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Development of KNN-EIM based hybrid model for brain MRI density range determination

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***Abstract*---**Data mining techniques are used in the medical data analysis to predict the hidden knowledge from the existing data. This work attempted to apply the data mining techniques to analysis the medical image focus to brain tumor evaluation. The affected tumor region range values. The work focused to evaluate the performance of clustering algorithms for medical image analysis via predicting the tumor affected area. It is achieved through analysing Brain MRI to identify the high-density neuron using the integrated approach of K-Means and Equal Interval clustering. The tumour affected area and its range values are identified using a clustering algorithm such as Equal Interval Method and K-Means approach. To enhance the accuracy of the affected region, the common affected high-density pixels are identified using a hybrid model through the Integration of K-Means and Equal Interval Method. It is evaluated according to time complexity and accuracy.

***Keywords*---**data mining, clustering, KNN, equal interval method.

Introduction

Human information processing and applications are servings as a source of inspiration to apply computing models and algorithms into medical image analysis.it is attempted to identify the tumor using clustering and classification techniques. Data clustering used to determine groups of similar objects where objects in a group will be similar (or related) to one another and different from (or unrelated to) the objects in other groups. A clustering method will produce high quality clusters with high low intra-cluster similarity and inter-cluster similarity [1]. This work mainly focused to analysis the Magnetic Resonance Image (MRI)

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brain image using existing datamining techniques such as Equal Interval Method (EIM), K-Means (KM) cluster, and development of hybrid model to find brain tumor. The hybrid method derived by integrating clustering models and determines neuron activeness, stress level and high-density tissues in the Brian MRI.

Review of Literature

In W. Frawley et. al. [2], untrivial extraction of implicit, previously unknown and perhaps significant information from data is referred to as the KDD. It may be used to find new information from current datasets. It might be continuous, distinct classifications or quantity. Ordinal or nominal data can be classified as categorical. Ch.Venkateswarlu and Abid Hussain[3] defined Data Mining as the mathematical core of the Knowledge Discovery in Database (KDD) process, which includes three key elements: (1) the use of algorithms to find patterns within the data, (2-3) the application of mathematical models to discovered patterns, and (3) the discovery of knowledge from the patterns and mathematical models. Multitudes of imaging modalities exist, ranging from the more common radiology, nuclear medicine, and optical imaging to image-guided intervention [4][5]. K-Means, Density-Based, Filtered, and Farther First clustering were all examined by G, et al. [6] in their study. The programme was used to develop and assess these clustering techniques. The K-Means method was shown to be the best of the algorithms and also delivered excellent results when a huge amount of data was used.

According to Ogwueleka et al. [7], a new approach for data collecting has been developed that consists of applying K-Means clustering using an Excel VBA macro for implementation. Cluster values derived by the program's cluster algorithm were utilised. Navneet Kaur [8] researched the topic of clustering, as well as other data mining approaches. They successfully applied Partitioning, Hierarchical, Grid, and density-based clustering methods. In hierarchical clustering, interconnectivity is the most important concept. Centroid-based partitioning assigns k-means to the partitions [9]. Density based clusters were discovered in a section of the dataset that had a greater density of points. This data analysis techniques for medical pictures and is linked to image clustering, segmentation, and classification. Medical imaging has helped in the identification and treatment of disease by allowing researchers to peer into the human body and study its interior components [10]. The usage of medical imaging techniques includes a range of technologies that are considered non-invasive ways for studying interior organs. Surgical operations are forbidden for doctors to examine at different regions and organs. It is effective in aiding in the detection and treatment of many health issues. K-Means and Perona Malik Anisotropic Diffusion (MD) segmentation was proposed by Masroor Ahmed et al. [11]. In this paper, they offer an effective automated approach for segmenting brain tumors from MR images for the extraction of tumor tissues.

Methodology

In order to determine the region of tumor that is influenced by the distance-based clustering techniques mentioned below, on the high-density digital data.

Clustering [12] is the process of organising objects into groups in which the objects that are grouped are more similar to each other. The following is a list of the approaches applied in this project.

Equal Interval Method

Clustering is the divided image results in five clusters, which are identified by digital values. Equal range value [13] is used to compute the distance measurements. For any cluster between 0 and 255, the number of values is 256. Each pixel is assigned to one of the five clusters depending on its value. The values are estimated to be impacted clusters, and hence, the high-density values are assumed. The similarity measure on clustered object is attempted using the following procedure.

Step 1: Fetch the MRI image
Step 2: Convert the fetched image into the nrrd file format.
Step 3: Convert and represent the images into cubical data set.
Step 4: Adopt the liner data set and compute the cluster index.
Step 5: Generate clusters using equal interval algorithm.
Step 6: Determination of similarity between different levels of clusters

K -Means Algorithm

The K-Means is a straightforward method for solving the clustering issue that uses no supervision [12]. For grouping a set of data points into k clusters, that should typically introduce k-mean clustering. This process is efficient at working with multidimensional vectors and has an above-average processing capacity. Thus, it measures distortion by measuring a distance, and so it does a better way of measuring the distortion of a data point relative to its cluster centre. The K-Means algorithm is a basic method which is repeatedly used to assign disease impacted images into K groups. A type of group process known as clustering divides items into several clusters, in which each object is placed in the right cluster with its own mean value[14]. The approach for classifying a given dataset utilises a simple, modest methodology. in the d-dimensional space are partitioned into k-clusters (assume k clusters) [15]. This will produce the collection of k clusters, each of which will represent the midpoint of a split dataset.

$$k = \sum_{j=1}^{k} \sum_{i=1}^{n} \left\| x_i^{(j)} - c_j \right\|^2 .$$

Equation 3.1

Where $\left\| x_i^{(j)} - c_j \right\|^2$ is a chosen distance measure between a data point and the cluster center c_j, is an indicator of the distance of the n data points from their respective cluster center.[16] The algorithm is composed of the following steps:

Step 1: Place k points into the space represented by the objects that are being clustered. These points represent the initial group centroids.

Step 2: Assign each object to the group that has the closest centroid.
Step 3: When all objects have been assigned, recalculate the positions of the k centroids.
Step 4: Repeat steps 2 and 3 until the centroids no longer move.

This produces a separation of the objects into groups from which the metric to be minimized can be calculated [17]. The clustering technique shows their efficiency in various fields [18], in this technique is expansive in the medical domain, the competence of *K-Means* was shown in many applications because of its performance.

Hybrid Approach

The cluster range values from Equal Interval Method and K-Means are fetched for each cluster and its common values are computed. The fetched affected cluster from the K-Means again is iterated with the EIM method. The more accurate results are obtained.

Step 1: Place k points into the space represented by the objects that are being clustered. These points represent the initial group centroids.
Step 2: Assign each object to the group that has the closest centroid.
Step 3: When all objects have been assigned, recalculate the positions of the k centroids.
Step 4: Repeat steps 2 and 3 until the centroids no longer move.
Step 5: Determine the minimum (Min) and maximum (Max) value form the Digital values.
Step 6: Determine the difference dx = Max – Min
Step 7: The Range R = dx / NC
Step 8: Fix the starting pixel value and End pixel values for each classification based on the range values.
Step 9: Process all row values and verify the range. According to the individual and combinational range values construct the classification data and sub image.
Step 10: Repeat the step 10 until all the classification to be processed.

As per the iterative results, the range intensity determines density of the affected slices. It determined the relationship between affected clusters and the model accuracy.

Construction of cubical database from MRI

MRI (Magnetic Resonance Imaging) is one of the popular and well-known methods for the three-dimensional observation of the brain and structures. It is quite limiting when it comes to image resolution. In stained sections, the resolution is good, but spatial aberrations are inherent in the staining process. Fetching data from the slicer's 3D download data base, the nrrd file is read. The N-dimensional raster data supported by nrrd is utilised in scientific visualisation and image processing. The neural network route analysis was done by Modha, et. al., who studied the MRI three-dimensional coordinated image to find out how far and how quickly the neuron was moving.[19] [20] The procedure to improve the speed of the neuron process utilises a similar method. MRI scans process the pictures, which are obtained, using Matlab, and convert them to two-dimensional images and values shown in figures 1.

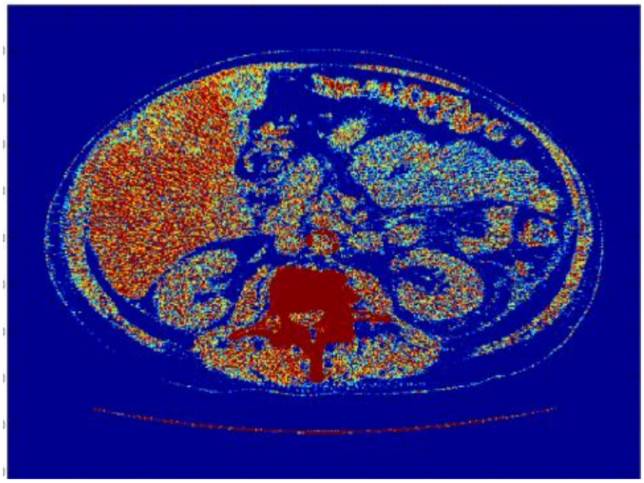

Figure 1. Converted MRI

Input for EMI Clustering

As a sequence of frames, the recorded .nrrd file was imported into the EIM Clustering application. One single set of input (figure 5.1 through figure 2) is provided below as an example.

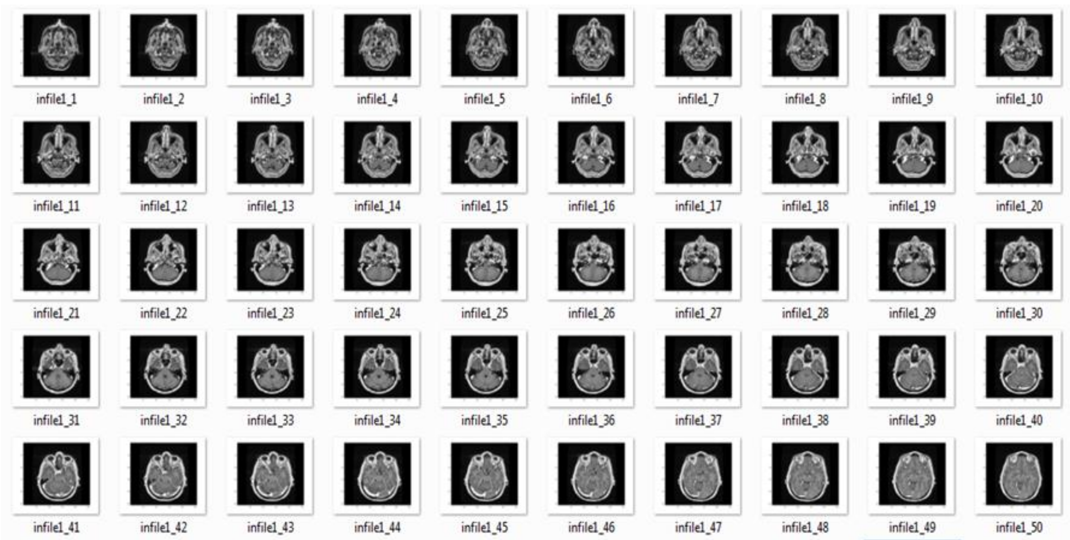

Figure 2. Input file frames

Table 1
Cluster Count and Range values for EIM method

F_ N0	# Pixel Cluster 1	Min Cluster 1	Max Cluster 1	# Pixel Cluster 2	Min Cluster 2	Max Cluster 2	# Pixel Cluster 3	Min Cluster 3	Max Cluster 3	# Pixel Cluster 4	Min Cluster 4	Max Cluster 4	# Pixel Cluster 5	Min Cluster 5	Max Cluster 5
1	498925	0	51	62092	52	102	79745	103	153	35325	154	205	403913	206	255
2	495314	0	51	61547	52	102	72908	103	153	42259	154	205	407972	206	255
3	491800	0	51	63358	52	102	72017	103	153	42377	154	205	410448	206	255
4	489814	0	51	62826	52	102	75485	103	153	41796	154	205	410079	206	255
5	488542	0	51	64819	52	102	76438	103	153	39441	154	205	410760	206	255
6	487699	0	51	61705	52	102	74477	103	153	41628	154	205	414491	206	255
7	485221	0	51	64941	52	102	73977	103	153	40171	154	205	415690	206	255
8	482485	0	51	65718	52	102	73479	103	153	42997	154	205	415321	206	255
9	478810	0	51	63904	52	102	75962	103	153	44814	154	205	416510	206	255
10	477842	0	51	62947	52	102	73858	103	153	46063	154	205	419290	206	255

The formed cluster images for each input frame is presented below from figure 3.

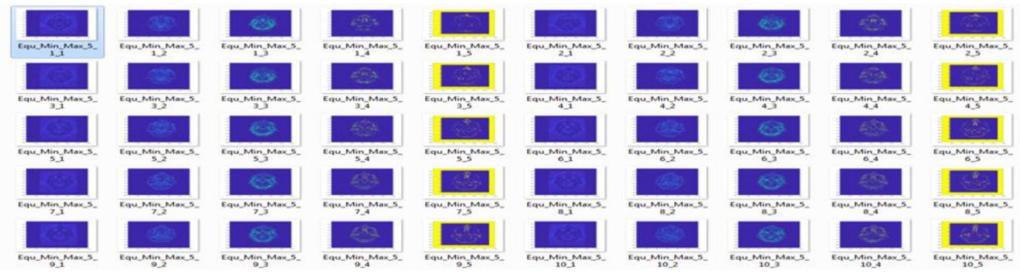

Figure 3. Clustered frames

Procedure for K-Means Squared Euclidian and EIM

The *K-Means Squared Euclidian (KMSE)-Equal Interval Method (*EIM) steps are presented below.

Step 1: Input the original MRI brain images.
Step 2: Convert into sequence of frames.
Step 3: Cluster the image using *K-Means Squared Euclidian* algorithm
Step 4: Get the clustered objects.
Step 5: Increment the value of *k*.
Step 6: Cluster dataset images
Step 7: Identify the affected cluster.
Step 8: Cluster the image using *EIM algorithm*.
Step 9: Get the clustered objects.
Step 10: Increment the value of *k*.
Step 11: Cluster dataset images
Step 12: Identify the affected cluster.
Step 13: Form the cluster image based on affected cluster range.
Step 14: Compute the average percentage of affected tumor.

Step 15: Compute the affected cluster average percentage and determine the level.

Range values from K-Means Squared Euclidian and EIM

The following frames and range values have been found in Table 2 as an impacted cluster using K-Means Squared Euclidian technique.

Table 2
Range values for affected cluster using K-Means Squared Euclidian algorithm

S.No	Frame	Cluster	No of Pixel	Min	Max
1.	77	3	415880	228	255
2.	78	4	428341	183	255
3.	80	3	452211	154	255
4.	82	2	450889	156	255
5.	83	1	1079996	0	255
6.	84	2	463033	152	255
7.	85	1	1079996	0	255
8.	86	4	449580	158	255
9.	87	3	211881	63	253
10.	88	3	418738	225	255
11.	89	5	430614	195	255
12.	90	3	203955	58	252
13.	91	1	1079996	0	255
14.	92	3	151554	99	237
15.	93	1	1079996	0	255
16.	94	1	1079996	0	255
17.	95	3	189129	50	252
18.	96	3	184364	52	253
19.	97	3	448635	157	255
20.	98	2	432121	183	255
21.	99	2	460911	150	255
22.	100	4	412189	248	255
23.	102	4	404296	254	255
24.	103	4	414077	247	255
25.	104	4	413195	247	255
26.	107	4	417258	239	255
27.	108	4	425100	215	255
28.	109	3	416632	244	255
29.	110	3	416711	245	255
30.	111	3	414506	247	255
31.	112	4	412505	250	255
32.	116	3	408428	251	255
33.	118	3	400668	205	255

Affected Clusters from K-Means Squared Euclidian and EIM

Each formed cluster algorithms are denoted with an index value and presented below in figure 4

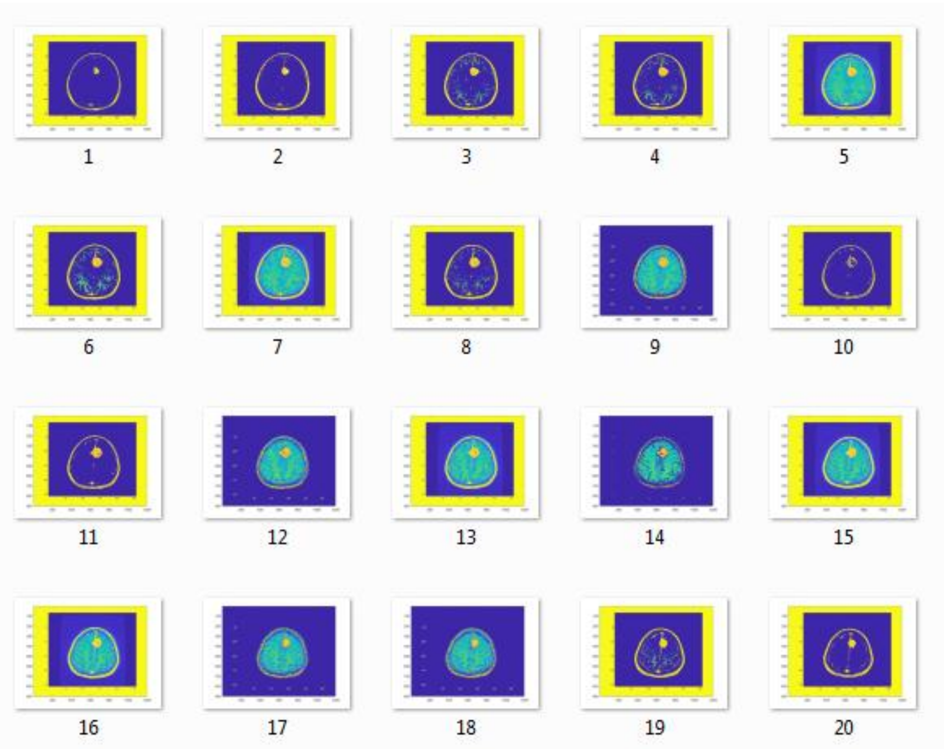

Figure 4. Affected Clusters from K-Means Squared Euclidian and EIM

Percentage of Affected Clusters from KMSE-EIM

The identified cluster ranges along with its average is computed and presented in table 3.

Table 3
Affected clusters and percentage and range values from KMSE-EIM method

S.No	Frame No	Affected Cluster	No of DNs	Min	Max	Total Pixel	Average
1.	77	5	344558	206	255	1080032	31.90
2.	78	5	347206	206	255	1080033	32.15
3.	80	5	347289	206	255	1080034	32.16
4.	82	5	348042	206	255	1080035	32.23
5.	83	5	347051	206	255	1080036	32.13
6.	84	5	348345	206	255	1080037	32.25
7.	85	5	347196	206	255	1080038	32.15
8.	86	5	348457	206	255	1080039	32.26
9.	87	5	214997	206	255	1080040	19.91

10.	88	5	345479	206	255	1080041	31.99
11.	89	5	348666	206	255	1080042	32.28
12.	90	5	214716	206	255	1080043	19.88
13.	91	5	348085	206	255	1080044	32.23
14.	92	5	211482	206	255	1080045	19.58
15.	93	5	347924	206	255	1080046	32.21
16.	94	5	347690	206	255	1080047	32.19
17.	95	5	213748	206	255	1080048	19.79
18.	96	5	214235	206	255	1080049	19.84
19.	97	5	348504	206	255	1080050	32.27
20.	98	5	348516	206	255	1080051	32.27
21.	99	5	348203	206	255	1080052	32.24
22.	100	5	343405	206	255	1080053	31.80
23.	102	5	344166	206	255	1080054	31.87
24.	103	5	343950	206	255	1080055	31.85
25.	104	5	343670	206	255	1080056	31.82
26.	107	5	345086	206	255	1080057	31.95
27.	108	5	347557	206	255	1080058	32.18
28.	109	5	344833	206	255	1080059	31.93
29.	110	5	344867	206	255	1080060	31.93
30.	111	5	344294	206	255	1080061	31.88
				Average			30.04

According to the observation, three clusters are removed and the range values are 206 to 255 for the whole detected clusters. The average cluster impacted is 30.04%. The same technique is applied to and detailed in the following K-Means City Block – EIM.

Percentage of affected Cluster and range values for KMCB-EIM

After identification, the common range values and the impacted percentages are computed. The range and percentages of affected clusters are shown in Table 4 below.

Table 4
Affected Cluster and range values for KMCB-EIM

S.No	Frame no	Affected Cluster	No of DNs	Min	Max	Total Pixel	Percentage
1	93	5	347362	206	255	1080032	32.16
2	97	5	346703	206	255	1080033	32.10
3	98	5	348317	206	255	1080034	32.25
					Average		32.17

According to the examination, the impacted pixels range from 206 to 255. It is a pixel with a high density of the afflicted clusters. The average number is 32.17%. The KMSE-EIM average is 30.04. The range of identification is the same, but the proportion of the region impacted is different.

Analysis of Hybrid Models

The common calculation range and identification of the area and percentage impacted is achieved using KMSQ-EIM and KMCB-EIM methods. For both approaches the common range is the same, but the proportion and performance differ. The proportion of the tumor in question and its fluctuations are shown in Table 5 below.

Table 5
Range and Percentage of Affected Area of Hybrid Algorithms

S. No	Images	No of Frames	% KMSE-EIM	% KMCB-EIM	Variation	Range From	Range To
1	RegLib_C01_MRMeningioma_1	130	30.04	29.55	0.49	206	255
2	RegLib_C01_MRMeningioma_2	112	32.17	35.51	3.34	206	255
3	RegLib_C01_MRMeningioma_3	148	30.14	31.10	0.96	206	255
4	RegLib_C01_MRMeningioma_4	96	62.34	64.44	2.10	206	255
5	RegLib_C01_MRMeningioma_5	115	49.65	47.50	2.15	206	255
6	RegLib_C01_MRMeningioma_6	141	23.16	20.40	2.76	206	255
7	RegLib_C01_MRMeningioma_7	95	34.86	38.62	3.76	206	255
8	RegLib_C01_MRMeningioma_8	94	72.55	70.10	2.45	206	255
9	RegLib_C01_MRMeningioma_9	117	22.45	22.78	0.33	206	255
10	RegLib_C01_MRMeningioma_10	117	35.64	33.77	1.87	206	255
11	RegLib_C01_MRMeningioma_11	127	37.89	41.50	3.61	206	255
12	RegLib_C01_MRMeningioma_12	117	62.34	64.78	2.44	206	255
13	RegLib_C01_MRMeningioma_13	134	21.64	24.65	3.01	206	255
14	RegLib_C01_MRMeningioma_14	135	42.43	41.39	1.04	206	255
15	RegLib_C01_MRMeningioma_15	98	35.65	38.97	3.32	206	255
16	RegLib_C01_MRMeningioma_16	114	60.11	60.36	0.25	206	255
17	RegLib_C01_MRMeningioma_17	113	70.45	71.25	0.80	206	255
18	RegLib_C01_MRMe	94	62.54	62.80	0.26	206	255

S. No	Images	No of Frames	% KMSE-EIM	% KMCB-EIM	Variation	Range From	Range To
	ningioma_18						
19	RegLib_C01_MRMeningioma_19	95	26.11	26.01	0.10	206	255
20	RegLib_C01_MRMeningioma_20	121	34.76	34.28	0.48	206	255
21	RegLib_C01_MRMeningioma_21	107	50.11	49.76	0.35	206	255
22	RegLib_C01_MRMeningioma_22	102	23.65	24.14	0.49	206	255
23	RegLib_C01_MRMeningioma_23	116	23.54	22.20	1.34	206	255
24	RegLib_C01_MRMeningioma_24	104	25.22	23.33	1.89	206	255
25	RegLib_C01_MRMeningioma_25	121	46.34	45.64	0.70	206	255
26	RegLib_C01_MRMeningioma_26	96	24.86	28.32	3.46	206	255
27	RegLib_C01_MRMeningioma_27	138	24.80	23.06	1.74	206	255
28	RegLib_C01_MRMeningioma_28	136	48.33	51.81	3.48	206	255
29	RegLib_C01_MRMeningioma_29	137	27.45	29.30	1.85	206	255
30	RegLib_C01_MRMeningioma_30	101	35.32	36.10	0.78	206	255
31	RegLib_C01_MRMeningioma_31	142	29.12	26.81	2.31	206	255
32	RegLib_C01_MRMeningioma_32	129	18.34	18.44	0.10	206	255
33	RegLib_C01_MRMeningioma_33	118	48.75	46.84	1.91	206	255
34	RegLib_C01_MRMeningioma_34	97	27.51	28.33	0.83	206	255
35	RegLib_C01_MRMeningioma_35	113	48.04	49.90	1.86	206	255
36	RegLib_C01_MRMeningioma_36	123	26.49	30.32	3.83	206	255
37	RegLib_C01_MRMeningioma_37	99	39.97	42.06	2.09	206	255
38	RegLib_C01_MRMeningioma_38	112	22.50	22.19	0.31	206	255
39	RegLib_C01_MRMeningioma_39	95	26.94	30.13	3.19	206	255
40	RegLib_C01_MRMeningioma_40	111	21.58	19.38	2.19	206	255
41	RegLib_C01_MRMe	105	36.75	34.59	2.15	206	255

S. No	Images	No of Frames	% KMSE-EIM	% KMCB-EIM	Variation	Range From	Range To
	ningioma_41						
42	RegLib_C01_MRMeningioma_42	95	30.96	33.16	2.21	206	255
43	RegLib_C01_MRMeningioma_43	135	21.90	20.88	1.02	206	255
44	RegLib_C01_MRMeningioma_44	102	19.49	23.12	3.63	206	255
45	RegLib_C01_MRMeningioma_45	116	20.37	19.56	0.81	206	255
46	RegLib_C01_MRMeningioma_46	91	62.20	59.86	2.34	206	255
47	RegLib_C01_MRMeningioma_47	92	25.30	24.99	0.31	206	255
48	RegLib_C01_MRMeningioma_48	135	23.14	20.26	2.88	206	255
49	RegLib_C01_MRMeningioma_49	131	22.76	23.18	0.42	206	255
50	RegLib_C01_MRMeningioma_50	121	17.01	15.05	1.96	206	255
51	RegLib_C01_MRMeningioma_51	102	44.11	42.59	1.52	206	255
52	RegLib_C01_MRMeningioma_52	104	23.71	24.76	1.05	206	255
53	RegLib_C01_MRMeningioma_53	109	32.19	30.53	1.66	206	255
54	RegLib_C01_MRMeningioma_54	114	38.64	39.26	0.62	206	255
55	RegLib_C01_MRMeningioma_55	121	25.44	23.71	1.73	206	255
56	RegLib_C01_MRMeningioma_56	92	40.38	40.28	0.10	206	255
57	RegLib_C01_MRMeningioma_57	114	20.05	17.50	2.55	206	255
58	RegLib_C01_MRMeningioma_58	104	34.49	34.96	0.46	206	255
59	RegLib_C01_MRMeningioma_59	97	53.66	52.91	0.75	206	255
60	RegLib_C01_MRMeningioma_60	108	38.90	37.64	1.26	206	255

The percentages of tumors impacted are indicated using KMSE-EIM and KMCB-EIM algorithms. The range values are the same, but the proportion affected varies according to the success of the clustering. The change is between 0.10 and 3.83 percentages. The afflicted area of the benign kind is less than the affected area of the malignant type. The fluctuation in the proportion of the benign entrance computed by means of a K-means Euclid Square - Equal interval technique by K-means City Block - Equal interval method shown in Table 6.

Table 6
Variations of KMSE-EIM vs KMCB-EIM for benign

S.No	Input IDs	No of Frames	% KMSE-EIM	% KMCB-EIM	Variations	Actual
1.	RegLib_C01_MRMeningioma_1	130	30.04	29.55	0.49	Benign
2.	RegLib_C01_MRMeningioma_2	112	32.17	35.51	3.34	Benign
3.	RegLib_C01_MRMeningioma_3	148	30.14	31.10	0.96	Benign
4.	RegLib_C01_MRMeningioma_6	141	23.16	20.40	2.76	Benign
5.	RegLib_C01_MRMeningioma_7	95	34.86	38.62	3.76	Benign
6.	RegLib_C01_MRMeningioma_9	117	22.45	22.78	0.33	Benign
7.	RegLib_C01_MRMeningioma_10	117	35.64	33.77	1.87	Benign
8.	RegLib_C01_MRMeningioma_11	127	37.89	41.50	3.61	Benign
9.	RegLib_C01_MRMeningioma_13	134	21.64	24.65	3.01	Benign
10.	RegLib_C01_MRMeningioma_14	135	42.43	41.39	1.04	Benign
11.	RegLib_C01_MRMeningioma_15	98	35.65	38.97	3.32	Benign
12.	RegLib_C01_MRMeningioma_19	95	26.11	26.01	0.10	Benign
13.	RegLib_C01_MRMeningioma_20	121	34.76	34.28	0.48	Benign
14.	RegLib_C01_MRMeningioma_22	102	23.65	24.14	0.49	Benign
15.	RegLib_C01_MRMeningioma_23	116	23.54	22.20	1.34	Benign
16.	RegLib_C01_MRMeningioma_24	104	25.22	23.33	1.89	Benign
17.	RegLib_C01_MRMeningioma_26	96	24.86	28.32	3.46	Benign
18.	RegLib_C01_MRMeningioma_27	138	24.80	23.06	1.74	Benign
19.	RegLib_C01_MRMeningioma_29	137	27.45	29.30	1.85	Benign
20.	RegLib_C01_MRMeningioma_30	101	35.32	36.10	0.78	Benign
21.	RegLib_C01_MRMeningioma_31	142	29.12	26.81	2.31	Benign
22.	RegLib_C01_MRMeningioma_32	129	18.34	18.44	0.10	Benign
23.	RegLib_C01_MRMeningioma_34	97	27.51	28.33	0.83	Benign

S.No	Input IDs	No of Frames	% KMSE-EIM	% KMCB-EIM	Variations	Actual
24.	RegLib_C01_MRMeningioma_36	123	26.49	30.32	3.83	Benign
25.	RegLib_C01_MRMeningioma_37	99	39.97	42.06	2.09	Benign
26.	RegLib_C01_MRMeningioma_38	112	22.50	22.19	0.31	Benign
27.	RegLib_C01_MRMeningioma_39	95	26.94	30.13	3.19	Benign
28.	RegLib_C01_MRMeningioma_40	111	21.58	19.38	2.19	Benign
29.	RegLib_C01_MRMeningioma_41	105	36.75	34.59	2.15	Benign
30.	RegLib_C01_MRMeningioma_42	95	30.96	33.16	2.21	Benign
31.	RegLib_C01_MRMeningioma_43	135	21.90	20.88	1.02	Benign
32.	RegLib_C01_MRMeningioma_44	102	19.49	23.12	3.63	Benign
33.	RegLib_C01_MRMeningioma_45	116	20.37	19.56	0.81	Benign
34.	RegLib_C01_MRMeningioma_47	92	25.30	24.99	0.31	Benign
35.	RegLib_C01_MRMeningioma_48	135	23.14	20.26	2.88	Benign
36.	RegLib_C01_MRMeningioma_49	131	22.76	23.18	0.42	Benign
37.	RegLib_C01_MRMeningioma_50	121	17.01	15.05	1.96	Benign
38.	RegLib_C01_MRMeningioma_52	104	23.71	24.76	1.05	Benign
39.	RegLib_C01_MRMeningioma_53	109	32.19	30.53	1.66	Benign
40.	RegLib_C01_MRMeningioma_54	114	38.64	39.26	0.62	Benign
41.	RegLib_C01_MRMeningioma_55	121	25.44	23.71	1.73	Benign
42.	RegLib_C01_MRMeningioma_57	114	20.05	17.50	2.55	Benign
43.	RegLib_C01_MRMeningioma_58	104	34.49	34.96	0.46	Benign
Min			17.01	15.05	0.10	
Max			42.43	42.06	3.83	
Average			27.82	28.10	1.74	

The calculated percentage of the KMSE-EIM technique is compared with the KMCB-EIM method. The lowest area percentage of the impacted KMSE-EIM technique is 17.01% and the highest is 42.43% for benign. The minimal area percentage affected by KMCB-EIM is 15.05%, while for the malignant the maximum is 42.06%. The variation between two methods is calculated, the smallest deviation is 0.1% and the largest is 1.74%. The average variance in the benign picture analysis is 1.74 percent. 15 frame differences out of 43 frames are less than 1 %. In KMSE-EIM method, the maximum impacted percentage is considerable. In the KMCB-EIM method, the minimal percentage is determined.

Conclusion

For K-Means Squared Euclidian the true positive is high - the method of equal interval compared to K-Means City Block - Equal Interval Method. For K-Means Squared Euclidian – Equal Interval Method, the False positive is reduced compared to K-Means City Bloc - Equal Interval Method. The KMSE-EIM value of 0.97 and the KMCB-EIM method value of 0.95 for benign, according to F1 values. The value of KMSE-EIM is 0.91 and the value of the KMCB-EIM method 0.88 is malignant. The KMSE-EIM is significant compared to the KMCB-EIM method, according to the computed F1 values. The precision, recall, f1-score, and support value performance measurements are significant for K-Means Squared Euclidian-Equal Interval Method compared with K-Means City Block – Equal Interval Method. Though it is less time for the K-Means city block - Equal Interval Method, K-Means Squared Euclidian- Equal Interval Method appreciate performance measures. Accuracy in the medical field is strongly suggested, thus K-Means Squared Euclidian- Equal Interval technique is determined as the best way among the two models created.

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