



**IJIRCCCE**

e-ISSN: 2320-9801 | p-ISSN: 2320-9798



# INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN COMPUTER & COMMUNICATION ENGINEERING

Volume 12, Issue 10, October 2024

**ISSN** INTERNATIONAL  
STANDARD  
SERIAL  
NUMBER  
INDIA

**Impact Factor: 8.625**



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# Learning on Brain Tumor Images for an Efficient Identification Approach by Fuzzy Color and Texture Histogram (FCTH) Filter and RGB Color Histogram Filter

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**ABSTRACT:** This study focuses on the classification and segmentation of brain tumors using a two-part dataset tailored for these specific tasks. The classification dataset involves categorizing brain tumors into four distinct classes: glioma, meningioma, pituitary tumors, and no tumor, while the segmentation dataset aims to detect the presence or absence of tumors and localize their positions if present. Various classifier combinations were evaluated, with models using FCTH (Fuzzy Color and Texture Histogram) filter consistently outperforming those utilizing RGBCHF (Red Green Blue Color Histogram Filter) features. Among the classifiers tested, FCTH combined with Support Vector Machine (SVM) achieved the highest performance metrics, including an accuracy of 80.51%, as well as high precision, recall, and ROC-PRC scores, indicating robust tumor classification capabilities. The segmentation task leverages a training-validation-test split to ensure precise tumor detection and localization, crucial for accurate diagnosis and treatment planning. This dual approach enhances the identification, categorization, and localization of brain tumors, contributing to more effective clinical decision-making.

**KEYWORDS:** Brain Tumour, IBK, Detection ,SVM, RGB Color Histogram

## I. INTRODUCTION

Brain tumors are among the most complex and life-threatening conditions, posing significant challenges to patients and healthcare professionals due to their diverse types, locations, and behaviors. They can arise from various cells and structures within the brain or surrounding tissues, leading to symptoms such as headaches, seizures, neurological deficits, and cognitive changes, depending on their size and location. Brain tumors can be broadly categorized into two types: benign and malignant. Benign tumors are non-cancerous and generally grow slowly, whereas malignant tumors are cancerous, often more aggressive, and capable of invading surrounding tissues or spreading to other parts of the brain or body.

The classification and early detection of brain tumors are critical for determining effective treatment strategies and improving patient outcomes. Tumors such as gliomas, meningiomas, and pituitary tumors vary greatly in their characteristics, and accurately distinguishing between these types can guide appropriate interventions, including surgery, radiotherapy, or chemotherapy. Furthermore, identifying the presence and precise location of tumors is crucial for planning targeted therapies, minimizing damage to healthy brain tissue, and improving prognosis.



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Recent advances in medical imaging and computational techniques, particularly in the fields of machine learning and deep learning, have paved the way for automated systems capable of classifying and segmenting brain tumors. These systems utilize various feature extraction and classification methods to analyze medical images, providing accurate predictions and detailed insights into tumor characteristics. By automating the process, such systems can reduce the burden on radiologists, increase diagnostic accuracy, and offer consistent, reproducible results across large datasets. This work organizes section 2 has literature survey, section 3 has materials and methods and section 4 has results and discussions and section 5 has conclusions.

### II. LITERATURE SURVEY

This work focuses the related works of this research. Vision Transformers (ViT) and Gated Recurrent Units (GRU) are advanced deep learning techniques [1] that have demonstrated significant capabilities in image classification and sequential data modeling, respectively. Prior research has often utilized convolutional neural networks (CNNs) to detect brain tumors in MRI scans, but the integration of ViT and GRU offers a novel approach by combining spatial feature extraction and temporal feature relationships. Literature shows that CNNs have faced limitations in capturing global image relationships, which ViTs can overcome through self-attention mechanisms. Similarly, GRUs have proven effective in managing sequential data dependencies. Recent studies have emphasized the importance of addressing data imbalance in medical imaging datasets. Incorporating various optimizers and employing rigorous cross-validation methodologies is consistent with best practices highlighted in existing literature for enhancing model robustness. Moreover, Explainable Artificial Intelligence (XAI) techniques such as SHAP, LIME, and attention maps align with recent trends in making AI models more interpretable for clinical applications, fostering trust among medical practitioners. The YOLO (You Only Look Once) family of models[2], including YOLOv7, is recognized for real-time object detection capabilities and has been adapted for various medical imaging tasks. Previous studies have demonstrated YOLO's potential in detecting abnormalities, but the detection of gliomas, meningiomas, and pituitary tumors remains a complex challenge due to their variable size, location, and shape. Literature [3-7] supports the need for transfer learning and fine-tuning in scenarios with limited data availability, as these techniques enhance model generalizability. Data augmentation and image enhancement techniques have also been frequently employed to improve model performance on medical image datasets. The incorporation of advanced modules, such as the Convolutional Block Attention Module (CBAM) and Spatial Pyramid Pooling Fast+ (SPPF+), aligns with emerging trends in deep learning for emphasizing salient image features and improving multi-scale feature fusion. Studies have further validated that specialized attention mechanisms and architectural modifications enhance the sensitivity and precision of medical image detection models. Author [8] reveals that while basic CNNs perform well on medical images, deeper models such as ResNet101, DenseNet121, and VGG architectures offer more robust feature representation. However, challenges in detecting early-stage Alzheimer's, marked by subtle brain changes, highlight the need for more refined models. Studies have consistently demonstrated the utility of MRI as a non-invasive tool for diagnosing Alzheimer's. Comparative analysis of different deep learning models and the emphasis on accuracy, recall, and AUC metrics reflect standard practices for evaluating model efficacy in medical imaging. This work [9] Deep learning has revolutionized digital pathology by automating complex image analysis tasks, including classification, detection, and segmentation. Existing literature highlights how the integration of pre- and post-processing techniques within deep learning pipelines can enhance model accuracy and performance. Pre-processing techniques, such as image normalization and augmentation, help optimize input data, while post-processing stages, like output refinement and error correction, further enhance model predictions. The adoption of these techniques across various medical imaging domains underscores their versatility. Research consistently shows that hybrid approaches combining traditional image processing with modern deep learning architectures yield superior outcomes, particularly in challenging tasks like nuclei and gland segmentation. This work[10] comparing CNN-based approaches with other pre-trained models, such as VGG16, VGG19, ResNet50, MobileNetV2, and InceptionV3, highlights the strengths and weaknesses of different architectures in handling medical imaging data. The high accuracy and robust performance reported for CNN-based models are consistent with findings from existing research, emphasizing their ability to generalize across different datasets. The trend of leveraging deep learning for automated diagnostics in healthcare has been well-documented, with studies emphasizing speed and accuracy to support clinical decision-making. This aligns with efforts to enhance diagnostic precision and reduce reliance on manual interpretation of medical images. This study[11] utilizes three BraTS datasets for classifying brain tumors into two categories, with each dataset containing four 3D MRI sequences per patient. The research is divided into two primary approaches: In the first approach, a hybrid model named TimeDistributed-CNN-LSTM (TD-CNN-LSTM) is proposed, combining 3D Convolutional Neural Networks (CNN)





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with Long Short-Term Memory (LSTM) networks, where each layer is wrapped with a TimeDistributed function. This methodology treats all four MRI sequences of each patient as a single comprehensive input, thereby capturing the complete set of tumor information available across different sequences. The model is optimized through ablation studies, focusing on refining the layer architecture and tuning hyperparameters to achieve the best possible performance. The second approach involves training a 3D CNN model separately for each MRI sequence, serving as a performance benchmark. Preprocessing techniques were applied to the datasets to maximize model performance and accuracy. Comparative analysis reveals that the TD-CNN-LSTM model outperforms the standalone 3D CNN, achieving a test accuracy of 98.90%. To further assess its reliability and generalization capability, the TD-CNN-LSTM model was evaluated using K-fold cross-validation. The integration of all MRI sequences within a single model input, combined with strong generalization, presents promising potential for enhancing medical research and aiding radiologists in accurate tumor diagnostics. This approach demonstrates the capacity for deep learning models to offer substantial improvements in the precision and efficiency of brain tumor detection.

### III. MATERIALS AND METHODS

The dataset borrowed from Kaggle data repository named as brain tumor mri dataset which is divided into two separate parts. The first part is a dataset created for classification. Here, brain tumors are divided into 4 different classes. These are: glioma, meningioma, pituitary and no tumor. Training and test separation is made in the folder.

The second part is created for segmentation. Here, two different classes are created only to detect the presence or absence of the tumor, and only for cases where the tumor is present, the coordinates of the tumor are in the labels folder.

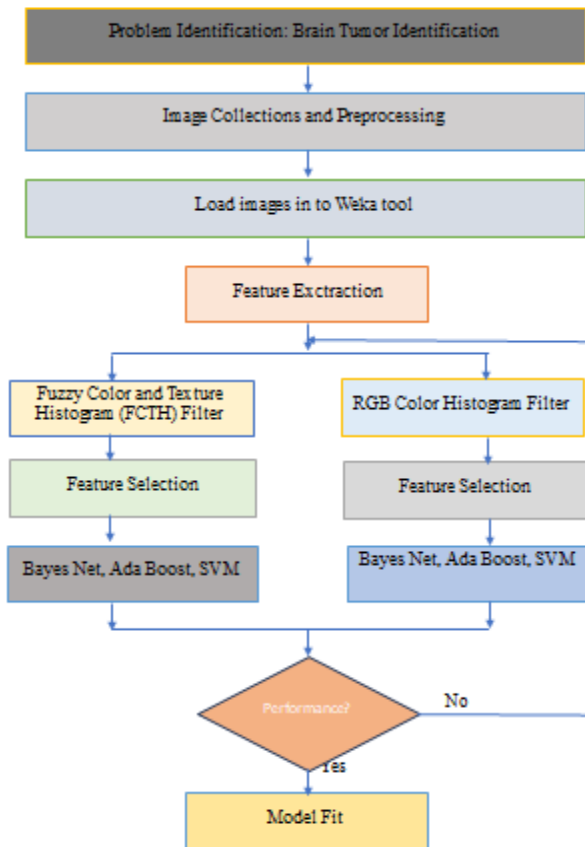


Figure 1: proposed system



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**Table 1: Classification Metrics**

S.No	Classifier	Accuracy	Precision	Recall	ROC	PRC
1	FCTH + NB	76.93%	0.81	0.76	0.84	0.84
2	FCTH + Ada Boost	77.62%	0.79	0.77	0.85	0.84
3	FCTH + SVM	80.51%	0.81	0.81	0.88	0.88
4	RGBCHF + NB	77.51%	0.77	0.77	0.85	0.84
5	RGBCHF + Ada Boost	75.28%	0.81	0.75	0.84	0.83
6	RGBCHF + SVM	74.57%	0.75	0.74	0.75	0.69

FCTH (Fuzzy Color and Texture Histogram (FCTH) Filter) + NB (Naive Bayes) achieves a moderate accuracy of 76.93%, with a strong precision of 0.81. The high precision means that when this model makes a prediction, it is often correct, indicating fewer false positives. However, the recall of 0.76 suggests that while it identifies many relevant instances, it still misses some. The ROC and PRC scores of 0.84 show this model's capability to differentiate between classes effectively.

FCTH Fuzzy Color and Texture Histogram (FCTH) Filter) + AdaBoost shows a slight improvement in accuracy and recall compared to Naive Bayes with FCTH, reaching 77.62% accuracy and 0.77 recall. This improvement suggests that AdaBoost, which works by boosting the focus on misclassified examples, better captures the complex relationships in the data. The precision is slightly lower than FCTH + NB at 0.79, but its stronger recall and ROC score of 0.85 highlight its capability to detect more relevant instances correctly.

FCTH Fuzzy Color and Texture Histogram (FCTH) Filter) + SVM (Support Vector Machine) has the highest accuracy at 80.51% and balanced precision and recall scores of 0.81 each. This indicates it excels in classifying instances correctly while minimizing both false positives and false negatives. The high ROC (0.88) and PRC (0.88) scores show that this model performs exceptionally well in distinguishing between classes. This combination stands out as the best-performing one among all, leveraging SVM's strength in handling high-dimensional data effectively.

RGBCHF (RGB Color Histogram Filter) + NB (Naive Bayes) model, achieve a slightly higher accuracy (77.51%) compared to FCTH + AdaBoost, with balanced precision and recall scores of 0.77. However, both metrics are slightly lower than their FCTH counterparts, indicating that RGBCHF's lack of texture features could make it less discriminative, leading to slightly reduced classification performance compared to FCTH-based combinations.

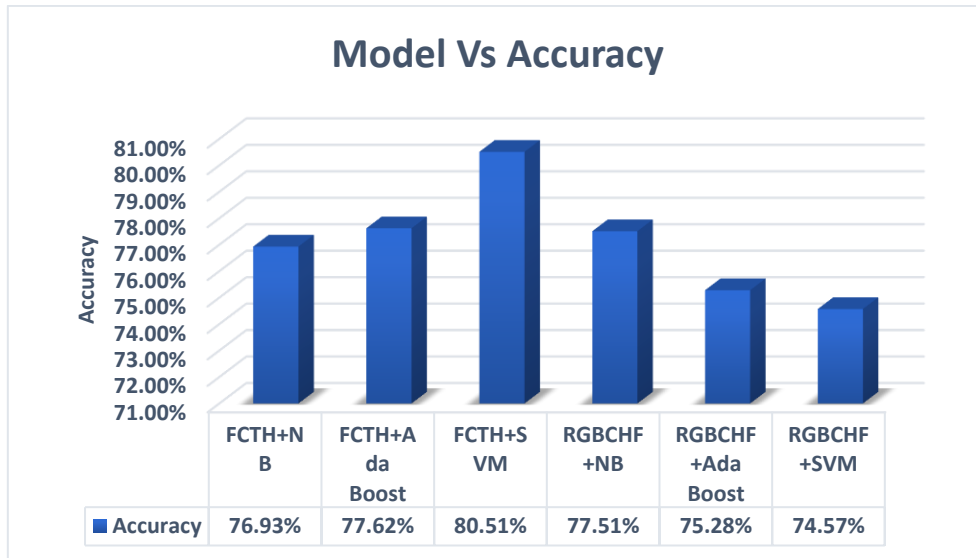
RGBCHF (RGB Color Histogram Filter)+ AdaBoost model shows high precision (0.81) but slightly lower recall (0.75). The high precision suggests fewer false positives, but the lower recall indicates more missed relevant instances. The overall accuracy is the lowest among AdaBoost models (75.28%), and the PRC (0.83) reflects slightly reduced performance, likely due to focusing solely on color features without texture.

RGBCHF (RGB Color Histogram Filter)+ SVM (Support Vector Machine) model has the lowest accuracy (74.57%) and relatively low precision (0.75), recall (0.74), and PRC (0.69). This indicates that SVM struggles with RGBCHF features, potentially because these features do not capture the necessary texture information to distinguish between classes effectively, resulting in lower overall performance.



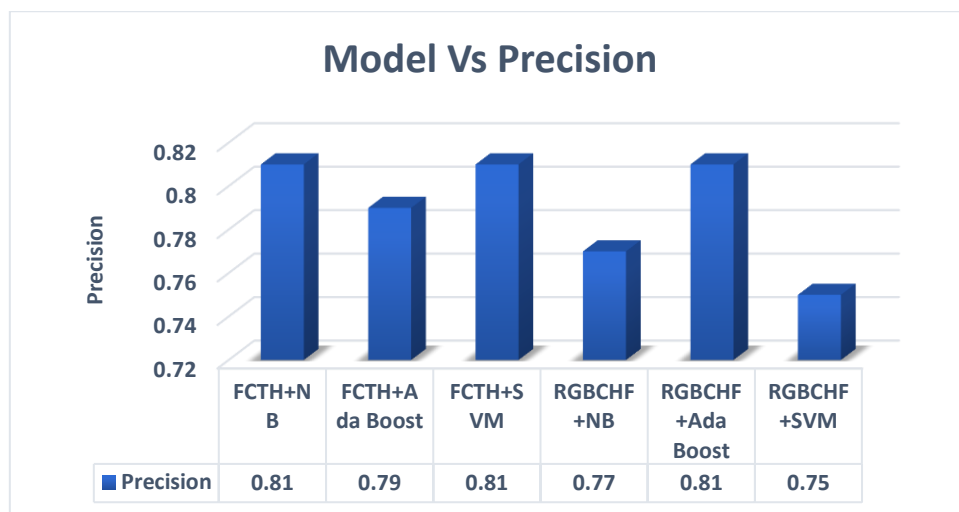
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**Figure 2: Model vs. Accuracy**

The "Model Vs Accuracy" chart 2 provides a visual representation of the accuracy achieved by different classifiers using FCTH and RGBCHF feature extraction methods. The combination of FCTH + SVM stands out with the highest accuracy, reaching approximately 80.51%, highlighting its superior performance over other classifier-feature combinations. In general, models using FCTH features tend to perform better than those using RGBCHF, indicating that the combined color and texture features in FCTH offer more robust information for classification. Comparatively, among the models using RGBCHF features, RGBCHF + NB achieves the highest accuracy, while RGBCHF + SVM shows the lowest. On the other hand, FCTH-based classifiers show a distinct improvement in performance, with FCTH + NB and FCTH + AdaBoost also achieving relatively high accuracy, although slightly lower than FCTH + SVM.



**Figure 3: Model vs. Precision**

The chart 3 shows that FCTH + NB and FCTH + SVM both achieve the highest precision, with a value of 0.81. This indicates that these models produce fewer false positives and are highly reliable in their positive predictions. RGBCHF + AdaBoost also achieves a precision of 0.81, suggesting good performance in terms of accurate positive predictions, although it is less consistent than FCTH-based models in other metrics. On the other hand, RGBCHF + NB and



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RGBCHF + SVM exhibit lower precision, with values of 0.77 and 0.75, respectively, demonstrating a higher likelihood of false positives compared to the FCTH-based models. FCTH + AdaBoost has a slightly lower precision of 0.79 compared to other FCTH combinations, indicating a modest drop in accuracy for its positive predictions.

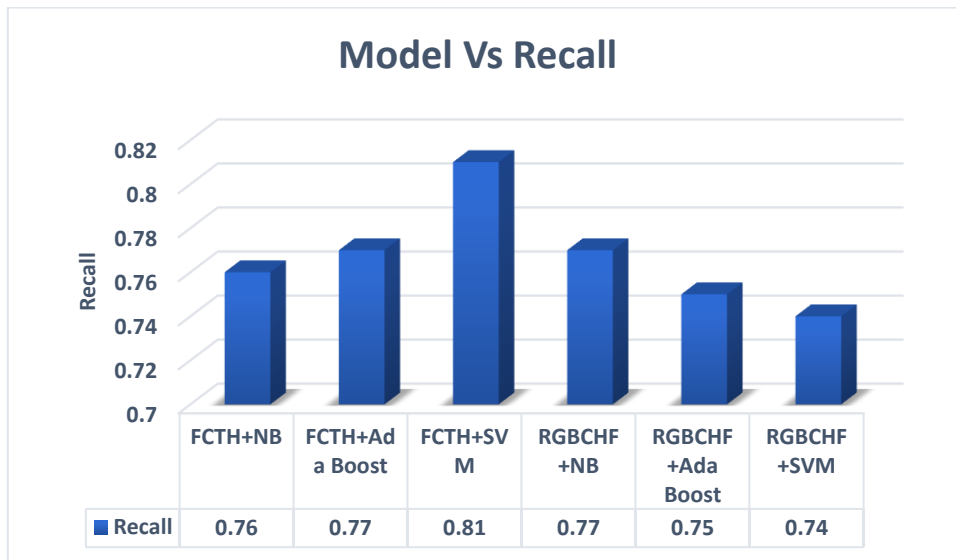


Figure 4: Model vs. Recall

In the chart 4 , FCTH + SVM achieves the highest recall value of 0.81, indicating that it is highly effective in identifying true positives. This suggests that this combination is capable of capturing a large portion of the relevant instances, making it useful in applications where missing relevant instances is costly. The FCTH + AdaBoost and RGBCHF + NB both achieve a recall of 0.77, demonstrating reasonably good sensitivity but slightly lower than FCTH + SVM. FCTH + NB has a slightly lower recall at 0.76, indicating a minor reduction in its ability to detect true positives compared to the top-performing FCTH-based model.

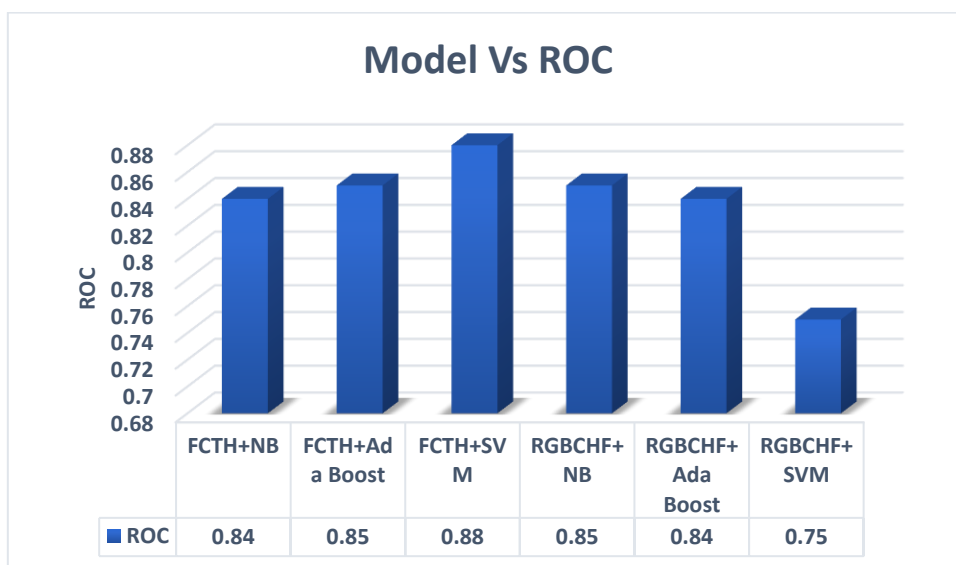


Figure 5: Model vs. ROC



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In this chart 5, FCTH + SVM achieves the highest ROC value at 0.88, demonstrating its superior capability to differentiate between positive and negative classes. This makes it a highly reliable model for classification tasks where distinguishing between classes is critical. FCTH + AdaBoost and RGBCHF + NB both achieve a ROC value of 0.85, showing solid performance in discriminating between classes. FCTH + NB and RGBCHF + AdaBoost follow closely with a ROC value of 0.84, indicating a slightly lower but still commendable ability to separate classes. The model with the lowest ROC value is RGBCHF + SVM, which has a value of 0.75. This indicates weaker performance compared to the other models, suggesting that it may struggle more with distinguishing between classes, possibly due to the limitations of the RGBCHF feature set.

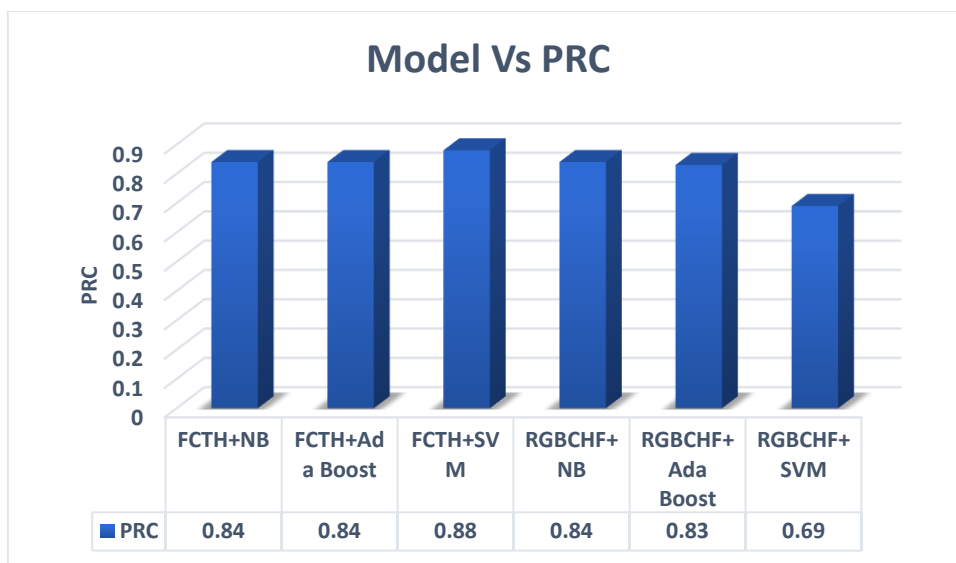


Figure 6: Model vs. PRC

This above chart 6, the highest PRC value is achieved by FCTH + SVM, with a score of 0.88. This indicates that this combination strikes the best balance between precision and recall, making it highly effective at correctly identifying true positives with fewer false positives and false negatives. FCTH + NB, FCTH + AdaBoost, and RGBCHF + NB each have a PRC value of 0.84, demonstrating strong performance as well. This suggests that these models provide good precision and recall, resulting in reliable classification outcomes. RGBCHF + AdaBoost has a slightly lower PRC value of 0.83, indicating a small decrease in its balance between precision and recall compared to other high-performing models. RGBCHF + SVM, however, exhibits the lowest PRC value at 0.69, highlighting its weaker ability to maintain a good trade-off between precision and recall. This suggests a higher likelihood of either missing true positives (lower recall) or misclassifying false positives (lower precision).

### IV. CONCLUSION

This work indicates that models using FCTH features generally outperform RGBCHF-based models. Among the tested classifiers, FCTH + SVM demonstrates the highest accuracy (80.51%) and strong precision, recall, ROC, and PRC values, making it a highly effective choice for tumor classification. The segmentation aspect focuses solely on detecting the presence of tumors and localizing them, providing critical support for identifying regions of interest, which is essential for accurate diagnosis and treatment planning.





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