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Kulczynski Similarity Index Feature Selection based Map Estimated Rocchio Classification for Brain Tumor Disease Diagnosis

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ABSTRACT
An early discovery of brain tumor is essentialto cure the disease completely.Classification isimportantissue to be resolved in disease diagnosis. The conventional techniques designed for brain tumor disease classification finds presence of disease. But, it failed to able the diagnosis performanceof brain tumor disease.Toconquerthelimits, proposed Kul Similarity Index Feature Selection based MAP Estimated Rocchio Classification (KSIFS-MERC) Technique is introduced. The proposed technique isemployed fortumor risk factor recognitionand patient data in their disease diagnosis viaimproved accuracy and lessertime utilization. The KSIFS-MERC methodinitially performs Kulczynski Similarity Index based Feature Selection (KSI-FS) process where KulSimilarity Index is used to find out the similarity between features for analyzing the feature as relevant or irrelevant. After the feature selection process, Maximum a Posteriori Probability (MAP) estimated Rocchio Classifier is used
to perform brain tumor disease diagnosis byenhanced accuracy. MAP estimated Rocchio Classifier precisely classifies patient as normal or abnormal according to maximum a posteriori probability result.By this way, KSIFS-MERC Technique increases the risk factor identificationand brain tumor syndromeanalysis performance as compared to existingmethods. Experimental evaluation ofKSIFS-MERC methodis performedthroughEpileptic Seizure Recognition Dataseton metricsnamely tumor diagnosis accuracy, tumor diagnosis time, andfalse positive rate with number of patients.Experimental outcomeshow that KSIFS-MERC methodis toimprovetumor diagnosis accuracy as well asminimize tumor diagnosis time when compared to conventional methods.

Keywords: Brain Tumor, Class Centroid, Kulczynski Similarity Index, MAP Estimated Rocchio Classifier, Minkowski Distance, Patient Data, Risk Factors

1. INTRODUCTION

Disease diagnosis is process of discovery out disease or condition matches the person's symptoms and signs. A diagnosis is a diagnostic process that considered as an attempt for feature selection and classification of an individual condition into separate and different categories that allow the medical decisions. A lot of research works have introduced various feature selection and classification techniques for risk factor identification as well as brain tumor disease diagnosis.However, classification accuracy as well as classification time performance were not sufficient. To address these issues, KSIFS-MERCmethoddesigned to enhance accuracy of brain tumor diseasediagnosis.

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Complex-valued classifiers were introduced in [1] to diagnose epilepsy byenhanced accuracy. But, time required forepilepsy diagnostic was very higher. An Ensemble Classifier was presented in [2]for increasing the performance of brain tumor disease diagnosis. However, diagnosis accuracy was not enough. A Gauss-Newton Representation Based Algorithm (GNRBA) was designed in [3]to breast cancer discovery.But, classification accuracy was not improved. A portable desktop prototype device was employed in [4] with the application of neural network for classifying malignant and benign tissue.However, failed toperform feature selection process by the portable desktop prototype device. A review of different machine learning techniques were developedto model cancer risk and cancer prognosis was analyzed in [5].

A Soft computing method of FCMs was performed in [6] tobrain tumor categorizationbyimproved accuracy.However, FPR of brain tumor diagnosis was more. Review of different data mining (DM)methodsdeveloped for the detection and prevention of brain tumor diseasebetween patients was analyzed in [7].Relationshipamong Parkinson disease as well asbrain tumor disease was presented in [8].But, the risk factors of brain tumor diseases were not analyzed. Tofind outhazard factors for women with ovarian cancer about recurrence, An Ensemble learning as well as five DM approaches was designed in [9]. For increasingdisease risk evaluation performance and to determineimportant risk features, ML and matrix factorization methods were combined in [10]. However, it failed to resolve the ratio of amount of patientstoincorrectlyclassify by designed method.

Tosolve above mentioned conventional drawbacks, KSIFS-MERCmethod is developed.The aims of contributions KSIFS-MERC method arefollowing as,

- To improve thebrain tumor syndromeanalysisaccuracyby classification as compared to existing methods,the KSIFS-MERCmethod is developed. KSIFS-MERCmethod is proposed with help of Kulczynski Similarity Index based Feature Selection (KSI-FS) and Maximum a Posteriori Probability (MAP) estimated Rocchio Classifier on contrary to conventional algorithms.

- To considerablyclassifythe risk factors (i.e. features) related to brain tumor syndrome with lesser time complexity as compared to existing method,KSI-FS algorithm is introduced in KSIFS-MERC method.Throughfeature selection process, the KSI-FSalgorithm choosesmedical features byenhancedKulczynski similarity index value as more important to predict the brain tumor disease.

- To decrease FPR of brain tumor disease recognitionwhen compared to existing algorithm, MAP estimated Rocchio Classifier is intended in the KSIFS-MERCTechnique. During the classification process, lesser distance between patient dataas well as centroid has larger probability to become a class member. This supports for KSIFS-MERC method toefficiently categorizepatient as normal or abnormal through enhanced accuracy.

2. Literature review

New technique was introduced [11] to find out risk factors related to remnant gastric cancer.But, the diagnosis accuracy of this method was lower. A novel data mining technique was developed in [12] for earlydetection of brain cancer.However, optimal features (symptoms) were not selected in this approach.

A semi-supervised techniquewas introduced in [13] for brain tumoranalysis. But,the time taken for brain tumor detection was higher. To improve classification accuracy of epileptic seizure recognition, An Ensemble Classifier was introduced [14] . However, disease diagnosis performance was not at the required level. To attain enhancedsensitivity,minimum false recognition rate of brain tumor disease, Bayesian linear discriminant analysis (BLDA) was presented [15] .However, disease diagnosis accuracy was poor.

For seizure recognitionthroughapplication of Support vector machine (SVM), Hilbert marginal spectrum analysis was developed in [16] . But, computational complexity was not solved.An effective feature extraction technique was presented in [17] for automated epileptic EEG signal classification. But, a number of patient data incorrectly classified was more. Radial basis function networks (RBFNNs) was utilized in [18]for classification of EEG signal to get higher accuracy for epileptic seizure discovery. However, time was not minimized. Naïve Bayes'classification and decision tree algorithms were introduced in [19]for finding the kind of brain tumor. However, the classification accuracy was very lower. Heterogeneous data fusion was presented in [20] for brain tumor classification. But, the false alarm rate of brain tumor identification was not reduced.

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To addresses the above limitations in brain tumor disease detection, the KSIFS-MERC Technique is designed which detailed described in below.

3. KUL SIMILARITY INDEX FEATURE SELECTION BASED MAP ESTIMATED ROCCHIO CLASSIFICATION TECHNIQUE

The Kul Similarity Index Feature Selection based MAP Estimated Rocchio Classification (KSIFS-MERC) methodis designed toenhance the braintumordisease diagnosis performance through risk factor identification. TheKSIFS-MERC method is designedthrough combining Kulczynski Similarity Index based Feature Selection (KSI-FS) in theRocchio Classification algorithm. When compared to conventional methods,the KSI-FS algorithm is developed in the KSIFS-MERCTechnique tofind outsignificant risk factors/variables which influence the braintumor diseasethroughlesser time complexity. From that, KSI-FS algorithmminimizes risk of overfittingas well asenhancesthe classificationcapability of KSIFS-MERC Technique to give better tumor prediction result.

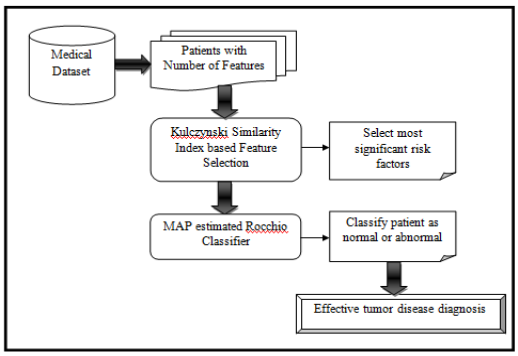

Figure 1 Architecture Diagram of the KSIFS-MERC Technique for Brain Tumour Disease Risk Factors Identification and Diagnosis

Furthermore, the KSIFS-MERC Technique designed MAPestimated Rocchio Classifier with help of maximum a posteriori probability to reduce FPR of brain tumor disease diagnosis. This aidsforKSIFS-MERCmethod to attain improved syndrome analysis of brain tumor show as compared to existing methods.

In above figure 1,describe theprocess of KSIFS-MERCmethodisachieving theimproved accuracy for brain tumor syndrome analysis with minimumnumber of risk factors.Initially, the input is finding the medical dataset (i.e.Brain cancer dataset). This dataset comprises a huge number of patient data '$P_1, P_2, .. P_n$'and theirmedical features '$F_1, F_2, .. F_n$'. In a disease diagnosis issue, put of features are illustrative of allvariation ofbrain tumor illness areessential. Aim of theKSIFS-MERC methodis find out presence of brain tumor disease more accurately with areduced number of features. Therefore, theKSIFS-MERC Technique applied KSI-FS algorithm to select feature subset(i.e. risk factors).Finally, KSIFS-MERC Technique developedMAP estimated Rocchio Classifier to identify brain tumor disease throughenhanced accuracy.

3.1 KulczynskiSimilarity Index based Feature Selection

Due to advances in differentmeasurements, medical datasetcomprises of relevant and irrelevant and unnecessaryfeatures.Removalof preciousfeaturessincethat datasets desiresathoroughsearch over sample space. Performance of classification modelsdepends on correctcollection of mainapplicable features.Eradicating redundant features reduce the size of medicaldataset to achieveimproved tumor disease diagnosis performance. Therefore,the Kulczynski Similarity Index based Feature Selection (KSI-FS) is designed in a KSIFS-MERCTechnique withaimingof choosing a subset of the relevant features from input medical dataset.The KSI-FS reduces data dimensionality by means of removing unrelated and redundant features and thereby speed ups thetumor risk factor identification process with higher accuracy. InKSIFS-MERCTechnique,Kulczynski(Kul) Similarity Indexis employed to quantify thecorrelation between features and tumor symptoms.This supports for KSI-FS to discover the essentialmedical features for brain cancersyndromeforecasting.

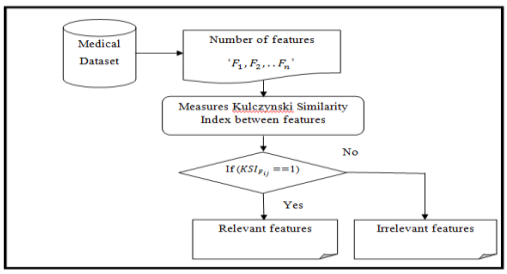

Figure 2 Processes of Kul Similarity Index based Feature Selection

From Figure 2,the KSI-FS algorithm initially measures the Kulczynski Similarity Index for everymedical feature inprovided dataset.From that, Kulczynski Similarity Index between medical features and tumor symptoms is mathematically determined using below,

$$KSI(P_i, S_i) = \frac{1}{2}\left(\frac{x}{x+y} + \frac{x}{x+z}\right) (1)$$

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From (1) 'P_i' represents the patient with number of features '$F_1, F_2, .. F_n$'whereas 'S_i' denotes number ofsymptom features related to tumor disease. Here, 'x' refers tonumber of features presents in both 'P_i' and 'S_i' whereas 'y'indicates the number of features present in patient record 'P_i' butnot occurs in 'S_i'. Besides, 'z' signifies number of features present in 'P_i' butnot occurs in 'S_i'. The output of the Kulczynski Similarity Index '$KSI_{F_{ij}}$'is ranges from 0 to 1.0. From that, the medical features with ahigherKulczynski similarity index isconsidered as more relevant to effectively carry out brain tumor disease forecast.

// Kul Similarity Index based Feature Selection Algorithm
Input: Medical dataset 'DS' with a number of patient data '$P_1, P_2, .. P_n$'; Number of features '$F_1, F_2, .. F_n$'
Output: Select relevant medical features for brain tumor disease diagnosis
Step 1:Begin
Step 2: **For** each medical feature '$F_i \in DS$'
Step 3: Determine Kul Similarity Index between 'F_i' and 'S_i' using (1)
Step 4: **If** ($KSI(F_i, S_i) == 1$)) **then**
Step 5: Feature 'F_i' is more relevant
Step 6: **Else**
Step 7: Feature 'F_i' is irrelevant
Step 8: **Endif**
Step 9: **End for**
Step 10:End

Algorithm 1 Kul Similarity Index based Feature Selection Algorithm

Algorithm 1 explains processes of KSI-FS. As shown in above algorithmic process, the KSI-FS algorithm initially takes a number of medical features from provided dataset as input. For each input medical feature, the KSI-FS algorithm applies the Kulczynski Similarity Index where it calculates the relationship between medical features and tumor symptoms. Based on the calculatedKulczynski similarity index value, then the KSI-FSalgorithm performsthe feature selection process. If the Kulczynski similarity index value '$KSI(F_i, S_i)$' is '1', afterwardmedical feature isconsidered relevant for discovering brain tumor disease. Otherwise, feature is considered as irrelevant. KSIFS-MERC Technique lessens dimensionality of features forobtaining betterbrain tumor disease diagnosis.

3.2 MAPestimated Rocchio Classifier

The MAPestimated Rocchio Classifieris designed in KSIFS-MERC Technique with intention of improving classification performance of brain tumor disease recognition.The MAPestimated Rocchio Classifier is proposed by combining aMAP estimation and Minkowski distance measurement in the existingRocchio classification algorithm. The main idea of MAP estimated Rocchio Classifier to denotesthe 'P_i' allpatient data as implement in a vector space.As a resultwhichpatient data bysimilar features have similar vectors. On contrary to conventional classification algorithms, Rocchio Classifier assigns class label to every patient data based on the designed MAPpurpose. Lesser distance between patient dataas well asspecified in vector space has dominated bybetter probability andclassify the patient datathatparticularclass i.e. normal or abnormal. Thus, MAPestimated Rocchio Classifier efficientlyperforms the brain tumor disease diagnosis throughenhanced accuracy as well aslesser time as compared to conventional methods.The process concerned in MAPestimated Rocchio Classifier is illustrated in below Figure 3.

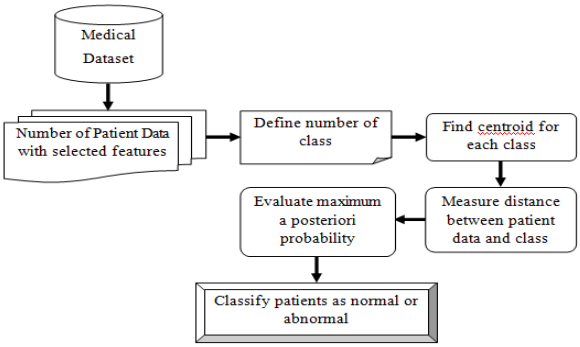

Figure 3 MAP estimated Rocchio Classifier Process

From above figure 3,represents the flow processes of MAP estimated Rocchio Classifier isto obtain theenhanceddiagnosis accuracy for brain tumor disease.Initially, the number of patient data and selected medical features as input givenMAP estimated Rocchio Classifier. Then, MAP estimated Rocchio Classifier initialize number of classes.In the KSIFS-MERCTechnique, a number of classesare defined as two namely normal and abnormal classes. After initializing the classes, MAP estimated Rocchio Classifier identify the centroid 'α' for each class 'c_i' using below mathematical expression,

$$\alpha_{(c_i)} = \frac{1}{|n_c|} \sum_{P_i \epsilon DS} v(P_i) \qquad (2)$$

From (2) '$\alpha_{(c_i)}$' represent the centroid of 'i^{th}' class whereas 'n' is a number of patient data in medical dataset 'DS'.'c' is denotes the class. '$v(P_i)$' specified asnormalized vector inpatient data 'P_i'.The centroid is obtained asmiddle of mass of its class members.Consequently, the MAP estimated Rocchio Classifierutilizes the Minkowski distance to calculate distance between data and centroid by belowmathematical formula,

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$$d_{ij} = \left(\sum_{i=1}^{n}\left(\left|\left(P_i - \alpha_j\right)\right|\right)^q\right)^{1/q} \quad (3)$$

From (3), 'α_j' denotes a 'j^{th}' class centroid and 'P_i' represents the 'i^{th}' patient data in the given medicaldataset. Here, 'N' point outs number of patient data as well as 'q' is parameter.After measuring distance, MAP estimated Rocchio Classifier evaluates the maximum a posteriori probability. Thismaximum a posteriori probability determination helps for MAP estimated Rocchio Classifier to find the highest probability of the patient data become member of specific class. MAP estimation assigns enhancedprobability to classifypatient tospecific class when distance amongpatient dataand which class centroid is extremely minimal.

In MAP estimated Rocchio Classifier, MAP is employed to find out maximum probability for everypatient become member of specific class using below mathematical representation,

$$\theta_{Map} = \arg\max \Pr\left(p_i \middle| \alpha_j\right) (4)$$

In equation (4), 'θ_{Map}'is a higher posteriori function, '$arg\ max$'is an argument of maximum probability '(Pr)' ofpatient data'(p_i)'inclusion to specificclass of centroid '(α_j)'.This process ofMAP estimated Rocchio Classifieris repeated until all the patient data are classified. The algorithmic process of MAP estimated Rocchio Classifier is explained in below.

// MAP estimated Rocchio Classifier Algorithm

Input: number of patient data '$P_1, P_2, .. P_n$' with selected medical features

Output: Enhanced disease diagnosis accuracy

Step 1: Begin

Step 2: Initialize number of class 'c_i'

Step 3: Determine centroid '$\alpha_{(c_i)}$' for each class using (2)

Step 4: **For** each patient data 'P_i'

Step 5: Calculate distance 'd_{ij}' between 'α_j' and 'P_i' using (3)

Step 6: Evaluate maximum a posteriori probability 'θ_{Map}' using (4)

Step 7: Classify the patient into a normal or abnormal class

Step 8: **End For**

Step 9:End

Algorithm 2 MAP estimated Rocchio Classifier

Algorithm 2 explains process of MAP estimated Rocchio Classifier. As shownin the above algorithmic steps, the MAP estimated Rocchio Classifier at first initialize the number of classes i.e. normal and abnormal class. Next, MAP estimated Rocchio Classifier computes centroid for every class and consequently estimates distance between each patient data and class centroid. After that, the MAP estimated Rocchio Classifier measures MAP which discoversmaximum probability for every patient becomes a member of specificclass. Finally, the MAP estimated Rocchio Classifier allocateclass label to the patientdepends on maximum a posteriori probability result. Thus, the KSIFS-MERCTechnique attains better diagnosis performance to correctlydiscover the presence/absence of brain tumor syndromebylesser amount of time.So, the KSIFS-MERCmethodenhancesdiagnosis accuracy as well asreduces diagnosis time ofbrain tumor syndrome as compared to conventional methods.

4. SIMULATION SETTINGS

The performance of proposedKSIFS-MERC Technique is implemented in Java language by using Epileptic Seizure Recognition Dataset.The Dataset [21] is obtained from UCI Machine Learning Repository to carry outsimulation process by Epileptic Seizure Recognition.This Epileptic Seizure Recognition Dataset comprises 5 files. Eachfilecontains 100 folders in every file havepatient's medical data i.e. a brain activity of the patient for 23.6 seconds.Forperforming the experimental process, the KSIFS-MERCTechnique considersanamount of patient medical data in series of 50-500 from Epileptic Seizure Recognition Dataset.

5. RESULTS AND DISCUSSION

Performance of KSIFS-MERC Technique is calculated in different parameters namely, tumor diagnosis accuracy, tumor diagnosis time and false positive rate and compared with existing Complex-valued classifier [1] and Ensemble classifier [2].

The performanceresults of proposed KSIFS-MERC Technique arediscussed in various metrics is measuredwith diverse number of patients and averagely ten results are depicted in below table and graph.

5.1 Tumor Diagnosis Accuracy(TDA)

Accuracy is defined asamount of patients accurately classified as normal or abnormal to total number of patient's. It iscalculated as,

$$TDA = \frac{\omega_a}{n} * 100 \quad (5)$$

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From (5), 'TDA' is adiagnosisaccuracy of brain tumor disease, 'n' is atotal number of patient and 'ω_a' is specified asnumber of patient which are accurately classified as normal or abnormal.The accuracy is measured in percentages (%).

ModelCalculation for TDA

- **Complex-valued classifier:** aamount of patients correctly classified as 40 and total number of patients is 50. TDA computed as,

$$TDA = \frac{40}{50} * 100 = 80\ \%$$

- **Ensemble classifier:** number of patients precisely classified in39 and total number of patients is 50. TDA obtained as,

$$TDA = \frac{39}{50} * 100 = 78\ \%$$

- **KSIFS-MERC method:** number of patients exactly classified is 43 and total number of patients is 50. TDA estimated as,

$$TDA = \frac{43}{50} * 100 = 86\%$$

TDAresult using KSIFS-MERCTechnique is compared with conventional Complex-valued classifier [1] and Ensemble classifier [2].Assume the 250 patient medical data usingEpileptic Seizure Recognition Dataset [21] for performing an experimentalprocess;KSIFS-MERC Technique obtains 93 % tumor diagnosis accuracy whereas Complex-valued classifier [1] and Ensemble classifier [2] gets 85 % and 88 %. In above achieved results, it significanttoamount of patients exactly classified as normal or abnormal using improved proposed KSIFS-MERCmethod. Hence, the KSIFS-MERCTechnique attains enhanced tumor diagnosis accuracy as compared to existing Complex-valued classifier [1] and Ensemble classifier [2]. Thus, KSIFS-MERC Technique enhances the TDA by 12 % and 19 % when compared [1] and [2].

Table 1 Tabulation for Tumor Diagnosis Accuracy

Number of Patients (n)	Tumor Diagnosis Accuracy (%)		
	Complex-valued classifier	Ensemble Classifier	KSIFS-MERC Technique
50	80	78	86
100	74	81	89
150	79	86	92
200	83	82	91
250	85	88	93
300	84	86	92
350	83	85	90
400	81	82	92
450	79	82	90
500	79	81	89

5.2 Tumor Diagnosis Time (TDT)

It measure time taken to find out presence and lackof brain tumor syndrome. The **TDT**is measured as,

$$TDT = n * t_s (6)$$

In equation (6), the detection time of brain tumor disease is determined. 'n' is a number ofpatient's data in which 't_s' specified in time utilizedtocategorizepresence and absence of brain tumor disease insingle patientdata. The TDT is calculated in millisecond (ms).

Sample Calculation for Tumor Diagnosis Time

- **Complex-valued classifier:** time takentoclassify one patient is 0.33 ms and total number of patients is 50. **TDT**is calculated as,

$$TDT = 50 * 0.33 = 17\ ms$$

- **Ensemble Classifier:** the time preferredtoclassify medical data of a one patient is 0.38 ms and total number of patients is 50. **TDT**is computed as,

$$TDT = 50 * 0.38 = 19\ ms$$

- **KSIFS-MERC Technique:** the time utilizedtoclassifyone patient data is 0.31 ms and whole number of patients is 50. **TDT**is evaluated as,

$$TDT = 50 * 0.31 = 16\ ms$$

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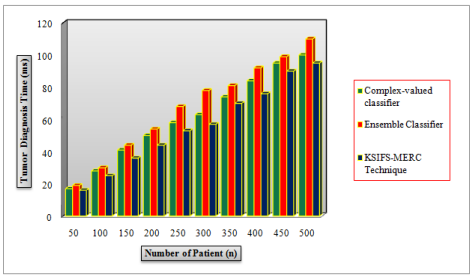

Figure 5 Experimental Result of Tumor Diagnosis Time versus Number of Patients

From above figure 5,describe theTDTbased ona different number of patients using existing methods and proposed KSIFS-MERC Technique. The KSIFS-MERCmethodpresents better diagnosis time for brain tumor disease as compared to Complex-valued classifier [1] and Ensemble classifier [2].This is because ofapplication of KSI-FS algorithm and MAP estimated Rocchio Classifier in the KSIFS-MERCTechnique than the existing works. Through the concepts ofKSI-FS algorithm, the KSIFS-MERCmethoddetermineskeyrisk factors (i.e. features) with a minimal timetodiagnosis brain tumor disease.

In order to categorize the patients as normal or abnormal by minimum time complexity by after identifying risk factors, the KSIFS-MERCTechnique exploits MAP estimated Rocchio Classifier.This helps for KSIFS-MERC method to minimizetimeneeded to detect presence andlack of brain tumor diseaseas compared to conventional methods.So, KSIFS-MERCTechnique decreasesTDT by 8 % and 17 % as compared to existing Complex-valued classifier [1] and Ensemble classifier [2].

5.3False Positive Rate(FPR)

FPR ismeasured the number of patient incorrectlyclassified as normal or abnormal to whole number of patients. FPR is mathematically formulated as,

$$FPR = \frac{\omega_{ia}}{n} * 100 \qquad (7)$$

From (7), FPA of tumor disease classification is measured. 'ω_{ia}' is a patient arewrongly classified as normal or abnormal.FPA is evaluated in percentages (%).

Sample Calculation forFPA

- **Complex-valued classifier:** amount of patient'swrongly classified in 14 and wholenumber of patients is 50. FPA is measured as,

$$FPR = \frac{14}{50} * 100 = 28\ \%$$

- **Ensembleclassifier:** amount of patients incorrectly classified in 15 and total number of patients is 50. FPA is formulated as,

$$FPR = \frac{15}{50} * 100 = 30\ \%$$

- **KSIFS-MERC Technique:**amount of patients inaccurately classified is 7 and total number of patients is 50. FPA is formulated as,

$$FPR = \frac{7}{50} * 100 = 14\ \%$$

The KSIFS-MERC methodusingdifferentnumber of patient's medical data Vs FPR of brain tumor disease classification evaluates the range of 50-500 from Epileptic Seizure Recognition Dataset.Experimental outcome of FPRusing KSIFS-MERCTechnique is compared with Complex-valued classifier [1] and Ensemble classifier [2]. When using the 400 patient medical data, KSIFS-MERC Technique obtains8 %FPRwhereas Complex-valued classifier [1] and Ensemble classifier [2] gets19 % and 18% respectively. As a result, the ratio of number of patients mistakenly classified as normal or abnormal using KSIFS-MERCTechnique is lesser. Hence,the proposedKSIFS-MERC Technique achievesa minimumFPR for tumor disease classification as compared to existing [1] and [2] methods. KSIFS-MERC method minimizes false positive rate by 50 % and 43% as compared to existing Complex-valued classifier [1] and Ensemble classifier [2].

Table 3 Tabulation for False Positive Rate

Number of Patients (n)	False Positive Rate (ms)		
	Complex-valued classifier	Ensemble Classifier	KSIFS-MERC Technique
50	20	22	14
100	26	19	11
150	21	14	8
200	17	18	9
250	15	12	7
300	16	14	8
350	17	15	10
400	19	18	8
450	21	18	10
500	21	19	11

6. SUMMARY

The proposed KSIFS-MERC method is employedforenhancing the efficiency of brain tumor disease diagnosis.Aim of KSIFS-MERC technique is achieved

through the supports of KSI-FS algorithm and MAP estimated Rocchio Classifier. By using the algorithmic processes of KSI-FS, KSIFS-MERC technique selects the minimal number of risk factors to accurately diagnosis the brain tumor as compared to existing works. Besides, KSIFS-MERC technique attains the less computational effort as MAP estimated Rocchio Classifierwork on fewer medical features to effectively classify the patients as normal and abnormal. Furthermore, KSIFS-MERC technique obtains the lower false positive rate through classifying brain tumor diseasesbased on the maximum a posteriori probability result. As a outcome, KSIFS-MERC technique givesimprovedbrain tumor syndromeanalysis performance as compared to conventionalmethods. The results of KSIFS-MERC technique is obtained indifferent metrics such as, TDA, TDT and FPR and compared bytwo conventional methods. Experimental results exposedtoKSIFS-MERC technique provide theincreased performance with improvement of tumor diagnosis accuracyand minimumtumor diagnosis time when compared to state of art of methods.

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