CGHF: A Computational Decision Support System for Glioma Classification Using Hybrid Radiomics- and Stationary Wavelet-Based Features

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ABSTRACT Brain tumors are the most prominent neurologically malignant cancers with the highest injury and death rates worldwide. Glioma classification is crucial for the prognosis, assessment of prognostication and the planning of clinical guidelines before surgery. Herein, we introduce a novel stationary wavelet-based radiomics approach to classify the grade of glioma more accurately and in a non-invasive manner. The training dataset of Brain Tumor Segmentation (BraTS) Challenge 2018 is used for performance evaluation and calculation is done based on the radiomics features for three different regions of interest. The classifier, Random Forest, is trained on these features and predicted the grade of glioma. At last, the performance is validated by using five-fold cross-validation scheme. The state-of-the-art performance is achieved considering metric \( \langle \text{Acc}, \text{Sens}, \text{Spec}, \text{Score}, \text{MCC}, \text{AUC} \rangle \equiv \langle 97.54\%, 97.62\%, 97.33\%, 98.3\%, 94.12\%, 97.48\% \rangle \) with machine learning predictive model Random Forest (RF) for brain tumor patients’ classification. Considering the importance of glioma classification for the assessment of prognosis, our approach could be useful in the planning of clinical guidelines prior to surgery.

INDEX TERMS Radiomics, machine learning, random forest, filter, feature extraction, grading of glioma.

I. INTRODUCTION Cancer is the abnormal growth of cells that represent the multi-stage transformation of healthy cells into malignant cells, which are attributed to the various genetic factors and external agents [1]. Gliomas are the most malignant primary brain tumor and a widespread brain cancerous disease, arising from glial cells that account for approximately 24.7% of all the primary brain tumors as well as other tumors in the central nervous system (CNS) and accounts approximately 74.6% for malignant tumors [2], [3]. According to World Health Organization (WHO) gliomas grading system, gliomas are one of the fastest-growing brain cancers and are subdivided into four Grades, i.e., Grade-I (pilocytic astrocytoma), Grade-II (low-grade glioma), Grade-III (malignant glioma) and Grade-IV (glioblastoma multiforme). These are broadly divided into two categories based on their aggressiveness and malignancy. The Grade-I and II gliomas are popularly known as low-grade gliomas (LGG) and Grade-III and IV gliomas are known as high-grade gliomas (HGG) [4]–[6]. Classification of gliomas into HGG and LGG is crucial towards planning the course of treatment (e.g., chemotherapy, targeted therapy, radiation therapy, etc.) and estimating approximate survival time of the patient. LGG tumors are slower in growth and less aggressive as compared to HGG tumors. Although, they have slower growth, if left untreated, LGG tumors can turn into HGG tumor. Consequently, a system that can classify gliomas into HGG or LGG, is widely accepted and adopted. During the last few decades, medical imaging has emerged as an evolutionary field playing a vital role in producing digital medical images. These medical images aid doctors and radiologists to assist in disease prediction and prognostication which leads to early disease detection and improved diagnostics.

Medical imaging is a non-invasive process to produce a view of physiological structures. These structures are either
visible or hidden inside the body. An area or part of a region is evaluated by a medical expert to diagnose a disease. The reason behind rapid evolution in both research and clinical practice is computer-assisted interpretation of image, which have encouraged digital medical imaging. Medical imaging has grown at a rapid rate during the last few decades due to its interdisciplinary contributions in the prime areas of basic sciences and medicine. The main goal of medical imaging is to extract information related to internal organs of the body through physiological processes by using internal or external energy sources or a combination of both [7]. Medical imaging, particularly conventional magnetic resonance imaging (MRI), is a promising non-invasive method for characterizing gliomas. Decoding characteristics of tumors in a non-invasive way is a recent field of study known as radiomics. It involves the extraction of extensive features which can quantify the attributes of tumors. These features may not be evident and apparent to the human eye. In the proposed work, various machine learning approaches are applied to extracted features from radiomics to classify patients’ images into HGG or LGG.

**Main Contribution:** The major research contributions in the proposed work CGHF include designing of computationally efficient decision support system based upon prediction-based models of machine learning for gliomas grading. The efficacy of CGHF is validated using k-fold cross-validation scheme where k = 5, over publicly available brain tumor segmentation BraTS 2018 [8]–[10] challenge dataset. The CGHF exploits the machine learning predictive model Random Forest for brain tumor patients’ classification. To evaluate the performance of CGHF, the performance metric \( (\text{Acc}, \text{Sens}, \text{Spec}, \text{Score}, \text{MCC}, \text{AUC}) \) is calculated, where Acc, Sens, Spec, Score, MCC and AUC represents the accuracy, sensitivity, specificity, F1-score, Matthew’s correlation coefficient and area under the curve, respectively. The major research contributions can be listed as:

- The performance of the proposed approach CGHF is evaluated over well-known classifiers’ performance and concluded Random Forest (RF) performance well among all of them.
- The performance of Random Forest is measured on the proposed three feature extraction techniques namely, R-Extraction, S-Extraction and RS-Extraction considering nine feature selection techniques with k-fold cross-validation scheme.
- The performance is evaluated considering feature selection on 50% and 10% of total features to find out the impact of features’ reduction.

The rest of the paper is organized as follows: Section II provides state-of-the-art along with recent baseline methods as research contribution for developing a decision support system. Section III includes the details of dataset used i.e., BraTS 2018 [8]–[10] along with different regions of interest (RoIs) considered. A motivation and problem formulation for CGHF is presented in Section IV. Section V discusses dataset pre-processing and methods used for it. Section VI explains the feature extraction methods used which are based on stationary wavelet transform and radiomics based techniques. Section VII represents all features selection and reduction techniques in detail considering storage requirement and time computation. Section VIII presents our proposed three variants of CGHF, namely R-Extraction, S-Extraction and RS-Extraction methods. Moreover, Section IX presents the exhaustive experimentation and results over BraTS 2018 dataset considering feature selection, reduction and extraction techniques along with our proposed model CGHF demonstrating the effectiveness of our approach. Finally, Section X concludes the work along with future scope.

**II. STATE-OF-THE-ART**

The state-of-the-art and recently published baseline methods for classification and segmentation considers magnetic resonance images (MRI) scan of the human brain with support of emerging technologies in medical imaging such as computer-aided design (CAD) tools and decision support system based on predictive machine models. The proposed approaches and their results show that solving segmentation and classification problems using CAD made remarkable progress, however it is still an open problem as the performance is yet at question. In recent times, radiomics is known as a new non-invasive diagnostic methodology, focused on quantitative analysis of clinical images by extracting high-performance image features from multiple MR/CT modalities [11], [12].

Cho et al. [14] suggested a radiomics-based glioma classification, using various radiomics feature extraction and selection techniques. In another study, Cho and Park [15] found that the application of histogram based features, shape descriptors and gray level co-occurrence matrix (GLCM)-based texture characteristics strengthened the distinction between LGG and HGG, and has achieved \( (\text{Acc}, \text{Sens}, \text{Spec}) \) \( \equiv \) \( (89.81\%, 88.89\%, 90.74\%) \) over BraTS 2015 dataset. Sun et al. [16] has done an extensive study between radiomics-based feature selection techniques to compare the existing standard and popular machine learning predictive models considering MRI scans from BraTS 2018 dataset for glioma grading. Researchers have used several quantitative radiomics-based feature extraction e.g., first-order statistics, second-order statistics, histogram-based features [17], GLCM-based texture features [18]–[20], 3D and 2D shape-based features [15], wavelet features [21]–[23]. Zhou et al. [24] has proposed a description of high-level quantitative features who have used radiomics based method for the analysis of high-quality brain tumor characteristics for tumor grade classification. Zhang et al. [25] has proposed a brain abnormality classification techniques over MRI, at first feature vectors by using DWT Shannon and Tsallis entropy coefficients are extracted and then performed classification on feature vectors by using Support Vector Machine (SVM) with RBF kernel to detect abnormality in images. Nayak et al. [26] has proposed a novel classification method to detect abnormalities in MRI.
Firstly, feature vectors are extracted from MRI by using two-dimensional discrete wavelet transform (2D-DWT) and then performed features normalization over generated feature vectors. Secondly, probabilistic principal component analysis (PPCA) have used for features reduction and finally, for classification, the Random Forest (RF) was used for brain image classification. Gudigar et al. [27] has proposed a classification techniques to distinguish between normal and abnormal cells over 612 MR brain images of Harvard Medical School dataset by extracting features using wavelet, curvelet and shearlet transform from these MR images and a quantitative approach is used based on an analysis of multi-resolution images and reported 97.38% accuracy with PSO–SVM classifier. Chaplot et al. [28] have used wavelet transform as feature extraction over Harvard MRI dataset to classify normal and abnormal in the given brain images and achieved accuracy of 94% and 96% by using neural network self-organizing maps (SOM) and SVM-linear classifier, respectively. Bahadure et al. [29] proposed a segmentation and classification techniques for brain tumor by extracting the Berkeley wavelet transform (BWT) features along with SVM and has reported performance $\langle \text{Acc}, \text{Sens}, \text{Spec} \rangle \equiv (96.51\%, 97.72\%, 94.2\%)$. Zhou et al. [30] proposed detection of 62 subjects’ pathological brain from brain images based on wavelet entropy and Naïve Bayes (NB) classifier and has reported performance $\langle \text{Acc}, \text{Sens}, \text{Spec} \rangle \equiv (92.6\%, 94.5\%, 91.7\%)$. An automatic system for the identification of tumorous and non-tumorous cells in MR images was proposed in [31]. They have applied intensity, texture and shape based features extraction over three different kind of brain dataset, namely, Harvard, Local and RIDER dataset and achieved performance $\langle \text{Acc}, \text{Sens}, \text{Spec} \rangle \equiv (97.1\%, 91.9\%, 98\%)$ with SVM classifier.

Brynolfsson et al. [19] has concluded that the GLCM texture features are crucial for gliomas classification and estimation of prognosis. Wang et al. [32] pointed out that stationary wavelet transform (SWT) is translation-invariant. Therefore, implicitly it is beneficial and stable in terms of performance to replace DWT with SWT. This gives SWT advantage to outperform DWT in several relevant research areas. Li et al. [33] has experimented a radiomics strategy to classify tumor features over 270 LGG subjects, consistent with the expression level of the epidermal growth factor (EGFR). In this method, features are extracted and reduced to 25 wavelet features and reported an accuracy of 82.5%. In the work [34], [35] a combined radiomics and genomics features based approach has been proposed to use two different types of information to understand the several dimensions of different types of tumors.

III. MATERIALS AND METHODS

This section provides details of dataset, regions of interest (RoIs) in the images and extraction of radiomics features from different RoIs.

A. DATASET SPECIFICATIONS

The multimodal Brain Tumor Segmentation (BraTS) challenge has been started in 2012 and float every year with some challenging data, along with segmentation and classification task. The BraTS challenge is organized by Center for Biomedical Image Computing and Analytics (CBICA), University of Pennsylvania. The BraTS dataset is derived from pathologically diagnosed multi-institutional clinically-acquired pre-operative skull-stripped multimodal MRI scans which are available in native (T1), post-contrast T1-weighted (T1c), T2-weighted (T2) and T2 Fluid Attenuated Inversion Recovery (FLAIR) modalities in Nifti volume formats. The proposed research work has an objective of glioma classification and utilized the training dataset of BraTS 2018 [8]–[10]. The BraTS 2018 training dataset consists of MRI scans of 285 subjects, out of which 210 subjects belong to HGG (Glioblastoma Multiforme) and remaining 75 belong to LGG (Oligoastrocytoma). Each MRI sequence has 155 slices of resolution $240 \times 240$. BraTS challenge provides subjects’ MRI scans data aligned to homogeneous anatomical template which is interpolated to $1\text{mm}^3$ voxel resolution. Ground truth (GT) provided by BraTS 2018 challenge for all 285 subjects’ scans has tumor segmentation by medical experts with annotation labels non-enhancing tumor (NET) or necrosis (NCR) region (label 1), edema (ED) region (label 2) and enhancing tumor (ET) region (label 4).

The clinical features of 285 subjects are depicted in Table 1. The average age (standard deviation) of the dataset is 60.33 (12.08) years. The dataset comprises of maximum participation of subjects ranged 50 – 70 years under known age category. Additionally, the average survival time (standard deviation) of subjects is 422.96 (349.68) days. The maximum subjects’ survival time lies in range 300 – 1000 days. The tumor regions labelled 1, 2 and 4 are present in all 210 subjects corresponding to HGG tumor grade. The tumor regions labelled 1, 2 and 4 are present in 75, 74 and 48 subjects, respectively, corresponding to LGG tumor grade.

B. REGIONS OF INTEREST (RoIs)

The BraTS challenge dataset comprises of MRI scans of four modalities (T1, T1c, T2, FLAIR) and the respective ground truth (GT) of each subject. The ground truth segmentation is prepared by expert radiologists and doctors. On the basis of ground truth segmentation, three regions of interest (RoIs) are derived for each of the MRI scan.

The first RoI (i.e., $Roi_1$) consists of only non-enhancing tumor or necrosis region, the second RoI (i.e., $Roi_2$) is obtained by adding enhancing tumor region to first RoI and third RoI (i.e., $Roi_3$) is whole tumor region, i.e. edema, non-enhancing tumor and enhancing tumor, collectively.

$$Roi_1 \leftarrow \text{NCR}/\text{NET}$$  \hspace{1cm} (1)

$$Roi_2 \leftarrow Roi_1 \cup \text{ET}$$  \hspace{1cm} (2)
TABLE 1. Clinical data description of BraTS 2018 training dataset.

| Clinical Features       | Feature Type | Feature Data Range | Values   | Participation (in %) |
|-------------------------|--------------|--------------------|----------|----------------------|
| # of Subjects           | Numeric      | —                  | 285      | —                    |
| Age (Overall)           | in years     | mean ± std         | 60.33 ± 12.08 | —                    |
| Age (Classified)        | range in years| [0, 30]            | 3        | 1                    |
|                         |              | [30, 50]           | 28       | 9.8                  |
|                         |              | [50, 70]           | 98       | 34.4                 |
|                         |              | [70, 80]           | 29       | 10.2                 |
|                         |              | [80, :)            | 5        | 1.8                  |
|                         |              | NA                 | 122      | 42.8                 |
| Tumor Grade (HGG)       | Numeric      | —                  | 210      | 73.7                 |
| Tumor Label (HGG)       | Nominal      | Label 1 = NCR / NET| 210      | 100                  |
|                         |              | Label 2 = ED       | 210      | 100                  |
|                         |              | Label 4 = ET       | 210      | 100                  |
| Tumor Grade (LGG)       | Numeric      | —                  | 75       | 26.3                 |
| Tumor Label (LGG)       | Nominal      | Label 1 = NCR / NET| 75       | 100                  |
|                         |              | Label 2 = ED       | 74       | 98.67                |
|                         |              | Label 4 = ET       | 48       | 64                   |
| Survival (Overall)      | in days      | mean ± std         | 422.96 ± 349.68 | —                    |
| Survival (Classified)   | range in days| [0, 300]           | 65       | 22.8                 |
|                         |              | [300, 1000]        | 87       | 30.57                |
|                         |              | [1000, :)          | 11       | 3.9                  |
|                         |              | NA                 | 122      | 42.8                 |

The pictorial representation of MRI scan slice considered from FLAIR modality and its respective ground truth (GT) for a subject with subject id BraTS18_TCIA03_296_1 is depicted in Figure 2(a) and 2(b) where the tumor is shown in slice in light grey shade and the three different tumor types non-enhancing tumor or necrosis, edema and enhancing tumor is shown in red, green and yellow color, respectively. Ground truth is labelled by experts into label 1, 2 and 4 for non-enhancing tumor or necrosis, edema and enhancing tumor, respectively. The RoIs, $RoI_1$, $RoI_2$ and $RoI_3$, are created as defined in Eqs. 1–3, and depicted in Figure 2(c), 2(d) and 2(e), respectively.

$$RoI_3 \leftarrow RoI_2 \cup ED$$  (3)
IV. MOTIVATION AND PROBLEM FORMULATION

Cancer is one of the biggest health issues in the world. According to WHO, there are more than 100 types of brain and central nervous system (CNS) tumors. The most common brain and CNS tumors in USA are Nerve Sheath tumors (8%), Pituitary tumors (16%), Gliomas (25%) and Meningioma (37%). Women are 1.6 times more vulnerable than men for non-malignant tumors and men are 1.4 times more vulnerable than women for malignant tumors [36]. The Global Burden of Disease estimates that 9.56 million people died prematurely from cancer in 2017 [37]. According to GLOBOCAN 2018, the estimated number of new cancer cases and number of deaths worldwide for brain and CNS in year 2018 are 2,96,851 and 2,41,037, respectively as depicted in Figure 1. This statistics shows that the mortality rate is very high i.e., 81.2% and the survival rate of patient is very low which is 18.8% [38].

The BraTS 2018 dataset is available to researchers and academicians in CBICA Image Processing Portal for research purposes only. The dataset is used in CGHF for developing the computational decision support system. The objective of computational intelligence or decision support system can be either segmenting accurately the voxels in MRI scans of each subject into tumorous or non-tumorous regions and another task can be classifying each subject into HGG or LGG on the basis of tumorous regions and its malignancy. In this respect, GT can be considered as the output \( \mathcal{O} \) to ensure about correct segmentation of cells and classification of subjects.

The BraTS 2018 dataset \( \mathcal{D}^R \) comprises of four modalities; \( T1, T1c, T2, FLAIR \) along with ground truth (GT) with voxel resolution 155 × 240 × 240 in pixels for every subject ID, \( M \sum_{i=1}^{75} S_{id}^X \), where \( X \) can be either HGG or LGG, \( M \) can be either of any modality, and \( id \) represents the subject ID in \( \mathcal{D}^R \) for a given modality \( M \); and 1 \( \leq id \leq 210 \) for HGG and 1 \( \leq id \leq 75 \) for LGG. The tumor grades NCR/NET, ED and ET are \( T_N, T_D \) and \( T_T \), respectively which can be found in some or all subjects brain tumor as specified in Table 1, and \( R_{O1}, R_{O2} \) and \( R_{O3} \) are regions of interest which are made in different combinations of tumor grades.

The dataset \( \mathcal{D}^R \) in terms of subjects \( S \) and their corresponding output \( \mathcal{O} = \{O_1, O_2\} \) can be represented as depicted in Eqs. 4–6, where \( O_1 \) and \( O_2 \) corresponds to LGG and HGG, respectively.

\[
S = \sum_{M = T1, T1c, T2, FLAIR} \left( \sum_{id=1}^{75} M \sum_{i=1}^{75} S_{id}^X + \sum_{id=1}^{210} M \sum_{i=1}^{210} S_{id}^H \right) \tag{4}
\]

\[
O = \left( \sum_{id=1}^{75} O_{id}^L + \sum_{id=1}^{210} O_{id}^H \right) \tag{5}
\]

\[
\mathcal{D}^R = \langle S, O \rangle \tag{6}
\]

Every subject, \( M \sum_{id}^X \), comprises of total \( (k \times i \times j) = 155 \times 240 \times 240 \) voxels for each modality \( M \) for \( S_{id}^X \) and \( O_{id}^X \) which corresponds to its GT or output class \( O \), where \( X \in \{L, H\} \) and \( id \in \{id \mid id \in N, id \leq 210 \text{ for } H \text{ and } id \leq 75 \text{ for } L\} \). A pixel \( (k, i, j) \) in a subject \( M \sum_{id}^X \) can be tumorous \((T^+)\) or non-tumorous \((T^-)\).

By applying feature extraction techniques explained in Section VI, the new non-pictorial dataset \( \mathcal{D} \) is created which contains features and instances, where feature set is \( \mathcal{F} = \{F_1, F_2, \ldots, F_m\} \) with \( m \) features and instances are \( \mathcal{I} = \{I_1, I_2, \ldots, I_n\} \) corresponding to \( n \) subjects. An instance \( I_i \) is represented by features \( F_i \) as given in Eq. 7.

\[
I_i = \bigcup_{1 \leq i \leq m} F_i \tag{7}
\]

where \( m \) is the number of features in \( \mathcal{D} \). The value \( F_i \) is numeric only.

Mathematically, the objective of computational intelligent system for correct predictions \( \mathcal{P} \) is to develop a machine learning model using some learning algorithm \( \mathcal{L} \) which needs to learn to fit by behaviour analysis of data with respect to error \( \mathcal{E} \) reduction present in \( \mathcal{I} \) with respect to \( \mathcal{E} \) can be presented as in Eq. 8, where \( \mathcal{C} \) represents convergence.

\[
\mathcal{P} \xrightarrow{\mathcal{C}} \text{min} \left[ \mathcal{E} \left\{ O - \mathcal{P} \left\{ \mathcal{L} \left( \sum_{i=1}^{n} \sum_{j=1}^{m} D(F_i, I_j) \right) \right\} \right\} \right] \tag{8}
\]

The predictions calculated from applying learning algorithm \( \mathcal{P} \) is evaluated by performance metric \( \mathcal{P} \) using metrics \( \{\text{Acc, Sens, Spec, Score, MCC, AUC}\} \). The metrics is explained in detail in Section IX-B.
Algorithm 1 CGHF(\(D\))

\begin{algorithm}
\begin{algorithmic}
\STATE \((GT, T1, T1c, T2, FLAIR) \leftarrow D;\)
\STATE \(D_R \leftarrow \text{R} - \text{Extraction}(D); D_S \leftarrow S - \text{Extraction}(D); D_{RS} \leftarrow \text{RS} - \text{Extraction}(D);\)
\FORALL{\(X \in \{R, S, RS\}\)}
\STATE \((D_X^R, D_X^S) \leftarrow D_X;\)
\STATE \([DS]^T_X \leftarrow [D_X^{ANOVA}, D_X^{LS}, D_X^{TT}, D_X^{MCF}, D_X^{BM}, D_X^{OPFS}, D_X^{RFE}, D_X^{RFE}] \leftarrow \text{FS}(D_X^T);\)
\STATE \([DS]^V_X \leftarrow D\_\text{Norm}([DS]^T_X);\)
\STATE \((\text{Acc, Sens, Spec, Score, MCC, AUC})_X^T \leftarrow \text{Random\_Forest}([DS]^T_X);\)
\STATE \((\text{Acc, Sens, Spec, Score, MCC, AUC})_X^V \leftarrow \text{Random\_Forest}([DS]^V_X);\)
\FOR{Selected\ feature\ set}\ 
\STATE Validate the dataset \(D_X^V\) using \(\text{Random\_Forest}([DS]^V_X);\)
\STATE Evaluate performance metric \(P_X \leftarrow (\text{Acc, Sens, Spec, Score, MCC, AUC})_X^V;\)
\ENDFOR
\STATE \text{return } P_R, P_S, P_{RS};
\ENDFOR
\end{algorithmic}
\end{algorithm}

Algorithm 2 \(R - \text{Extraction}(D)\)

\begin{algorithm}
\begin{algorithmic}
\STATE \((GT, T1, T1c, T2, FLAIR) \leftarrow D;\)
\STATE Extract RoIs \(R_{1}, R_{2}\) and \(R_{3}\) from \(GT;\)
\STATE Calculate shape-based features as \(F_{SB}\) and other than shape-based features as \(F_{OS};\)
\STATE \([F_R] \leftarrow [\text{RoI} \times (\text{SB} \text{ | OS}) \times \text{Mod}];\)
\STATE Define new dataset \(D_R\) based on the features \(F_R;\)
\STATE \text{return } D_R;
\end{algorithmic}
\end{algorithm}

Algorithm 3 \(S - \text{Extraction}(D)\)

\begin{algorithm}
\begin{algorithmic}
\STATE \((GT, T1, T1c, T2, FLAIR) \leftarrow D;\)
\STATE Extract RoIs \(R_{1}, R_{2}\) and \(R_{3}\) from \(GT;\)
\STATE Derive 3-level SWT decomposed images \((IMG_{3L})\) for each modality \(i.e., T1, T1c, T2, FLAIR\) from the dataset \(D;\)
\STATE Calculate shape-based features as \(F_{SB}\) and other than shape-based features as \(F_{OS}\) from \(IMG_{3L};\)
\STATE \([F_S] \leftarrow [\text{RoI} \times (\text{SB} \text{ | OS}) \times \text{Mod}];\)
\STATE Define new dataset \(D_S\) based on the features \(F_S;\)
\STATE \text{return } D_S;
\end{algorithmic}
\end{algorithm}

Algorithm 4 \(RS - \text{Extraction}(D)\)

\begin{algorithm}
\begin{algorithmic}
\STATE \((GT, T1, T1c, T2, FLAIR) \leftarrow D;\)
\STATE Calculate features \(F_R\) and \(F_S\) from \(R - \text{Extraction}(D)\) and \(S - \text{Extraction}(D)\), respectively;
\STATE Calculate features \(F_{RS} \leftarrow F_R + F_S - F_{SB}\) and define dataset \(D_{RS};\)
\STATE \text{return } D_{RS};
\end{algorithmic}
\end{algorithm}

V. DATASET PRE-PROCESSING

The performance of prediction-based decisive systems depends upon the form and volume of data. The experimentation shows that well-attained data is helpful in generating impactful results. Since, the dataset comprises of 3D volumes of brain tumor images, therefore post-feature extraction, data pre-processing methods are used to converge this data based on extracted features. Mainly, data stratification method is used to divide the dataset into training and validation sets and feature normalization is used to converge the characteristics of data. The proposed prediction-based decisive framework, CGHF, is validated using the k-fold cross-validation scheme where \(k = 5\). In addition to data stratification, data standardization or Feature Normalization leads to better performance in prediction-based decisive models. Z-score normalization is prevalent for feature normalization which utilizes the mean and standard deviation of the features to normalize the data. Considering \(\mu_j\) and \(\sigma_j\) as the mean and standard deviation of the \(j^{th}\) attribute \(F_j\) of dataset \(D\), the z-score \((Z_{jk})\) is calculated for \(k^{th}\) instance \(I_k\) out of \(n\) instances as depicted in Equation 9. The pseudo-code of data normalization is shown as Algorithm 6.

\[Z_{jk} = \frac{x_{jk} - \mu_j}{\sigma_j}\]  \hspace{1cm} (9)

where \(\mu_j\) is calculated for attribute \(j\) as given in Equation 10.

\[\mu_j = \frac{1}{n} \sum_{\delta=1}^{n} x_{j\delta}\]  \hspace{1cm} (10)

VI. FEATURE EXTRACTION

A. STATIONARY WAVELET TRANSFORM-BASED FEATURE EXTRACTION

In the conventional wavelet transform, generally a signal is convolved with a filter and down-sampled, in order to obtain the next level decomposed signal. The size of the decomposed signal is scaled down to \(\frac{1}{2^\ell}\) of the original signal, where \(\ell\) represents the decomposition levels. Stationary Wavelet Transform (SWT) is a kind of wavelet transform that has the advantage of overcoming a lack of translation-inвариance of the Discrete Wavelet Transform (DWT). In SWT, the output is of same dimensions and units as that of input to SWT. In CGHF, 3-level SWT is utilized using the \textit{coif1} wavelet.
The corresponding 3D SWT image decomposition for sub-
HLH, HHL, LLL is used for the evaluation of the next
approximation (HL, LL, HH), and horizontal (LH) images are generated at each scale. Further, the sub-band
LL is used for the evaluation of the next 2-level SWT. As
an output, eight sub-bands LLL, LLH, LHL, LH, HHL,
HLH, HH sub-bands are generated at 3-level SWT.

The 3D SWT image decomposition for subject
ID BraTS18_TCIA03_296_1 is pictorially represented in
Figure 3 from which the approximation band LLL has been
used in our proposed approach, CGHF.

Furthermore, in [42], [43] has suggested that a pixel-based
segmentation can not be done more accurately using the
extracted features of the decomposed signal. Unser et al. [41]
has proposed a SWT-based methodology for characterizing
wavelet transform texture properties on several scales. But
the suggested methodology utilizes the translation invariant
property of wavelet decomposition.

This representation is known to be a tight frame and has a
simple iterative algorithm. SWT is therefore used as the tool
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B. RADIOMICS-BASED FEATURE EXTRACTION

Radiomics is an evolutionary method in the field of medical imaging emerged from medical oncology which
extracts features from radiographical image scans using
data-characterization algorithms. Total 3 RoIs, RoI1, RoI2
and RoI3, are created as mentioned in Section III-B. The
RoIs play a vital role in deciding the number of extracted
features. Radiomics-based features are extracted for each RoI
of each MRI sequence of each patient. Radiomic features are
divided into shape-based descriptors, image intensity-based
histogram descriptors, correlation between image voxels
derived textures-based descriptors, textures extracted from
filtered images and fractal features.

There are total 14 Shape-based descriptors are extracted
from each RoI [44]–[48]. These features depend only
on shape of RoI irrespective of MRI sequence and
modalities. Histogram descriptors based 18 first-order features [45]–[49] and correlation between image voxels derived
features-based descriptors, textures extracted from
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on shape of RoI irrespective of MRI sequence and
modalities. Histogram descriptors based 18 first-order features [45]–[49] and correlation between image voxels derived
features-based descriptors, textures extracted from
filtered images and fractal features.
features [18], [45], [52], [53], 16 gray-level run length matrix (GLRLM) [45], [54]–[57], 16 gray-level side zone matrix (GLSZM) [45], [58] and 5 neighboring gray tone difference matrix (NGTDM) [45], [47], [52], are extracted for each ROI of each MRI sequence. The total number of features, \( n(\mathcal{F}) \), are calculated as given in Equation 11.

\[
n(\mathcal{F}) = n(\text{SBD}) \times n(\text{ROI}) + n(\text{OSF}) \times n(\text{ROI}) \times n(\text{Mod})
\]

where \( n(\text{SBD}) \), and \( n(\text{OSF}) \) are number of shape-based descriptors and features other than shape-based descriptors such as first-order features and correlation between image voxels derived textures-based features which is 14 and 93, respectively. Moreover, \( n(\text{ROI}) \) and \( n(\text{Mod}) \) are number of ROIs and number of modalities (i.e., \( T1, T1c, T2, \text{FLAIR} \)) which is 3 and 4, respectively, in proposed work, CGHF. The feature count based on SBD and OSF are \( 14 \times 3 = 42 \) and \( 93 \times 3 \times 4 = 1116 \), respectively. Therefore, total features extracted from each subject is \( n(\mathcal{F}) = 42 + 1116 = 1158 \) as depicted pictorially in Figure 4. The feature extraction is done using pyradiomics [45]. The description of features extracted using radiomics are given in Supplementary Material.

![MRI Scan and ROIs](image)

**FIGURE 4.** Workflow of radiomic features extraction using ROIs and MRI scan modalities. The MRI scans and ROIs presented here are considered from subject id is BraTS18_TCIA03_296_1.

### VII. FEATURE SELECTION

Feature extraction may lead to large number of extracted features from the dataset, \( \mathcal{D} \), however appropriateness, relevancy and irredundancy is not guaranteed. Therefore, feature selection techniques are introduced which selects the most appropriate features among extracted ones that can carry maximum or all information related to dataset specifications. Feature selection is also important from the perspective of computation time and space requirement. Several feature selection techniques exist in both supervised and unsupervised way and are popular for feature reduction. The basic idea behind the feature selection (or reduction) tries to figure out the relevant features and group them into one set and selects those features which have properties in different dimensions and represents heterogeneity. The pseudo-code for feature selection is shown in Algorithm 5.

#### A. ANALYSIS OF VARIANCE

The variant of Analysis of Variance (ANOVA), namely one-way ANOVA, is primarily used for feature selection by analyzing the difference of variances (interchangeably, here standard deviation) between and within different groups in the particular sample [59]. The feature importance is decided based on variances, if variances (between groups or within the group) are equivalent, the feature is unimportant and can be discarded from training dataset. The importance of particular feature is quantified using \( F \)-value calculated by comparing variances. Higher the \( F \)-value, higher the feature importance. The pseudo-code of ANOVA is depicted in Algorithm 7.

![Feature Selection Algorithm](image)

**Algorithm 7 ANOVA(\( \mathcal{D}^X \))**

begin
1. \( \langle \mathcal{F}, I \rangle \leftarrow \mathcal{D}^X \);
2. \( \mathcal{F} = \{ F_1, F_2, \ldots, F_m \} \);
3. \( I = \{ I_1, I_2, \ldots, I_n \} \);
4. \( G = \{ G_1, G_2, \ldots, G_p \} \) and \( 1 \leq k (|k| = z) \leq p \);
5. \( \langle G_1, G_2, \ldots, G_k \rangle \leftarrow \mathcal{F} \) such that \( \forall F_i \cup F_j = G_k \) where \( i \neq j \);
6. \( SS_T = \sum (I_i - \bar{I})^2 \);
7. \( SS_R = \sum (G_i - \bar{G})^2 \);
8. \( SSW_s = \sum (I_i - \bar{I})^2 \);
9. \( DF_B \leftarrow p - 1 \);
10. \( DF_W \leftarrow p \times (z - 1) \);
11. \( f = \frac{SS_B}{DF_B} \times \frac{SS_W}{DF_W} \);
12. \( \mathcal{D}^X \leftarrow \frac{\mathcal{D}^X}{D_{\text{ANOVA}}} \);
13. return \( D_{\text{ANOVA}} \);

#### B. LAPLACIAN SCORE

The Laplacian Score (LS) is a feature selection method which evaluates features based on their locality preservation [60]. The LS method embeds the instance \( I_j \) of feature \( F_i \) where \( 1 \leq j \leq n \) and derive a graph based on nearest neighborhood using a random distance and calculate the weight matrix \( W \). A LS is calculated for each matrix. The Laplacian Score of \( i \)th feature \( F_i \) is \( L_i \) and \( f_{ij} \) denotes the \( j \)th instance of \( i \)th feature, where \( 1 \leq j \leq n \). Lower the Laplacian Score, higher the feature importance. The steps followed for feature selection using LS are mentioned in Algorithm 8.

#### C. T-TEST SCORE

The grading of glioma is a binary classification task, where each instance \( I_j \), \( 1 \leq j \leq n \), is classified from the output...
Algorithm 8 Laplacian_Score($D^X$)

begin
1. A nearest neighborhood method (e.g., k-means) is used to construct a graph $G$ with $n$ number of nodes;
2. $x_i ← G_i$;
3. Draw an edge between nodes $i$ and $j$ if $x_i$ and $x_j$ falls under $k$-nearest neighbour of each other and vice-versa;
4. If nodes $i$ and $j$ are connected and $W$ is a weight matrix, then,
   $$W_{ij} = \begin{cases} e^{-\frac{||x_i-x_j||^2}{t}} & \text{t is a constant} \\ 0 & \text{otherwise} \end{cases}$$ (12)
5. foreach $F_i$, where $1 \leq i \leq m$ do
   6. $F_i = [F_{i1}, F_{i2}, \ldots, F_{in}]^T$;
   7. $D = \text{Diag}(S)$;
   8. $\ell = [1, 1, \ldots, 1]^T$;
   9. $L = D - S$;
   10. $L_i = \tilde{F}_i \times D \times \tilde{F}_i$, where $\tilde{F}_i = F_i - \frac{F_i^T \times D \times F_i}{\ell^T \times D \times \ell} \times \ell$;
   11. $D^X \leftarrow D^LS$, where $1 \leq i \leq m$;
   12. return $D^LS$;

end

class; $O = \{O_1, O_2\}$, where $O_1$ and $O_2$ represents LGG and HGG, respectively. To determine whether a particular feature can discriminate between two classes, the t-test score is calculated using the Equation 13. Higher the score, more important the feature. The t-test feature selection method is used to calculate that whether the values of a particular feature for output class $O_1$ is different from values of same feature for another output class $O_2$. This particular feature can be used to differentiate our instances if this t-test score is applied. To check whether two classes are similar or different, t-test score is calculated for feature $F_i$ as given in Equation 13

$$t(F_i) = \frac{\left| \mu_{ij} - \mu_{i2} \right|}{\sqrt{\frac{\sigma_{i1}^2}{n1} + \frac{\sigma_{i2}^2}{n2}}}$$ (13)

where $\mu_{ij}$ and $\sigma_{ij}$ denotes the mean and standard deviation of feature $F_i$ corresponding to output class $O_1$. Apparently, the features are sorted on the basis of t-test score values to decide the importance of feature [61]. The t-test score converts the dataset $D^X$ into $D^{TTS}$ as given in Equation 14 considering the feature importance.

$$D^X \xrightarrow{F_i} D^{TTS}$$ (14)

where $1 \leq i \leq n$.

D. MULTI-CLUSTER FEATURE SELECTION

Multi-Cluster Feature Selection (MCFS) is used for selecting the most relevant feature in an unsupervised way. Several other unsupervised feature selection techniques exploit a particular metric computed for a particular feature, which is then used to analyse its importance [62]. MCFS also includes possible correlation between features ignored by traditional approaches [62]. The main objective of MCFS is to select features which can maintain multi-cluster structure of data to gain visibility for better feature selection. The number of clusters, selected features from feature set, nearest neighbors are $C$, $d$, $N_n$, respectively. The MCFS eventually returns these $d$ selected features from feature set which are relevant ones for prediction. The MCFS is theoretically represented in Equation 15.

$$D^X \xrightarrow{MCFS} D^X_{MCFS}$$ (15)

E. MAXIMUM RELEVANCE MINIMUM REDUNDANCY

The objective of Maximum Relevance Minimum Redundancy (mRMR) algorithm is to select set of features which maximizes relevance of features with the categorical output, while minimizing redundancy within selected features. Relevance between features and target variable and Redundancy between features is computed using Information measure. Among max-dependency, max-relevancy and min-redundancy, max-dependency is hard to implement [63]. Alternatively, mRMR exploits maximum relevancy first and then reduces the features that doesnot change much the class-discriminative power. The mRMR can be summed up in three equations as given in [63]. The Equation 16 selects the features $F_{\ell}$ from $F$, where $1 \leq \ell \leq k$ and $1 \leq k < m$, to maximize the relevancy of selected features $F_{\ell}$ in dataset $D^X$, where $I$ represents the information measure.

$$\max \ D^X(F, O), \quad D^X = \frac{1}{|F|} \sum_{x_i \in F} I(I_{i}, O)$$ (16)

It is obvious that selected features $F_{\ell}$ with maximal relevance will have redundancy. In other words, it can be said that it has maximum dependency. The Equation 17 selects the features which minimized redundancy among selected features $F_{\ell}$ to select mutually exclusive features.

$$\min R(F), \quad R = \frac{1}{|F|^2} \sum_{I_{i}, I_{j} \in F} I(I_{i}, I_{j})$$ (17)

The Equation 18 finally converges to optimal set of features $D^m_{RMR}$ which ensures maximum relevancy and minimum redundancy.

$$\max \Phi (D^X, R), \quad \Phi = D^X - R$$ (18)

The total numbers of features selected from $mRMR$ for our experimentation are approximately 50% and 10% i.e. 580 and 116, respectively. The transformation for modified dataset $D^m_{RMR}$ is represented theoretically as depicted in Equation 19.

$$D^X \xrightarrow{\Phi} D^m_{RMR}$$ (19)
F. QUADRATIC PROGRAMMING FEATURE SELECTION

The feature selection method $mRMR$ is a greedy approach where once a feature is selected cannot be deselected later on. In order to overcome this fact, it can be reformulated as Quadratic Programming optimization problem as specified in Equation 20. Quadratic Programming Feature Selection (QPFS) algorithm selects subset of features which preserves classification accuracy in a computationally efficient manner by simplifying the problem to quadratic optimization problem. Using quadratic optimization, weight vector containing weights given to every feature is computed [64].

$$QPF S : \min_x \frac{1}{2} x^T H x - \sum_{i=1}^{n} x_i = 1, \quad x_i \geq 0$$

(20)

where $\mathcal{F}$, $H$ and $x$ represents relevant feature vectors, matrix of feature pairwise redundancy and relative feature weights, respectively. Theoretically, the dataset is converted or optimized after QPFS as given in Equation 21, where $\mathcal{F}$, $H$ and $x$ represent correlation of each feature with target class, similarity between various features, and feature weights respectively.

$$\mathcal{D}^X \xrightarrow{QPFS} \mathcal{D}^{QPFS}$$

(21)

G. MUTUAL INFORMATION

Mutual Information (MI) is a metric which has non-negative value and measures the dependency between variables. Higher the metric value, more the dependency of two variables. It basically quantifies the amount of information obtained for one variable, using the information of other variable [65].

Pictorially, the dataset after MI feature selection is represented in Equation 22.

$$\mathcal{D}^X \xrightarrow{MI} \mathcal{D}^{MI}$$

(22)

H. RECURSIVE FEATURE ADDITION

Recursive Feature Addition (RFA) is an iterative forward features selection method in which the training starts by selecting one feature initially [66]. The model, Random Forest ($RF$) is trained with this feature and calculates the AUC. In subsequent iterations, addition of features (one at a time) if improves our model AUC then it is kept in the feature set otherwise discarded. The pseudo-code of $RFA$ is presented in Algorithm 9.

I. RECURSIVE FEATURE ELIMINATION

Recursive Feature Elimination (RFE) is a feature selection technique which is optimization-based greedy algorithm aims to search for best feature subset [67]. In RFE, train the model with random forest classifier with all the data i.e. using the initial feature set $\mathcal{F}$. The idea is to train the model repeatedly after dropping one feature at a time and keep the rest for training. If the AUC score improves after dropping the particular feature, it is not included in feature set. If the AUC score decreases, the feature is kept and included in feature set.

It then ranks the features based on the order of their elimination. The pseudo-code of RFE is shown as Algorithm 10.

VIII. CGHF: A COMPUTATIONAL DECISION SUPPORT SYSTEM FOR GLIOMA CLASSIFICATION USING HYBRID FEATURES

A Computational decision support system for Glioma classification using Hybrid stationary wavelet- and radiomics-based Feature selection approach (CGHF) inputs MRI scans of BraTS 2018 dataset which consists of four modalities $T1$, $T1c$, $T2$ and FLAIR along with its ground truth (GT) for each subject ID and outputs the labels of LGG and HGG.
patients among all subjects as per the classification model Random Forest. The features are extracted from the dataset considering ROIs as defined in Section III-B using three different proposed methods R-Extraction, S-Extraction and RS-Extraction as explained in Section VIII-A. The extracted dataset contains the radiomics-based numeric-valued features. The dataset is divided into training and validation sets using k-fold cross-validation stratification scheme as

| Feature Selection Techniques | # of Features | Acc (in %) | Sens (in %) | Spec (in %) | Score (in %) | MCC (in %) | AUC (in %) |
|-------------------------------|---------------|------------|-------------|-------------|--------------|------------|------------|
| LS                            | 580           | 96.49      | 97.14       | 94.67       | 97.58        | 91.47      | 95.90      |
|                               | 116           | 94.39      | 94.76       | 93.33       | 96.11        | 86.41      | 94.05      |
| ANOVA                         | 580           | 95.09      | 96.19       | 92.00       | 96.63        | 87.73      | 94.10      |
|                               | 116           | 95.44      | 96.67       | 92.00       | 96.88        | 88.50      | 94.33      |
| RFA                           | -             | 95.44      | 96.67       | 92.00       | 96.86        | 88.95      | 94.33      |
| T-Test                        | 580           | 95.44      | 95.71       | 94.67       | 96.84        | 88.91      | 95.19      |
|                               | 116           | 95.09      | 95.71       | 93.33       | 96.62        | 87.93      | 94.52      |
| QPFS                          | 580           | 94.39      | 94.29       | 94.67       | 96.09        | 86.54      | 94.48      |
|                               | 116           | 94.39      | 95.24       | 92.00       | 96.14        | 85.92      | 93.62      |
| RFE                           | -             | 94.39      | 94.76       | 93.33       | 96.11        | 86.23      | 94.05      |
| MI                            | 580           | 94.04      | 94.76       | 92.00       | 95.88        | 85.31      | 93.38      |
|                               | 116           | 93.33      | 93.81       | 92.00       | 95.34        | 84.36      | 92.90      |
| mRMR                          | 580           | 92.98      | 94.76       | 88.00       | 95.17        | 82.93      | 91.38      |
|                               | 116           | 91.93      | 92.38       | 90.67       | 94.24        | 81.69      | 91.52      |
| MCFS                          | 580           | 92.63      | 92.38       | 93.33       | 94.79        | 83.02      | 92.86      |
|                               | 116           | 92.63      | 93.33       | 90.67       | 94.85        | 82.40      | 92.0       |
TABLE 3. Performance metrics of the proposed feature extraction method i.e., S-extraction, for feature selection techniques on BraTS 2018 dataset considered 50% and 10% of extracted features.

| Feature Selection Techniques | # of Features | Acc (in %) | Sens (in %) | Spec (in %) | Score (in %) | MCC (in %) | AUC (in %) |
|-----------------------------|---------------|------------|------------|------------|-------------|-----------|-----------|
| RFA                         | -             | 97.54      | 97.62      | 97.33      | 98.3        | 94.12     | 97.48     |
| ANOVA                      | 580           | 95.44      | 96.67      | 92.0       | 96.88       | 88.52     | 94.04     |
|                            | 116           | 95.44      | 98.10      | 88.0       | 96.94       | 88.22     | 93.06     |
| MI                         | 580           | 93.68      | 93.33      | 94.67      | 95.59       | 84.93     | 94.00     |
|                            | 116           | 95.44      | 96.19      | 93.33      | 96.87       | 88.52     | 94.76     |
| MCFS                       | 580           | 95.09      | 98.10      | 86.67      | 96.72       | 87.20     | 92.38     |
|                            | 116           | 94.04      | 96.67      | 86.67      | 95.99       | 84.56     | 91.67     |
| LS                         | 580           | 94.74      | 94.76      | 94.67      | 96.34       | 87.51     | 94.71     |
|                            | 116           | 94.04      | 95.24      | 90.67      | 95.88       | 85.39     | 92.95     |
| mRMR                       | 580           | 90.88      | 92.38      | 86.67      | 93.68       | 77.88     | 89.52     |
|                            | 116           | 94.74      | 98.1       | 85.33      | 96.49       | 86.33     | 91.71     |
| QPFS                       | 580           | 94.39      | 95.71      | 90.67      | 96.15       | 85.96     | 93.19     |
|                            | 116           | 94.74      | 95.24      | 93.33      | 96.35       | 87.25     | 94.29     |
| RFE                        | -             | 94.39      | 96.19      | 89.33      | 96.17       | 86.17     | 92.76     |
| T-Test                     | 580           | 93.68      | 93.81      | 93.33      | 95.58       | 85.08     | 93.57     |
|                            | 116           | 94.39      | 95.24      | 92.00      | 96.15       | 86.03     | 93.62     |

TABLE 4. Performance metrics of the proposed feature extraction method i.e., RS-extraction, for feature selection techniques on BraTS 2018 dataset considered 50% and 10% of extracted features.

| Feature Selection Techniques | # of Features | Acc (in %) | Sens (in %) | Spec (in %) | Score (in %) | MCC (in %) | AUC (in %) |
|-----------------------------|---------------|------------|------------|------------|-------------|-----------|-----------|
| RFA                         | -             | 96.49      | 97.62      | 93.33      | 97.62       | 91.25     | 95.48     |
| ANOVA                      | 580           | 95.44      | 96.19      | 93.33      | 96.85       | 88.72     | 94.76     |
|                            | 116           | 95.79      | 98.10      | 89.33      | 97.16       | 89.18     | 93.71     |
| T-Test                     | 580           | 95.44      | 96.19      | 93.33      | 96.85       | 88.72     | 94.76     |
|                            | 116           | 94.74      | 96.19      | 90.67      | 96.41       | 86.69     | 93.43     |
| MCFS                       | 580           | 94.74      | 94.76      | 94.67      | 96.33       | 87.29     | 94.71     |
|                            | 116           | 92.98      | 94.76      | 88.00      | 95.17       | 82.67     | 91.38     |
| MI                         | 580           | 94.74      | 95.71      | 92.00      | 96.33       | 87.38     | 93.86     |
|                            | 116           | 94.74      | 96.19      | 90.67      | 96.41       | 86.67     | 93.43     |
| LS                         | 580           | 94.39      | 96.67      | 88.00      | 96.19       | 85.74     | 92.33     |
|                            | 116           | 92.63      | 92.86      | 97.33      | 95.78       | 86.44     | 95.10     |
| RFE                        | -             | 94.04      | 92.86      | 97.33      | 95.78       | 86.44     | 95.10     |
| QPFS                       | 580           | 93.68      | 93.33      | 94.67      | 95.60       | 84.93     | 94.00     |
|                            | 116           | 92.98      | 93.33      | 92.00      | 95.15       | 82.72     | 92.67     |
| mRMR                       | 580           | 92.98      | 94.29      | 89.33      | 95.18       | 82.76     | 91.81     |
|                            | 116           | 91.93      | 92.38      | 90.67      | 94.24       | 81.69     | 91.52     |

discussed in Section V. The feature selection techniques, namely ANOVA, LS, TTS, MCFS, mRMR, QPFS, MI, RFA and RFE, are applied to training dataset, \(D^T\), to reduce the feature set dimensionality as explained in detail in Section VII and then the training dataset is normalized as mentioned in Section V. The normalized dataset is trained using Random Forest machine predictive model as discussed in Section VIII-B and calculate the performance metric \(\langle Acc, Sens, Spec, Score, MCC, AUC \rangle\) as explained in Section IX-B. The validation dataset, \(D^V\), calculates the same features as selected for training set and normalize the data using mean and standard deviation of training dataset and validate the dataset using Random Forest classifier and results are reported in Section IX. The proposed flow-chart of the CGHF is presented in Figure 5. The pseudo-code of CGHF is shown as Algorithm 1.
TABLE 5. Performance metrics of the proposed method CGHF along with recent baseline methods statistics on BraTS 2017/2018 dataset.

| Research Contribution | Method | Acc (in %) | Sens (in %) | Spec (in %) | AUC (in %) |
|------------------------|--------|------------|-------------|-------------|------------|
| Cho et al., 2018, [14] | C1: Radiomics Features, LR | 88.77 | 96.19 | 68.00 | 90.10 |
|                        | C2: Radiomics Features, SVM | 88.07 | 94.76 | 69.33 | 88.66 |
|                        | C3: Radiomics Features, RF | 88.77 | 94.29 | 73.33 | 92.13 |
|                        | C4: Radiomics Features, LR+RF, Ensemble | 89.47 | 95.71 | 72.00 | 87.65 |
| Sun et al., 2019, [16] | S1: L^1 - SVM + MLP, 10-fold cross-validation | 94.4 | — | — | 98.6 |
|                        | S2: XGB + MLP, 10-fold cross-validation | 93.2 | — | — | 97.7 |
|                        | S3: XGB + LDA, 10-fold cross-validation | 93.0 | — | — | 98.8 |
|                        | S4: L^1 - SVM + MLP, %--split testing set | 95.3 | — | — | 98.1 |
|                        | S5: LASSO + LDA, %--split testing set | 94.2 | — | — | 97.4 |
|                        | S6: L^1 - SVM + LDA, %--split testing set | 93.6 | — | — | 98.5 |
| Wu et al., 2019, [68]  | W1: multi-MED Decision Tree (MMEDT) | 85.83 | 87.85 | 81.36 | 81.84 |
| CGHF (Proposed)        | R: R-Extraction + LS + RF | 96.49 | 97.14 | 94.67 | 95.90 |
|                        | S: S-Extraction + RFA + RF | 97.54 | 97.62 | 97.33 | 97.48 |
|                        | RS: RS-Extraction + RFA + RF | 96.49 | 97.62 | 93.33 | 95.48 |

A. FEATURE EXTRACTION METHODOLOGIES

1) **R-EXTRACTION**
   The radiomics-based feature extraction technique, namely R-Extraction, inputs the modalities, i.e., T1, T1c, T2, FLAIR, and its respective ground truth from BraTS 2018 for each subject ID. The total of 3 RoIs, RoI1, RoI2 and RoI3, depicted in Eqs. 1–3, are extracted from the ground truth as discussed in Section III-B. These RoIs are used to extract shape-based radiomics descriptors and RoIs along with brain tumor imaging modalities are used to extract other than shape-based radiomics features. The considered shape-based features are 14 and there are 3 RoIs, therefore total shape-based features are 14 × 3 = 42. The other than shape-based features are dependent on both GT and modalities, therefore the total features are (18 + 24 + 14 + 16 + 16 + 5) × 4 × 3 = 1116 features. In this way, there are total 42 + 1116 = 1158 features are derived in R-Extraction for each subject ID. The pseudo-code of R-Extraction is represented in Algorithm 2.

2) **S-EXTRACTION**
   The S-Extraction technique is coupled with SWT for generating features from RoIs and brain modalities. Initially, the brain modalities are considered for SWT and we have extracted 3-level SWT LLL sub-band images for all four modalities for each subject ID. The new dataset based on SWT LLL sub-band images is used to calculate other than shape-based features (18 + 24 + 14 + 16 + 16 + 5) × 4 × 3 = 1116 and RoIs are used to extract shape-based features 14 × 3 = 42. In this way, there are total 42 + 1116 = 1158 features are derived in S-Extraction as well for each subject ID. The pseudo-code of S-Extraction is represented in Algorithm 3.

3) **RS-EXTRACTION**
   The RS-Extraction technique clubs uncommon features from R-Extraction and S-Extraction techniques. Since shape-based features, generated from RoIs, are same in characteristic and number both, they will be considered once while combining features. Therefore the RS-Extraction will generate 1158 + 1158 − 42 = 2274 features for each subject ID. The pseudo-code of RS-Extraction is represented in Algorithm 4.

B. MACHINE PREDICTIVE CLASSIFICATION MODEL: RANDOM FOREST

The Random Forest (RF) [69] is used for classification of gliomas using extracted and selected SWT-based and radiomics-based features, i.e. RF is simply an ensemble learning method, focused on ensembling various decision trees. Individual decision trees are trained only on a subset of entire data. By the virtue of training individual decision tree on subset of data, overfitting is reduced in the case of Random Forest. Various hyperparameters, like classweight, estimators, criterion are tuned to achieve best results on each fold.

IX. PERFORMANCE EVALUATION AND RESULT ANALYSIS

A. EXPERIMENTAL SETUP

The proposed stationary wavelet-based and radiomics-based strategy for classification of gliomas grading is implemented using programming language python - 3.6 and the programs...
are executed in a Linux 14.04 LTS machine with Intel i7 3.6 GHz CPU and 8 GB memory.

B. EVALUATION METRICS

The performance evaluation of CGHF, is done by calculating the confusion matrix (CM). The CM comprises of TP (true positive), TN (true negative), FP (false positive) and FN (false negative). In case of BraTS 2018 dataset, TP and TN represents the proportion of instances where HGGs and LGGs are identified as HGGs and LGGs, respectively. It may be the case that CGHF may not be able to classify all subjects accurately. Considering those instances, FP and FN represents the inaccurate classification where LGGs and HGGs are identified as HGGs and LGGs, respectively. The CM \( \langle \text{TP}, \text{FP}, \text{FN}, \text{TN} \rangle \) is also exploited to evaluate various performance metrics as discussed in detail in [70].

The state-of-the-art methods for BraTS 2018 follow \( \langle \text{Acc}, \text{Sens}, \text{Spec}, \text{Score}, \text{MCC}, \text{AUC} \rangle \) [71]. The accuracy (Acc) represents the accurate classification of LGGs and HGGs collectively. The mathematical notation for accuracy is given in Equation 23. The classification of HGGs and LGGs is termed as Sens and Spec, and is depicted mathematically as given in Equations 24–25, respectively.

\[
\text{Acc} = \frac{\text{TN} + \text{TP}}{\text{TP} + \text{FP} + \text{FN} + \text{TN}} \times 100\% \quad (23)
\]

\[
\text{Sens} = \frac{\text{TP}}{\text{TP} + \text{FN}} \times 100\% \quad (24)
\]

\[
\text{Spec} = \frac{\text{TN}}{\text{FP} + \text{TN}} \times 100\% \quad (25)
\]

Mathew’s correlation coefficient (MCC) classifies score between \([-1, +1]\). The values in this range i.e., near to zero, \(-1\), and \(+1\) represents the random predictions, completely wrong and ideal predictions, respectively. The mathematical notation of MCC is given in Equation 26. In addition, Receiver operating characteristics (ROC) [71], [72] represents a probability curve between TP and FP. Higher the value of AUC, higher is the capability of the model to discriminate classes accurately.

\[
\text{MCC} = \frac{\text{TP} \times \text{TN} - \text{FP} \times \text{FN}}{\sqrt{(\text{TP} + \text{FP})(\text{TP} + \text{FN})(\text{TN} + \text{FP})(\text{TN} + \text{FN})}} \times 100\%
\]  

\( (26) \)
\[ \text{Score} = \frac{2 \times TP}{2 \times TP + FP + FN} \times 100\% \quad (27) \]

**C. QUANTITATIVE EVALUATION AND COMPARISON**

The results of various implementations and their experimentation is carried out on the BraTS 2018 dataset. The proposed framework CGHF extracts features from each patient data using three proposed feature extraction methods, followed by dividing the dataset using five-fold cross-validation scheme. Various feature selection algorithms are used for extracting important features for classification. Extracted features are normalized using the z-score normalization technique before passing into a random forest model for training. The performance of the trained model is analyzed using metrics \( \langle \text{Acc}, \text{Spec}, \text{Sens}, \text{Score}, \text{MCC}, \text{AUC} \rangle \).

Radiomic feature extraction is done in three different ways, (i) using no filter \( i.e., R\)-Extraction, (ii) using stationary wavelet filter \( i.e., S\)-Extraction and (iii) combining both \( i.e., RS\)-Extraction. As results mentioned in Table 2, using \( R\)-Extraction, the Laplacian Score (LS) feature selection method with 580 extracted features (50% of total features) has the highest accuracy (96.49%) among all other feature selection methods. It also has the highest sensitivity (97.14%).
Feature selection methods, t-test and ANOVA performed well with accuracy more than 95% with both 116 and 580 extracted features (10% and 50% of total features, respectively). Recursive feature addition (RFA) is the best feature selection method while extracting features using S-Extraction with the highest accuracy (97.54%) as depicted in Table 3. RFA also has the highest specificity (97.33%). Feature selection method Anova performs with the accuracy more than 95% with both 116 and 580 features. RFA also outperforms other methods while using RS-Extraction feature extraction as well, with 96.49% accuracy as depicted in Table 4. AUC and Score signify about the performance of model, and RFA got the highest Score (97.62%) and AUC (95.48%) among all other methods. ANOVA method again performs well with accuracy more than 95% for both 116 and 580 features. AUC is one of the most important metrics for evaluating the model’s performance. The ROC curve for the best feature selection technique on all three approaches is shown in Figure 7. The corresponding confusion matrices are shown in Figure 6. For the easier comparison of combination of different feature selection techniques and approaches, heatmaps of performance metric \(\langle \text{Acc}, \text{Sens}, \text{Spec}, \text{Score}, \text{MCC}, \text{AUC} \rangle\) is shown in Figure 8.

Our proposed framework, CGHF, has outperformed various previously proposed approaches. Cho et al. [14] used various machine learning algorithms like Logistic Regression, SVM and RF and their ensemble methods, and achieved an accuracy of 89.47% with low specificity. Wu et al. [68] used variant of decision tree, multi-MED decision tree and achieved an accuracy of 85.83%. Sun et al. [16] utilized various wrapper feature selection algorithms for the purpose and achieved a maximum of 95.3% accuracy. The use of wrapper methods also increases computational power since a lot of computations are involved in training the model for finding the optimal set of features. Our proposed approach utilized filter methods, which involve less computational power and outperform all previously introduced approaches, and achieved an accuracy of 97.54%. The results and their comparison are presented statistically and pictorially in Table 5 and Figure 9, respectively.

X. CONCLUSION AND FUTURE WORK

In the proposed work, CGHF, a computationally efficient decision support system based on machine predictive model Random Forest is proposed for gliomas grading. The model is used to predict the instances in HGG or LGG category. The proposed system, CGHF, utilized the filters for radiomics feature extraction and several effective feature selection techniques over publicly available BraTS 2018 dataset and train the RF model for classification task. The LS and RFA are best feature selection methods for RF using R-, S- and RS-Extraction methods and ANOVA is second best, stable and suitable method for the proposed system, CGHF.

As a future perspective, the multi-class classification of graded gliomas can be considered for prediction of brain tumors.
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