especially for glioma, demand a transparent and comprehensive diagnostic framework that not only ensures high accuracy but also fosters interpretability for clinical decision-making. To meet this need, an interpretable artificial intelligence (AI) approach is proposed, combining machine learning (ML) and deep learning (DL) models enriched by explainable artificial intelligence (XAI) techniques. The approach focuses on enhancing prediction accuracy while ensuring the process remains understandable and traceable by medical professionals. Patient-centric data such as clinical histories and genetic profiles are integrated to enable more personalized diagnostics. A multi-stage methodology is adopted, employing multiple feature selection techniques including Vital Feature Selection (FS), Mutual Information FS, Principal Component Analysis (PCA) FS, and Pearson Correlation Coefficient FS. These techniques help in reducing dimensionality and improving model generalization without losing critical predictive markers. A combination of classical ML algorithms and advanced ensemble methods such as the Voting Classifier is utilized to maximize glioma grading accuracy. The Voting Classifier exhibits perfect performance, achieving 100% accuracy using essential features and mutual information-based selection. In contrast, deep learning models, particularly Convolutional Neural Networks (CNNs), achieve commendable results with 91% accuracy when PCA-based features are applied and 90% with Pearson coefficient-based features. The fusion of these techniques under the umbrella of interpretable AI ensures not only high performance but also enables medical experts to understand the decision pathways involved in classification outcomes. This transparency bridges the gap between black-box AI systems and real-world clinical applicability. Overall, the integration of diverse feature selection strategies, patient-specific data, robust machine learning models, and explainable frameworks presents a significant leap toward precise, trustworthy, and interpretable brain tumor prognosis.

Keywords: Glioma, molecular makeup, explainable artificial intelligence (XAI), SHAP, LIME, QLattice

1. INTRODUCTION:

Glioma is a important type of central nervous system (CNS) malignancy, springing up from glial cells inside the brain or spinal cord [1]. Those neoplasms originate from glial cells, which might be wholesome cerebral cells that help and safeguard neuronal cells. Strange proliferation of these glial cells effects in tumor formation that can infiltrate and damage adjoining mind or spinal cord tissue [2].

Gliomas showcase varying ranges of malignancy, with glioblastoma identified as the most aggressive and malignant form, generally labeled as grade IV via the "world fitness organization (WHO) [6]. Glioblastoma, also referred to as Glioblastoma Multiforme (GBM)", is infamous for its fast proliferation and capability to invade healthy brain tissue, rendering it one of the most lethal types of brain cancer.

Gliomas are classified by using grade and type consistent with histological parameters, which suggest the predicted level of differentiation and the tumor's potential for aggressive proliferation. The WHO classifies gliomas into categories I-IV, with grade I tumors usually being benign and predominantly curable, regularly determined in kids. Those tumors have sluggish increase and may often be addressed with surgical intervention. "Grade II gliomas, encompassing oligodendrogliomas, astrocytomas, and oligoastrocytomas", predominantly afflict adults and are classified as low-grade, despite the fact that possess the capacity to progress into higher-grade tumors over time [5]. "Grade III gliomas, which include anaplastic astrocytomas and anaplastic oligodendrogliomas", exhibit extra invasiveness and aggressiveness in comparison to grade II tumors, resulting in expanded remedy problem and a higher propensity for dissemination to surrounding tissues [5].

According to the WHO, the maximum perilous variation of glioblastoma is grade IV glioma, or Glioblastoma Multiforme, characterized via its fast and unregulated proliferation, alongside its potential to invade adjacent cerebral tissues. GBM is a really aggressive neoplasm frequently unresponsive to traditional therapeutic modalities, including surgical procedure, radiotherapy, and chemotherapy, which exacerbates its extended loss of life price [6]. The symptoms of glioma may additionally vary based totally at the tumor's length and place within the mind or spinal cord; however, established signs encompass complications, nausea, and memory impairment, changes in personality, visible disturbances, and speech problems. Those signs and symptoms emerge as the tumor expands and exerts strain on adjoining brain tissue, compromising its capability. The prognosis and survival rate of glioma sufferers are appreciably tormented by the tumor's grade, vicinity, and rate of development, with decrease-grade gliomas generally being greater amenable to remedy than the especially competitive "glioblastoma multiforme (GBM)".

2. OBJECTIVES:

The goal is to build an interpretable AI-driven diagnostic framework that accurately predicts glioma progression by leveraging personalized data, effective feature selection techniques, and high-performing machine learning algorithms.

(1) To develop a transparent diagnostic system that combines machine learning and deep learning algorithms with explainable AI to enhance glioma classification accuracy and enable clinicians to understand the decision-making process.

(2) To apply diverse feature selection techniques—Vital FS, Mutual Information FS, PCA FS, and Pearson Coefficient FS—to identify the most significant markers contributing to accurate glioma grading and prognosis.

(3) To integrate personalized patient data, including clinical history and genetic information, with optimized ensemble classifiers and CNNs, aiming to improve predictive performance and support precision healthcare strategies.

3. REVIEW OF LITERATURE/ RELATED WORKS:

Current advancements inside the studies of gliomas, especially regarding their categorization and grading, have highlighted the developing significance of current imaging strategies, machine learning, and radiomics evaluation to beautify diagnostic precision. Gliomas, originating from glial cells inside the mind or spinal cord, are classified into 4 classes by means of the "world health organization (WHO)", from benign Grade I tumors to the fantastically malignant Grade IV glioblastomas. numerous observe initiatives have targeting creating dependable techniques to exactly outline and grade gliomas utilising clinical and molecular characteristics, alongside superior imaging technology, to deepen the comprehension of those tumors and growth affected person outcomes.

Finch et al. [7] performed a comprehensive evaluation of latest development in glioma research that specialize in person gliomas and highlighting the significance of genetic and molecular markers in their categorization and diagnosis. Their research emphasized that improvements in genetics and

molecular biology have greater the comprehension of glioma pathophysiology, facilitating greater precise categorization and subtle tailored treatment approaches. They also examined the increasing significance of "artificial intelligence (AI) and machine learning (ML)" methodologies inside the identification of biomarkers that useful resource in glioma class and forecast affected person treatment responses. The incorporation of these techniques into medical exercise is expected to convert glioma analysis and remedy inside the next years.

Ouerghi et al. [28] investigated glioma category through MR image radiomics evaluation, revealing that sophisticated photo processing methods can markedly enhance glioma grading. Radiomics, the extraction of excessive-dimensional characteristics from clinical images, has grown to be an amazing instrument in oncology. Via the evaluation of MRI scans from glioma patients, Ouerghi et al. identified precise textural developments that correspond with tumor grade, offering a non-invasive approach for glioma grading. This study complements the present evidence for the application of imaging biomarkers inside the analysis and analysis of gliomas. Tian et al. [9] hired multiparametric MRI photographs to formulate a radiomics-based totally technique for glioma grading. Their studies utilized textural features received from diverse MRI modalities to evaluate glioma tumor heterogeneity, hence enhancing the precision of glioma grading. Multiparametric imaging affords vital facts, improving the sensitivity and specificity of glioma type.

Cho et al. [30] further elucidated the software of radiomics in glioma grading by employing radiomic analysis for the categorization of gliomas primarily based on MRI statistics. Their research targeting creating a device able to autonomously classifying gliomas into their corresponding categories thru the evaluation of MRI-derived traits. The have a look at emphasized the importance of characteristic extraction in radiomics, as the choice of the maximum pertinent capabilities can notably beautify model overall performance. Their studies indicated that radiomic indicators acquired from conventional MRI sequences may distinguish among low- and high-grade gliomas, supplying a promising approach to assist in scientific decision-making.

Machine learning (ML) has extensively contributed to glioma classification. Wu et al. [11] hired a mutual records-based totally feature selection method using radiomic facts to decorate the class accuracy of gliomas. Their studies highlighted the importance of characteristic selection techniques, as unprocessed radiomic statistics often consists of redundant or needless facts that can decrease the efficacy of predictive models. Utilizing reciprocal records for feature selection enabled the identification of the maximum informative factors that improved the accuracy of glioma grading. this technique has been appreciably applied in recent glioma grading research, highlighting the growing importance of characteristic engineering in the creation of dependable machine learning models for medical applications.

Cao et al. [32] investigated different developments in MRI functions for glioma category, offering a quantitative model to differentiate decrease-grade gliomas from glioblastomas the usage of clinically pertinent MRI characteristics. Their research indicated that combining clinical and imaging data could beautify the understanding of glioma grading, thereby facilitating the early detection of malignant gliomas. The quantitative version they created integrated MRI-derived characteristics with scientific elements to improve the diagnostic precision of glioma grading, underscoring the importance of interdisciplinary strategies in glioma diagnosis.

Digital pathology, at the side of machine learning, has emerged as a useful instrument for glioma type. Rathore et al. [13] performed a study reading virtual pathology pix with machine learning approaches to categorise gliomas. This system emphasised the automatic exam of histopathology pix for the detection and grading of gliomas, utilising tissue styles and cellular attributes. Their studies highlighted the potential of integrating classical histology with contemporary machine learning methodologies to beautify the precision and efficacy of glioma grading. The advancement of state-of-the-art algorithms for automated photo processing in pathology can lessen human error and yield more reliable and reproducible effects.

Alongside MRI and virtual pathology, genetic abnormalities and molecular biomarkers have garnered massive cognizance in glioma studies. Tasci et al. [20] presented an intensive dataset encompassing scientific and mutation characteristics associated with gliomas, highlighting huge mutations in genes consisting of "IDH1, IDH2, TP53, and ATRX", which might be diagnosed for his or her impact on glioma analysis and grading. Their dataset is an essential useful resource for lecturers seeking to

create fashions that combine genetic and molecular records into glioma grading. The amalgamation of genomic records with radiomic and clinical traits offers a promising road for future glioma studies, probably facilitating greater tailored and targeted healing alternatives for sufferers.

The studies on glioma grading underscores the increasing significance of present day imaging techniques, radiomics, and machine learning in improving diagnostic precision and clinical decision-making. The amalgamation of many statistics sources, such as clinical characteristics, MRI-derived textural functions, histopathological pictures, and genomic facts, might beautify the reliability and accuracy of glioma grading structures. Regardless of good sized improvements on this area, sizable efforts remain necessary to decorate these methodologies and comprise them into wellknown medical practice. The integration of artificial intelligence, clinical imaging, and molecular information is predicted to convert the prognosis, class, and remedy of gliomas in the approaching future. Modern research in glioma grading has considerable promise to decorate patient effects, facilitate early detection, and provide customized remedy regimens customized to unique tumor characteristics.

Table 1: Literature Survey Comparison Table

Sl .No	Area & Focus of the Research	The result of the Research	Reference
1	Genetic markers and AI for glioma diagnosis and treatment enhancement	Improved glioma categorization using AI and genetic profiling integration	A. Finch, G. Solomou, V. Wykes. et. al.., (2021). [7]
2	Radiomics-based MR image analysis for non-invasive glioma grading	Textural MRI features correlate strongly with tumor malignancy levels	H. Ouerghi, O. Mourali, and E. Zagrouba (2022) [28]
3	Multiparametric MRI radiomics for evaluating tumor heterogeneity in gliomas	Enhanced grading accuracy by combining multiple MRI texture features	Q. Tian, L. Yan, X. Zhang, (2018) [9]
4	Mutual information-based feature selection for glioma classification	Significant accuracy boost in grading using optimized radiomic features	Y. Wu,B.Liu,W.Wu (2018) [11]
5	Integration of clinical and genetic mutation data for gliomas	Robust dataset improved modeling of gene-based glioma prognosis	E. Tasci, K. Camphausen, A. V. Krauze et.al. (2020) [20]

4. MATERIALS AND METHODS:

The cautioned technique seeks to improve glioma prognosis via the mixing of “machine learning, deep learning, and explainable artificial intelligence (XAI) methodologies”. The system initiates the utility of various feature selection techniques, such as vital “featureselection (FS), Mutual records FS, principal component analysis (PCA) FS, and Pearson Coefficient FS”, to ascertain the maximum pertinent diagnostic markers. This system ensures that completely the maximum vast features are covered for version training, improving the precision and readability of forecasts. a selection of machine learning algorithms, including “Random forest, Logistic Regression, decision Tree, KNN, SVM (Linear and Sigmoid), and Ridge Classifier”, are utilized to assemble initial models. Ensemble strategies, such as stacking (Stack-1 and Stack-2) and voting classifiers, are hired to amalgamate the outputs of diverse classifiers to decorate performance. Moreover, “deep learning methodologies,

consisting of artificial Neural Networks (ANN) and Convolutional Neural Networks (CNN)", are utilized for classy function extraction and forecasting. The closing technique is to provide a clear and extremely specific diagnostic instrument for glioma analysis.

Fig 1: Proposed Architecture

The picture illustrates a machine learning system for glioma type. The technique commences with data processing, succeeded by characteristic engineering employing techniques together with PCA and FS. The processed records is finally divided into training and testing subsets. Various machine learning models, together with "Random forest, decision Tree, and SVM", are educated and evaluated on the statistics. The efficacy of these models is assessed via standards which include "accuracy, precision, recall, and F1-score".

4.1 Dataset Collection:

The Glioma Grading dataset comprises 839 entries and 24 columns, offering many features pertinent to glioma tumor diagnosis and grading. The columns comprise Grade (tumor grade), Gender, Age at diagnosis, Race, and genetic markers including "IDH1, TP53, ATRX, PTEN, EGFR, CIC, MUC16, PIK3CA, NF1, PIK3R1, FUBP1, RB1, NOTCH1, BCOR, CSMD3, SMARCA4, GRIN2A, IDH2, FAT4, and PDGFRA". All columns contain non-null values, with numerical data indicating the presence or absence of genetic mutations, tumor features, and patient demographics, hence enabling analysis for glioma prognosis and prediction.

Table 2: Dataset Collection Table

Attributes	
1. Grade	13. PTEN
2. Gender	14. EGFR
3. Age_at_diagnosis	15. CIC
4. Race	16. MUC16
5. IDH1	17. PIK3CA
6. TP53	18. NF1
7. ATRX	19. PIK3R1
8. FUBP1	20. RB1
9. NOTCH1	21. BCOR
10. CSMD3	22. SMARCA4
11. GRIN2A	23. IDH2
12. FAT4	24. PDGFRA

4.2 Pre-Processing:

Pre-processing includes data cleaning and formatting, conducting "exploratory information analysis (EDA)" to become aware of tendencies, extracting pertinent capabilities, and deciding on substantial characteristics to optimize model performance.

4.2.1 Data Processing

Data processing entails the cleaning and practise of the dataset for analysis. replica data entries are diagnosed and removed to preserve facts integrity. Drop cleansing gets rid of extraneous or inappropriate columns that do not useful resource the prediction technique. Label encoding is applied

for categorical variables like 'Gender' and 'Race' to transform them into numerical values, consequently rendering them suitable for machine learning strategies. These approaches facilitate the optimization of the dataset, making sure its preparedness for next evaluation and model improvement.

4.2.2 Exploratory Data Analysis

EDA includes comprehending the dataset's structure and distribution through visible and statistical strategies. analyzing the hyperlinks among the attributes and the intention variable 'Grade' famous insights into the records's styles, correlations, and probable outliers. precis statistics, consisting of mean, median, and standard deviation, are computed for numeric columns, at the same time as records visualizations, including histograms and field plots, are produced to assess statistics distribution and come across notable developments or anomalies.

4.2.3 Feature Extracting

Feature extraction is the method of identifying pertinent characteristics from the dataset for model education. The target variable, 'Grade', is prominent from the features, constituting the based variable (y) and independent variables (X). The capabilities, consisting of age, gender, and genetic markers, are selected for their significance and capacity association with glioma grading. Selecting pertinent features ensures that the version concentrates at the maximum influential variables, thereby enhancing prediction accuracy and minimizing information noise.

4.2.3 Feature Selection

Characteristic selection is critical for reinforcing model performance with the aid of discerning and maintaining just the maximum informative statistics. The essential feature technique identifies characteristics in keeping with their significance to the target variable. The Mutual-data technique assesses the correlation between every characteristic and the target, identifying features with great reliance. The PCA approach diminishes the dataset's dimensionality while retaining variance, therefore facilitating model simplification. The computer technique identifies functions that optimize information variance, as a result improving the model's prediction overall performance.

4.3 Training & Testing:

Dividing the dataset into training and testing subsets is critical for assessing version efficacy. The information is partitioned, normally in an 80/20 or 70/30 ratio, with the majority allotted for model training and the minority special for testing. This division facilitates model validation, guaranteeing that the educated version generalizes successfully to novel, unobserved statistics. The test set assesses the version's performance for accuracy, precision, recall, and additional metrics.

4.4 Algorithms:

“Random Forest”is utilized for its capacity to manage giant datasets and mitigate overfitting. The aggregation of predictions from numerous decision trees boosts accuracy and robustness in figuring out glioma grades, making use of an ensemble learning approach for elevated diagnostic reliability.
“Logistic Regression”is hired for binary class, mainly to distinguish between low-grade and high-grade gliomas. Reference [14] Its interpretability and efficiency render it ideal for elucidating the correlation between diagnostic markers and the opportunity of glioma occurrence, presenting big insights for clinical practitioners.
“Decision Trees”are hired to simulate decision-making techniques and classify gliomas according to diverse traits. [15] Their intuitive framework facilitates the sincere interpretation of ways numerous indicators affect category, allowing healthcare specialists to realize important variables in prognosis and therapy making plans.
“K-Nearest Neighbors (KNN)”is utilized for its straightforwardness in categorization programs. [16] It identifies the nearest information factors in feature space to categorise gliomas, so successfully finding similarities in patient statistics and improving diagnosis accuracy based on proximity.

"Support Vector Machine (SVM) with a linearkernel" is applied for its efficacy in excessive-dimensional spaces. It establishes a hyperplane to differentiate numerous glioma grades, rendering it appropriate for linear class duties and enhancing prediction accuracy based on diagnostic markers.
"SVM with a sigmoidkernel"is utilized to perceive non-linear relationships in the dataset. Mapping functions right into a better-dimensional area enables the type of complicated patterns in glioma prognosis, consequently boosting prediction overall performance and presenting more subtle insights.
"Stack-1 (RF + LR + DT + KNN with LR as Meta Model)":
"Stack-1 combines Random Forest, Logistic Regression, Decision Tree, and KNN", making use of their respective benefits to decorate type precision. Employing Logistic Regression because the Meta model improves selection-making via synthesizing predictions from numerous algorithms, yielding a dependable final prediction for glioma diagnosis.
"AdaBoost"is applied to improve the precision of weak classifiers thru the aggregation of their predictions. [19] It emphasizes misclassified examples, improving version overall performance through successive iterations. This versatility renders it useful in improving glioma class and making sure extra dependable diagnostic effects.
"CatBoost"is applied for its talent in coping with express functions efficiently without requiring enormous preprocessing. The gradient boosting framework improves predictive accuracy by figuring out problematic interconnections within the records, rendering it especially effective for evaluating several diagnostic markers in glioma diagnosis.
"LightGBM"is employed for its rapidity and efficacy in dealing with big datasets. The gradient boosting framework helps rapid training and superior performance, rendering it green for glioma classification and improving the gadget's predictive competencies whilst optimizing computational resources.
"XGBoost"is utilized for its sturdy gradient boosting techniques that enhance performance and precision. The control of absent information and evaluation of function importance decorate glioma category, making certain robust and reliable predictions derived from several diagnostic indicators.
"Stack-2 (AdaBoost + CatBoost + LGBM + XGB with LR as Meta Model)":"Stack-2 combines AdaBoost, CatBoost, LightGBM, and XGBoost, utilizing Logistic Regression"because the Meta version. This ensemble method improves anticipated accuracy through combining the strengths of many algorithms, ensuing in more advantageous class effects in glioma diagnosis through collaborative choice-making.
"Final Stack (Stack-1 + Stack-2)": The final Stack integrates the findings from Stack-1 and Stack-2, amalgamating various machine learning methodologies to improve class efficacy. This comprehensive ensemble technique makes use of the benefits of various algorithms, making certain reliable and specific glioma analysis via joint predictions.
The "**Ridge Classifier"**is utilized to cope with multicollinearity worries within the dataset. The software of L2 regularization improves model stability and overall performance, facilitating effective glioma class at the same time as keeping interpretability and lowering overfitting inside the examination of diagnostic markers.
"C4.5"is utilized for constructing decision trees from training data. It adeptly manages each specific and continuous variables, rendering it suitable for glioma category. Its potential to formulate intelligible choice regulations improves transparency inside the diagnostic procedure.
"Classification and Regression Trees (CART)"are hired to explain and categorize glioma grades using binary tree topologies. This approach facilitates explicit decision-making techniques, allowing healthcare employees to recognise the ramifications of diverse diagnostic indicators on glioma type.
"Voting Classifier (Bag with RF + DT"): The voting Classifier consolidates predictions from Random forest and decision Tree models to enhance class precision. By integrating the strengths of many algorithms, it gives you a robust final prediction for glioma diagnosis, minimizing the risk of misclassification and enhancing universal diagnostic reliability.
"Artificial Neural Networks (ANN)"are utilized for their potential to figure tricky patterns interior records. Their multi-layer structure improves predictive accuracy by taking pictures complex correlations amongst diagnostic indicators, rendering them effective for determining glioma grades based on non-linear interactions.

"Convolutional Neural Networks (CNN)"are employed for the analysis of imaging information, particularly MRI photographs. Their potential to extract spatial hierarchies and functions renders them optimal for improving glioma type accuracy, facilitating extra effective diagnoses based on visible facts patterns and attributes.

5. RESULTS AND DISCUSSION:

Accuracy: The accuracy of a test refers to its ability to properly distinguish between affected person and healthful cases. to assess the accuracy of a test, one must compute the ratio of true positives and proper negatives throughout all assessed cases. this may be expressed mathematically as:

$$"Accuracy = \frac{TP + TN}{TP + FP + TN + FN} (1)"$$

Precision: Precision assesses the percentage of correctly categorised cases amongst the ones identified as tremendous. therefore, the system for calculating precision is expressed as:

$$"Precision = \frac{\text{True Positive}}{\text{True Positive} + \text{False Positive}} (2)"$$

Recall:recall is a metric in machine learning that assesses a version's potential to recognize all pertinent times of a particular magnificence. it's far the share of as it should be predicted fantastic observations to the whole actual positives, providing insights into a version's efficacy in figuring out occurrences of a specific elegance.

$$"Recall = \frac{TP}{TP + FN} (3)"$$

F1-Score: The F1 score is a metric for evaluating the accuracy of a machine learning version. It amalgamates the precision and keep in mind metrics of a version. The accuracy metric quantifies the frequency of authentic predictions generated by a version for the duration of the entire dataset.

$$"F1\ Score = 2 * \frac{Recall\ X\ Precisio}{Recall + Precisio}$$

AUC-ROC Curve: The AUC-ROC Curve is a metric for comparing classification performance throughout distinct threshold levels. ROC plots the true positive rate as opposed to the fake positive charge. The AUC measures the model's standard ability to distinguish across instructions, with a higher AUC signifying superior version performance.

$$"AUC = \sum_{i=1}^{n-1} (FPR_{i+1} - FPR_i) \cdot \frac{TPR_{i+1} + TPR_i}{2} (5)"$$

MCC: The Matthews coefficient, or Matthews correlation coefficient (MCC), is a overall performance indicator utilized for binary classifiers in machine learning. It assesses the correlation among predicted and real binary effects by reading all 4 components of a confusion matrix.

$$"MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN}} (6)"$$

Jaccard: The Jaccard index is a metric hired to assess the similarity and variety of sample units. it's far generally defined because the ratio of two quantities (areas or volumes), mainly the size of the intersection divided by the size of the union, sometimes called intersection over union (IoU).

$$"Jaccard = \frac{|A \cap B|}{|A \cup B|} (7)"$$

In Tables 1 and 2, the "voting Classifier (Boosted DT + ExtraTree)" attained the most accuracy and overall performance among all sampling strategies—important feature, "Mutual-info FS, PCA FS, and pc FS". It continually surpassed competing algorithms throughout all measures, which include "accuracy, precision, bear in mind, F1 score, AUC score, MCC, and Jaccard score".

In Tables 3 and 4, the CNN attained the most accuracy and performance across all sampling strategies: important function, Mutual-information "FS, PCA FS, and laptop FS". It consistently exceeded competing algorithms across all measures, consisting of "accuracy, precision, recall, F1 score, AUC score, MCC, and Jaccard score".

Table 3: Performance Evaluation Metrics–Important Feature

Model	Accuracy	Precision	Recall	F1_ Score	AUC_ Score	MCC	Jaccard_ Score
Random Forest	0.810	0.810	0.810	0.809	1.000	0.615	0.682
LogisticRegression	0.833	0.847	0.833	0.832	0.912	0.680	0.716
DecisionTree	0.815	0.840	0.815	0.815	0.918	0.656	0.690
KNN	0.827	0.827	0.827	0.827	0.943	0.647	0.707
SVM-Linear	0.845	0.868	0.845	0.844	0.911	0.714	0.733
SVM-Sigmoid	0.298	0.305	0.298	0.301	0.775	-0.457	0.180
Stack-1	0.839	0.847	0.839	0.838	0.947	0.686	0.725
AdaBoost	0.845	0.855	0.845	0.844	0.938	0.700	0.734
CatBoost	0.857	0.871	0.857	0.856	0.915	0.729	0.752
LGBM	0.851	0.857	0.851	0.850	0.988	0.707	0.743
XGBoost	0.839	0.844	0.839	0.838	0.982	0.683	0.725
Stack-2	0.851	0.853	0.851	0.850	0.976	0.701	0.743
Final Stack	0.845	0.849	0.845	0.844	0.960	0.693	0.734
Ridge Classifier	0.857	0.880	0.857	0.856	0.912	0.738	0.751
C4.5	0.768	0.769	0.768	0.766	1.000	0.534	0.626
CART	0.804	0.804	0.804	0.803	1.000	0.604	0.674
VotingClassifier	**1.000**	**1.000**	**1.000**	**1.000**	**0.876**	**1.000**	**1.000**
ANN	0.833	0.834	0.833	0.833	0.876	0.663	0.716
CNN	0.821	0.821	0.821	0.821	1.000	0.642	0.697

Graph 1: Comparison Graphs – Important Feature

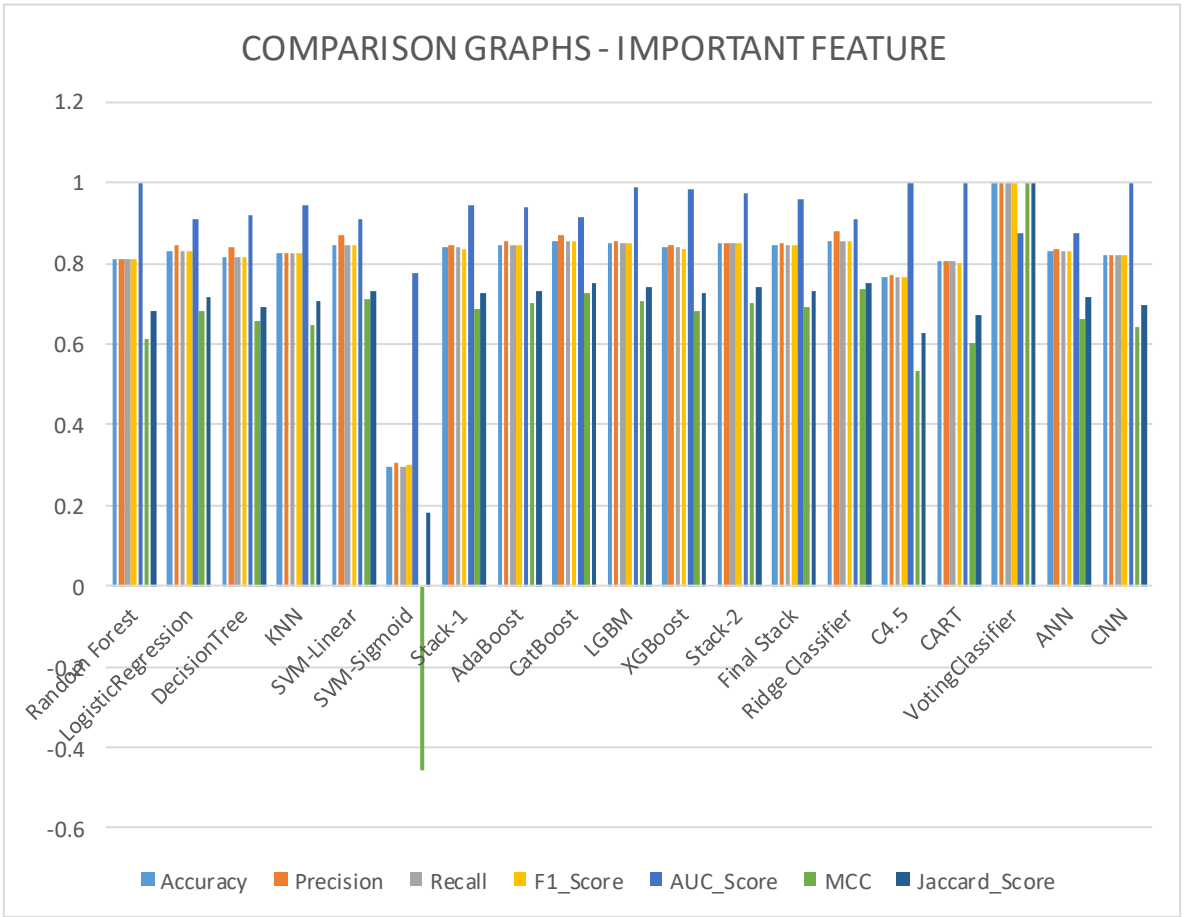


Table 4: Performance Evaluation Metrics – Mutual-Info FS

Model	Accuracy	Precision	Recall	F1_ Score	AUC_ Score	MCC	Jaccard_ Score
Random Forest	0.774	0.798	0.774	0.779	1.000	0.538	0.627
LogisticRegression	0.875	0.875	0.875	0.875	0.917	0.746	0.778
DecisionTree	0.857	0.857	0.857	0.857	0.923	0.710	0.751
KNN	0.839	0.845	0.839	0.840	0.950	0.672	0.722
SVM-Linear	0.881	0.882	0.881	0.881	0.915	0.762	0.788
SVM-Sigmoid	0.381	0.429	0.381	0.401	0.792	-0.311	0.232
Stack-1	0.845	0.846	0.845	0.846	0.978	0.684	0.732
AdaBoost	0.863	0.863	0.863	0.863	0.940	0.723	0.760
CatBoost	0.863	0.863	0.863	0.863	0.906	0.723	0.760
LGBM	0.833	0.840	0.833	0.835	0.988	0.660	0.713
XGBoost	0.833	0.838	0.833	0.834	0.980	0.659	0.714
Stack-2	0.833	0.840	0.833	0.835	0.980	0.660	0.713
Final Stack	0.845	0.849	0.845	0.846	0.980	0.684	0.731
Ridge Classifier	0.869	0.870	0.869	0.869	0.917	0.738	0.769
C4.5	0.774	0.798	0.774	0.779	1.000	0.538	0.627
CART	0.768	0.801	0.768	0.775	1.000	0.528	0.618
VotingClassifier	**1.000**	**1.000**	**1.000**	**1.000**	**0.879**	**1.000**	**1.000**
ANN	0.565	0.690	0.565	0.604	0.879	0.069	0.376
CNN	0.756	0.816	0.756	0.768	1.000	0.507	0.597

Graph 2: Comparison Graphs –Mutual-Info FS

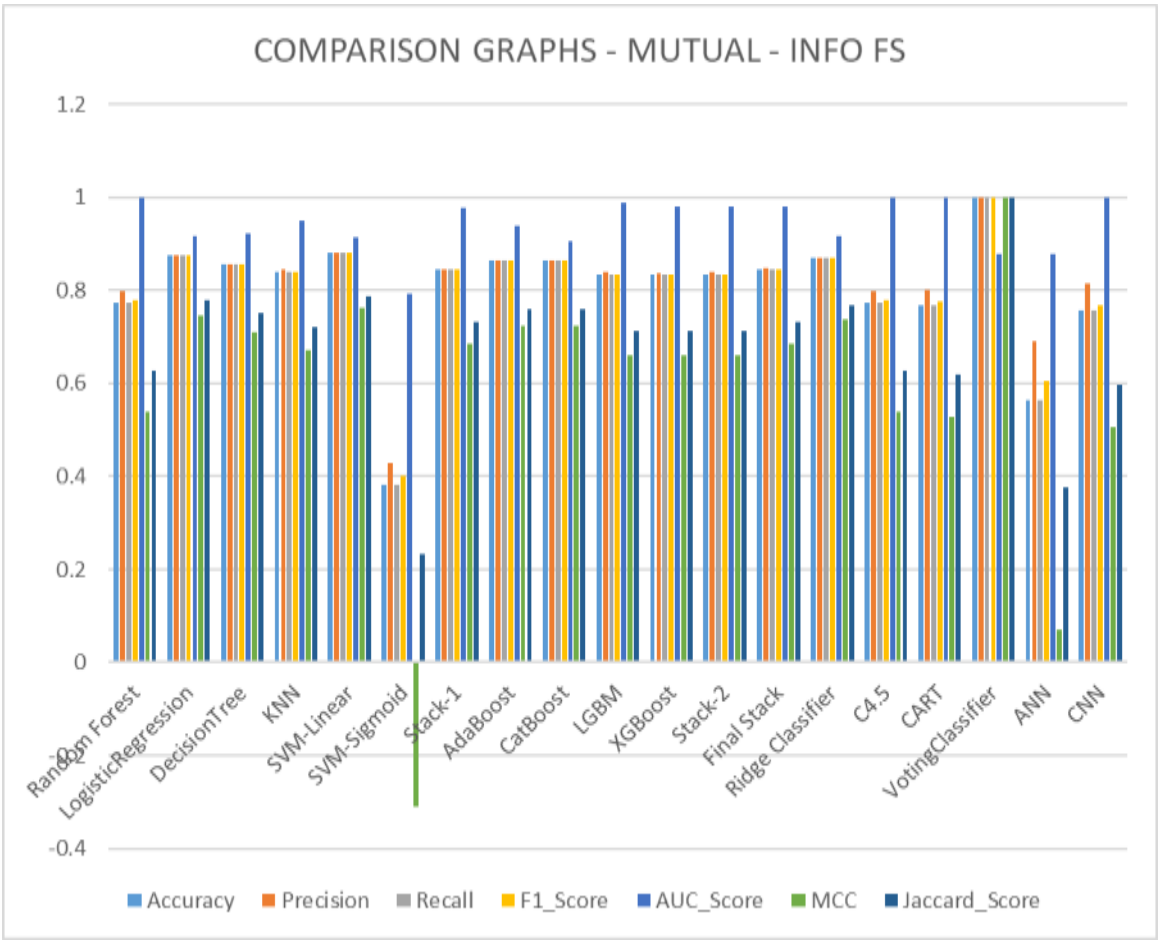


Table 5: Performance Evaluation Metrics – PCA FS

Model	Accuracy	Precision	Recall	F1_Score	AUC_Score	MCC	Jaccard_Score
Random Forest	0.869	0.874	0.869	0.868	0.916	0.742	0.770
LogisticRegression	0.869	0.876	0.869	0.868	0.908	0.744	0.770
DecisionTree	0.869	0.874	0.869	0.868	0.900	0.742	0.770
KNN	0.869	0.874	0.869	0.868	0.896	0.742	0.770
SVM-Linear	0.873	0.881	0.873	0.872	0.903	0.753	0.776
SVM-Sigmoid	0.813	0.813	0.813	0.813	0.811	0.620	0.687
Stack-1	0.865	0.869	0.865	0.864	0.911	0.733	0.764
AdaBoost	0.873	0.879	0.873	0.872	0.911	0.751	0.776
CatBoost	0.869	0.877	0.869	0.868	0.889	0.746	0.770
LGBM	0.857	0.864	0.857	0.856	0.899	0.721	0.752
XGBoost	0.865	0.869	0.865	0.864	0.914	0.733	0.764
Stack-2	0.873	0.877	0.873	0.872	0.908	0.749	0.776
Final Stack	0.865	0.869	0.865	0.864	0.910	0.733	0.764
Ridge Classifier	0.869	0.877	0.869	0.868	0.908	0.746	0.770
C4.5	0.869	0.874	0.869	0.868	0.918	0.742	0.770
CART	0.869	0.874	0.869	0.868	0.918	0.742	0.770
VotingClassifier	0.889	0.897	0.889	0.888	0.902	0.785	0.801
ANN	0.579	1.000	0.579	0.734	0.902	0.000	0.336
CNN	**0.915**	**0.916**	**0.915**	**0.915**	**0.920**	**0.825**	**0.845**

Graph 3: Comparison Graphs –PCA FS

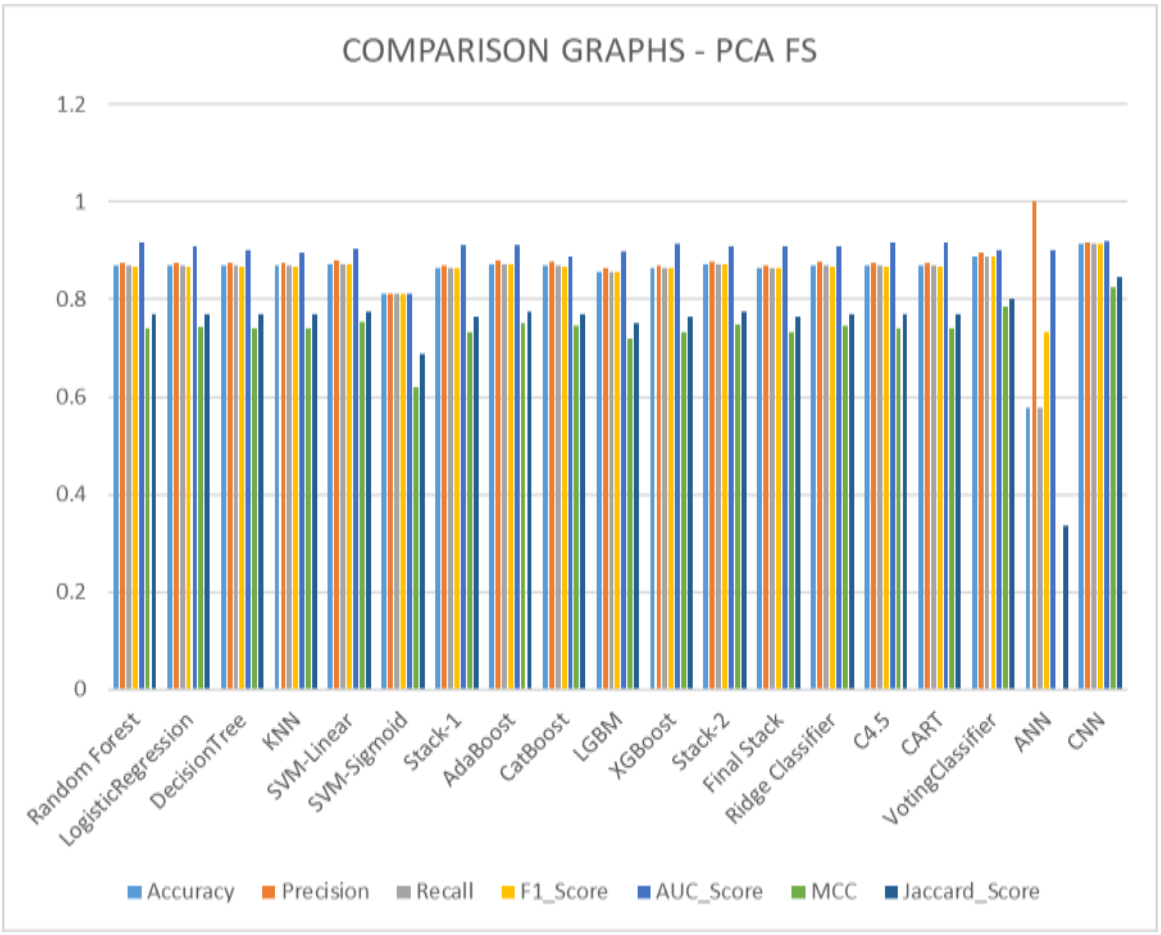
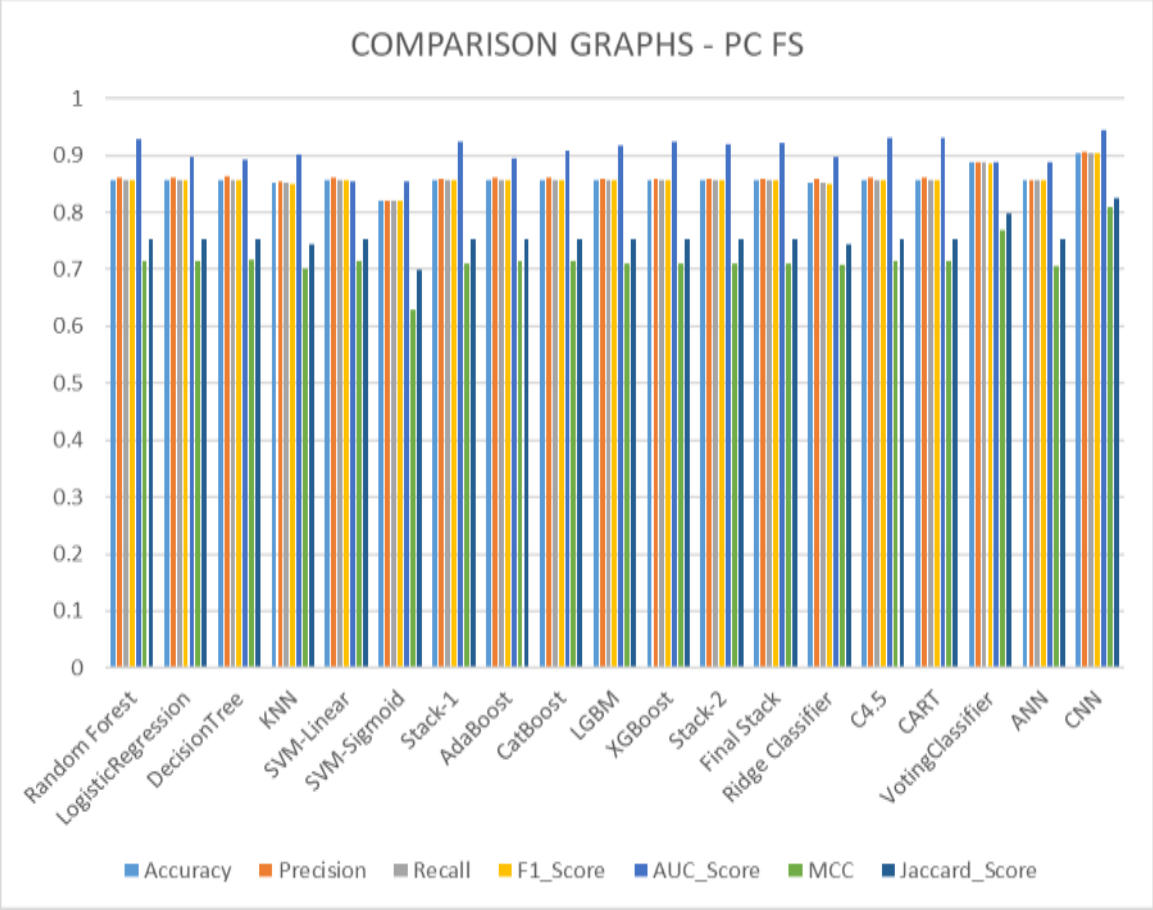


Table 6: Performance Evaluation Metrics – PC FS

Model	Accuracy	Precision	Recall	F1_Score	AUC_Score	MCC	Jaccard_Score
Random Forest	0.857	0.861	0.857	0.856	0.928	0.714	0.753
LogisticRegression	0.857	0.861	0.857	0.856	0.897	0.714	0.753
DecisionTree	0.857	0.863	0.857	0.856	0.893	0.717	0.753
KNN	0.851	0.854	0.851	0.850	0.902	0.700	0.744
SVM-Linear	0.857	0.861	0.857	0.856	0.854	0.714	0.753
SVM-Sigmoid	0.821	0.821	0.821	0.821	0.854	0.628	0.699
Stack-1	0.857	0.859	0.857	0.856	0.923	0.710	0.753
AdaBoost	0.857	0.861	0.857	0.856	0.895	0.714	0.753
CatBoost	0.857	0.861	0.857	0.856	0.908	0.714	0.753
LGBM	0.857	0.859	0.857	0.856	0.918	0.710	0.753
XGBoost	0.857	0.859	0.857	0.856	0.923	0.710	0.753
Stack-2	0.857	0.859	0.857	0.856	0.919	0.710	0.753
Final Stack	0.857	0.859	0.857	0.856	0.921	0.710	0.753
Ridge Classifier	0.851	0.859	0.851	0.850	0.897	0.707	0.744
C4.5	0.857	0.861	0.857	0.856	0.931	0.714	0.753
CART	0.857	0.861	0.857	0.856	0.931	0.714	0.753
VotingClassifier	0.887	0.887	0.887	0.886	0.889	0.768	0.798
ANN	0.857	0.857	0.857	0.856	0.889	0.705	0.752
CNN	**0.904**	**0.907**	**0.904**	**0.903**	**0.945**	**0.809**	**0.826**

Graph 4: Comparison Graphs –PC FS



In Graphs (1, 2, 3, and 4), accuracy is depicted in light blue, precision in orange, recall in gray, F1-score in yellow, AUC score in blue, MCC in green, and Jaccard score. The voting Classifier surpasses all different algorithms throughout all standards, exhibiting the greatest values relative to the alternative models. The aforementioned graph truely depicts these details.

6. CONCLUSION:

Timely identification and intervention for glioma tumors can decorate their prognosis and mitigate potential complications. The advised method makes use of a synthesis of "machine learning, deep studying, and explainable artificial intelligence (XAI)" to obtain particular and interpretable results in glioma grading. The system effectively detects important diagnostic indicators for greater predictive accuracy thru the application of numerous feature selection strategies, which includes important "feature selection, Mutual records FS, PCA FS, and Pearson Coefficient FS". The voting Classifier exhibited superior performance most of the studied algorithms, accomplishing 100% accuracy for essential function and Mutual records feature selection. The CNN model confirmed outstanding performance, with 91% accuracy with PCA feature selection and 90% with Pearson coefficient feature selection. The effects underscore the efficacy of integrating trendy machine learning models with deep learning methodologies, making certain each advanced overall performance and transparency in glioma diagnosis. The system's capacity to supply specific, personalized predictions can substantially facilitate early prognosis and treatment, enhancing patient outcomes.

The future potential of this system encompasses the enhancement of feature selection methodologies and the research of sophisticated deep learning architectures, which includes Transformer models, to reap more accuracy. Furthermore, which includes multi-modal data assets, inclusive of genomic and scientific statistics, may additionally augment the system's predictive capability. The real-time application in medical environments, along with ongoing version retraining with new information, will enhance predictions, consequently helping in the development of individualized treatment techniques and improving patient care in glioma prognosis.

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