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An automated detection and classification approach in MRI tumor diagnosis

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ABSTRACT
In the process of image coding, external noises impact a lot in processing efficiency. In the application of medical image processing, this effect is more, important due to its finer content details. It is required to minimize the noise effect with preserving the image content information, without losing the image generality. Towards the objective of image denoising, in this work, a dynamic block coding approach for noise minimization in medical image processing is presented. The second observing factor in region segmentation is the marking of small region patterns which are derived due to misclassification of actual and detected regions. the complexity of detection logic, due to recurrent coding is an additional factor to observe. In this paper, a new recurrent coding approach of region segmentation is proposed, overcoming the issue of region marking, discontinuity issue and small region miss-classification. The suggested approach is a simpler and robust to region detection, test over different MRI samples.

KEYWORDS
Denoising, medical image processing, dynamic block coding, MRI images, classification

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I. INTRODUCTION

Current developments have led to attaining higher coding efficiency in image processing applications and its utilization. In different level of applications, medical image processing has its own importance. In the area of medial image coding, finer details coding and preservation is of prime importance. Towards the accuracy in image coding, various approaches were developed in past, to achieve the objective of image quality improvement. Various well-established techniques, such as median filtering are successfully used in gray scale imaging. Median filtering approach is particularly adapted for impulsive noise suppression. It has been shown that median filters present the advantage to remove noise without blurring edges since they are nonlinear operators of the class of rank filters and since their output is one of the original gray values [1][2]. The extension of the concept of median filtering to color images is not trivial. The main difficulty in defining a rank filter in color image is that there is no ”natural” and unambiguous order in the data [3][4]. During the last years, different methods were proposed to use median filters in color medical image processing [5][6]. Whatever the vector filtering method, the challenge is to detect and replace noisy pixels whereas the relevant information is preserved. But it is recognized that in some MRI image areas most of vector filters blur thin details and image edges [7][8][9]. Generally impulse noise contaminates medical images during data acquisition by camera sensors and transmission in the communication channel. [10] proposed a two-phase algorithm. In the first phase of this algorithm, an adaptive median filter (AMF) is used to classify corrupted and uncorrupted pixels; in the second phase, specialized regularization method is applied to the noisy pixels to preserve the edges and noise suppression. The main drawback of this method is that the processing time is very high because it uses a very large window size of 39 x 39 in both phases to obtain the optimum output; in addition, more Complex circuitry is needed for their implementation. [11] proposed a sorting based algorithm in which the corrupted pixels are replaced by either the median pixel or neighborhood pixel in contrast to AMF and other existing algorithms that use only median values for replacement of corrupted pixels. At higher noise densities this algorithm does not preserve edge and fine details satisfactorily. In this paper a novel robust estimation based filter is proposed to remove fixed value impulse noise effectively. The proposed filter removes low to high density fixed value impulse noise with edge and detail preservation upto a noise density of 90%. Recently, nonlinear estimation techniques are gaining popularity for the problem of image denoising. The well-known Wiener filter for minimum mean-square error (MMSE) estimation is designed under the assumption of wide-sense stationary signal and noise a random process is said to be stationary when its statistical characteristics are time domain invariant [12]. For most of the natural MRI images, the stationary condition is not satisfied. In the past, many of the noise removing filters were designed with the stationary assumption. These filters remove noise but tend to blur edges and fine details. This algorithm fails to remove impulse noise in high frequency regions such as edges in the MRI image. To overcome the above mentioned difficulties a nonlinear estimation technique for the problem of medical image denoising has been developed based on robust statistics. Robust statistics addresses the problem of estimation when the idealized assumptions about a system are occasionally violated. The contaminating noise in an image is considered as a violation of the assumption of time domain coherence of the medical image intensities and is treated as an outlier random variable [12]. [13] Developed a robust parameter estimation algorithm for the medical image model that contains a mixture of Gaussian and impulsive noise. In [12] a robust estimation based filter is proposed to remove low to medium density Gaussian noise with detail preservation. Though these techniques were developed for filtration of Gaussian or impulsive noise they are been developed for gray level images and are not suitable for color images. In this paper a modified approach to time domain median filter is proposed for the noise removal in digital medical images. The paper is further presented in six sections. Where conventional time domain filtration methods and their limitations were presented in Section 2. Section 3 outlines the proposed modified median filtration approach for MRI images. The simulation observations were presented in section 4.

II. PROPOSED SYSTEM OUTLINE

In the approach of medical image processing, automated image recognition for tumor detection has its own significance. And automate system can provide a early stage analysis and decision based on the image data passed with more effective way. An approach of automated processing medical image data analysis system is presented in figure 1. The system basically consists of a preprocessing stage, feature extraction and classification stage. The primary requirement of any image coding system is to process the image to an extent of maximum accuracy retaining the image integrity.

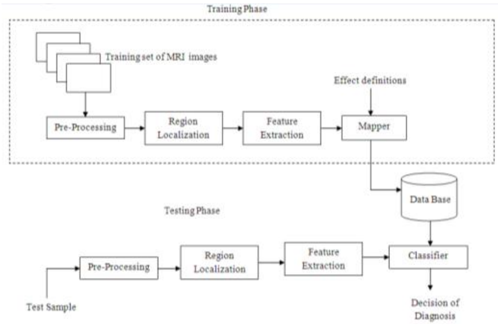


Figure 1: Proposing system architecture for the automated Diagnosis system

In the pre-processing unit the given sample is processed for a standard processing size, extracting the pixel values and performing filtration to eliminate noise effects. The process of denoising was observed in various literatures to eliminate noise effects at preprocessing level. In recent approach towards denoising of MRI sample at preprocessing median filtration was suggested [3]. Wherein median filtration are effective under a discrete level of noise effect, under dynamic noise variations the immunity is reduced. In the operation of median filtration, The values of the pixel in the window are stored and the median – the middle value in the sorted list (or average of the middle two if the list has an even number of elements)-is the one plotted into the output image. The median filtered image g(x, y) can be obtained from the median pixel values in a neighborhood of (x, y) in the input image f(x, y), as defined by the following formula:

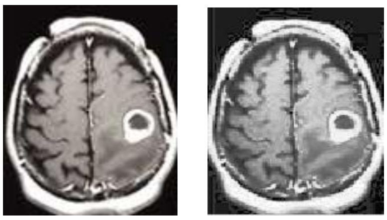
$$MdF(x_i) = Median(\|x_i\|^2) \quad (1)$$

Where, i = 1…. N

These filtration techniques were found to be effective in gray scale images. When processed over color images these filtration techniques give lesser performance. To achieve accurate reconstruction of medical image the median filtration technique is modified to time domain median filtration. The Time domain Median Filter is a uniform smoothing algorithm with the purpose of removing noise and fine points of medical image data while maintaining edges around larger shapes. Segmentation subdivides an image into its constituent parts of objects, the level to which this subdivision is carried depends on the problem being solved, that is, the segmentation should stop when the edge of the tumor is able to be detected.i.e. the main interest is to isolate the tumor from its background. The main problem in the edge detection process is that the cancer cells near the surface of the MRI is very fatty, thus appears very dark on the MRI, which is very confusing in the edge detection process. To overcome the problem, two steps were performed. First, histogram equalization has been applied to the image to enhance the gray level near the edge. Second, thresholding the equalized image in order to obtain a binarized MRI with gray level 1 representing the cancer cells and gray level 0 representing the background.

a) Histogram Equalization

The histogram of an image represents the relative frequency of occurrences of the various gray levels in the image. Histogram modeling techniques (e.g. histogram equalization) provide a sophisticated method for modifying the dynamic range and contrast of an image by altering that image such that its intensity histogram has a desired shape. Unlike contrast stretching, histogram modeling operators may employ non-linear and non-monotonic transfer functions to map between pixel intensity values in the input and output images. Histogram equalization employs a monotonic, non-linear mapping which re-assign the intensity values of pixels in the input image such that the output image contains a uniform distribution of intensities. Figure. 2 shows the effect of histogram equalization on MRI.



(a) (b)

Figure 2. a) The original MRI b) Histogram equalized MRI

b) Thresholding

The segmentation is determined by a single parameter known as the intensity threshold. In a single pass, each pixel in the image is compared with this threshold. If the pixel's intensity is higher than the threshold, the pixel is set to white, in the output. If it is less than the threshold, it is set to black. Segmentation is accomplished by scanning the whole image pixel by pixel and labeling each pixel as object or background according to its binarized gray level. Binarization is carried out using the thresholding. Thresholding is a simple technique for image segmentation. It distinguishes the image regions as objects or the background. Although the detected edges are consisting of tumor edges and non-tumor edges in every block, they can distinguish due to the fact that the intensity of the tumor edges is higher than that of the non-tumor edges. Thus, an appropriate threshold can be selected to preliminarily remove the non-tumor edges in the block. A dynamic thresholding value is calculated as the target threshold value *T*. The target threshold value is obtained by performing an equation on each pixel with its neighboring pixels. Two mask operators are used to obtain mask equation and then calculate the threshold value for each pixel in the 3 detail sub-bands. Basically, the dynamic thresholding method obtains different target threshold values for different sub-band images. Each block ***es*** is then compared with *T* to obtain a binary image (***e***).

The threshold *T* is determined by,

$$T = \frac{\sum (es(i,j) \text{ X } s(i,j))}{\sum s(i,j)} \qquad (2)$$

where

$$s(i,j)=\text{Max}(\,|\,g1 ** es(i,j)\,|,|g2 ** es(i,j)|) \qquad (3)$$

and

$$g1=[\,-1\ 0\ 1], \qquad g2=[-1\ 0\ 1]^{t}$$

In the above eqn.,"* *" denote two-dimensional linear convolution.
applying similar operations to each pixel, all S (i, j) elements can be determined for each block. threshold 'T' is then be computed, and the binary edge image (***e***) is then given by,

$$e(i,j)=\begin{cases} 255, \text{ if } es(i,j) > T \\ 0 \quad , \text{ otherwise} \end{cases} \qquad (4)$$

c) Region localization

The fundamental enhancement needed in MRI is an increase in contrast. Contrast between the brain and the tumor region may be present on a MRI but below the threshold of human perception. Thus, to enhance contrast between the normal brain and tumor region, a Segmentation filter is applied to the digitized MRI resulting in noticeable enhancement in image contrast. Segmentation filters work by increasing contrast at edges to highlight fine detail or enhance detail that has been blurred. Tumor edges are generally short and connected with each other in different orientation. Morphological dilation and Erosion operators are used to connect isolated candidate tumor edges in each block of the binary image.

1	1	1
1	1	1
1	1	1

Figure 3. Structuring elements

To compute the erosion of a binary input image by a given structuring element, each of the *foreground* pixels in the input image is considered. If for *every* pixel in the structuring element, the corresponding pixel in the image underneath is a foreground pixel, then the input pixel is left as it is. The structuring element consists of a pattern specified as the coordinates of a number of discrete points relative to some origin. Figure 3 shows a number of different structuring elements of various sizes. In each case the origin is marked by a ring around that point. The origin does not have to be in the center of the structuring element, but often it is. As seen from the figure, structuring elements that fit into a 3×3 grid with its origin at the center are the most commonly seen type. When a morphological operation is carried out, the origin of the structuring element is typically translated to each pixel position in the image in turn, and then the points within the translated structuring element are compared with the underlying image pixel values.

III. ADAPTIVE LEARNING APPROACH

The proposed modified approach works as explained below,

1) Calculate the time domain depth of every point within the mask selected.
2) Sort these time domain depths in descending order.
3) The point with the largest time domain depth represents the Time domain Median of the set. In cases where noise is determined to exist, this representative point is used to replace the point currently located under the center of the mask.
4) The point with the smallest time domain depth will be considered the least similar point of the set.
5) By ranking these time domain depths in the set in descending order, a time domain order statistic of depth levels is created.
6) The largest depth measures, which represent the collection of uncorrupted points, are pushed to the front of the ordered set.
7) The smallest depth measures, representing points with the largest time domain difference among others in the mask and possibly the most corrupted points, and they are pushed to the end of the list. This prevents the smoothing by looking for the position of the center point in the time domain order statistic list. The image inter relation error is then minimize using a least mean error (LMSE) estimation. The Least Mean Square (LMS) algorithm is an adaptive algorithm, which uses a gradient-based method of steepest decent. LMS algorithm uses the estimates of the gradient vector from the available data. LMS incorporates an iterative procedure that makes successive corrections to the weight vector in the direction of the negative of the gradient vector, which eventually leads to the minimum mean square error. Compared to other algorithms LMS algorithm is relatively simple; it does not require correlation function calculation nor does it require matrix inversions. From the method of steepest descent, the weight vector equation is given by;

$$w(n+1) = w(n) + 1/2\mu[-\Delta(E\{e^2(n)\})] \quad (5)$$

Where μ is the step-size parameter and controls the convergence characteristics of the LMS algorithm; $e^2(n)$ is the mean square error between the output y(n) and the reference signal which is given by,

$$e^2(n) = [d^*(n) - w^h x(n)]^2 \quad (6)$$

The gradient vector in the above weight update equation can be computed as

$$\Delta_w(E\{e^2(n)\}) = -2r + 2Rw(n) \quad (7)$$

In the method of steepest descent the biggest problem is the computation involved in finding the values r and R matrices in real time. The LMS algorithm on the other hand simplifies this by using the instantaneous values of covariance matrices r and R instead of their actual values i.e.

$$R(n) = x(n)x^h(n) \ (8)$$
$$R(n) = x(n)d^*(n) \quad (9)$$

Therefore the weight update can be given by the following equation,

$$W(n+1) = w(n) + \mu x(n)[d^*(n) - w(n)x^h(n)] (10)$$

The LMS algorithm is initiated with an arbitrary value w(0) for the weight vector at n=0. The successive corrections of the weight vector eventually leads to the minimum value of the mean squared error. Therefore the LMS algorithm can be summarized in following equations;

$$Output, (n) = x(n)w^h(n)] \quad (11)$$

$$Error, e(n) = d^*(n) - y(n) \quad (12)$$

$$Weight, w(n+1) = w(n) + \mu x(n)e^*(n) \quad (13)$$

This computed weight provides an optimal value for noise elimination. Using this noise limit, the images are Denoised and passed for higher grid interpolation. The experimental result obtained for the developed system is as illustrated in the following section.

IV. SVM CLASSIFIER MODEL

In machine learning, support vector machines (SVMs, also support vector networks) are supervised learning models with associated learning algorithms that analyze data and recognize patterns, used for classification and regression analysis. Given a set of training examples, each marked for belonging to one of two categories, an SVM training algorithm builds a model that assigns new examples into one category or the other, making it a non-probabilistic binary linear classifier. An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. New examples are then mapped into that same space and predicted to belong to a category based on which side of the gap they fall on. In addition to performing linear classification, SVMs can efficiently perform a non-linear classification using what is called the kernel trick, implicitly mapping their inputs into high-dimensional feature spaces.More formally, a support vector machine constructs a hyper plane or set of hyper planes in a high- or infinite-dimensional space, which can be used for classification, regression, or other tasks. Intuitively, a good separation is achieved by the hyper plane that has the largest distance to the nearest training-data point of any class (so-called functional margin), since in general the larger the margin the lower the generalization error of the classifier.Whereas the original problem may be stated in a finite dimensional space, it often happens that the sets to discriminate are not linearly separable in that space. For this reason, it was proposed that the original finite-dimensional space be mapped into a much higher-dimensional space, presumably making the separation easier in that space. To keep the computational load reasonable, the mappings used by SVM schemes are designed to ensure that dot products may be computed easily in terms of the variables in the original space, by defining them in terms of a kernel function k(x,y) selected to suit the problem. The hyper planes in the higher-dimensional space are defined as the set of points whose dot product with a vector in that space is constant. The vectors defining the hyper planes can be chosen to be linear combinations with parameters α_i of images of feature vectors x_i that occur in the data base. With this choice of a hyper plane, the points x in the feature space that are mapped into the hyper plane are defined by the relation:

$$\sum_i \alpha_i k(x_i, x) = constant. \quad (14)$$

Note that if k(x,y) becomes small as y grows further away from x, each term in the sum measures the degree of closeness of the test point x to the corresponding data base point x_i. In this way, the sum of kernels above can be used to measure the relative nearness of each test point to the data points originating in one or the other of the sets to be discriminated. Note the fact that the set of points x mapped into any hyper plane can be quite convoluted as a result, allowing much more complex discrimination between sets which are not convex at all in the original space.

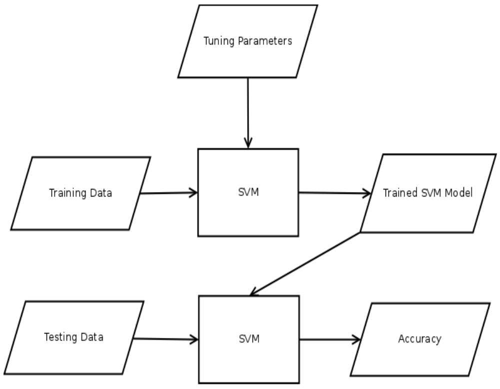


Figure.4: SVM classifier working

V. EXPERIMENTAL RESULTS

To test the accuracy of the modified time domain median filter, a medical image with corruption applied by some means is applied. To estimate the quality of a reconstructed MRI image, first calculate the Root-Mean-Squared Error between the original and the reconstructed image. The Root-Mean-Squared Error (RMSE) for an original image I and reconstructed MRI image R is defined by,

$$RMSE(I,R) = \sqrt{\frac{1}{I_w \times I_h}} \sum_{i=0}^{I_w} \sum_{j=0}^{I_h} \|(i,j) - R(i,j)2 \quad (15)$$

The algorithm for the Modified Time domain Median Filter (MSMF) requires two parameters. The first parameter considered is the size of the mask to use for each filtering operation. The second parameter, threshold ζ, represents the estimated number of original points for any given sample under a mask. A collection of ten MRI images of various sizes was used in these tests. These images are a variety of textures and subject matter. The texture of these MRI images impact on the threshold chosen than the window mask size.

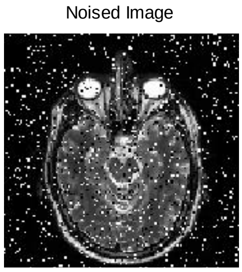
The tests to determine the best mask size were conducted in this manner:

1. Each of the ten MRI images in the collection was artificially distorted with ρ=0.0, ρ=0.05, ρ=0.10, and ρ=0.20 noise composition, resulting in 40 images.
2. Each of the forty medical noisy images was then reconstructed using the SMF with mask sizes of N=3, N=5, and N=7 (the second argument, threshold

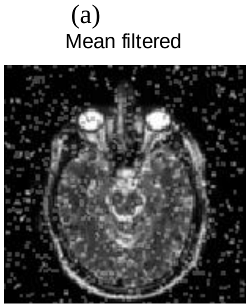
ζ, is set to 1), resulting in 120 reconstructed medical images.

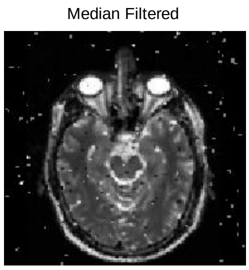
3. The Root-Mean-Squared Error was computed between all 120 reconstructed MRI images and the originals. The RMSE is a simple estimation score of the difference between two MRI images. An ideal RMSE would be zero, which means that the algorithm correctly identified each noisy point and also correctly derived the original data at that location in the signal. For the evaluation of the work a performance evaluation is carried out for various samples and the result obtained were as shown below

For the evaluation of the work a performance evaluation is carried out for various samples and the results obtained were as shown below. As seen in figure 2, a mask size of 3 clearly outperformed the other tested sizes of 5 and 7. Neither the amount of noise, the size of the MRI image, nor the subject matter of the image effects on which mask size performed the best. Less thorough tests were run on higher mask sizes such as 9 and 11. With each increase in mask size, the RMSE of each test increased. Most of the medical images are images of various scenes, such as portrait shots, nature shots, animal shots, scenic shots of snow-capped mountains and sandy beaches. When comparing the Adaptive Masking Filter, the Adaptive Masking Filter, the Masking Filter, and the Mean Filter, a 2000 image subset of the 59,895 images were used.

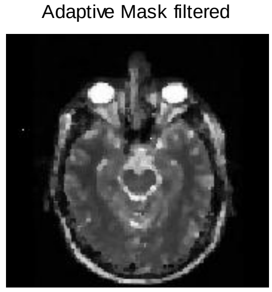


(a) (b)





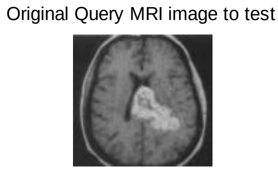
(c) (d)



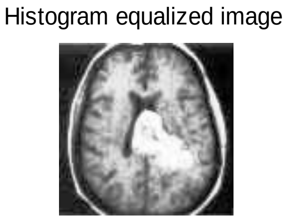
(e)

Fig 5 (a) Original MRI sample for processing (b) noised image sample at variance of 0.1 (c) mean filter output of noise image sample (d) median filter output for the same noised sample (e) obtained filtered output using proposed AMF filtration

Fig 5 illustrates the obtained result observation for given MRI sample, affected by salt pepper noise at a variance of 0.1. The estimation using Adaptive mask filter is observed to be more effective in estimation in comparison to the conventional filtration approaches. Due to the usage of block mask processing, the surrounding pixels were processed with low region noise distribution in comparison to the existing filtration approach.

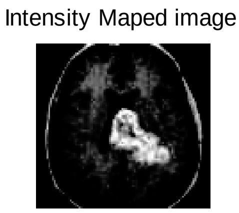


(a)



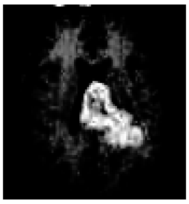
(b)

Figure 6. (a) Original Test sample (b) Histogram equalized image



(a)

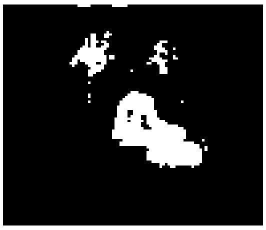
Extracted Region without outer Skull Region



(b)

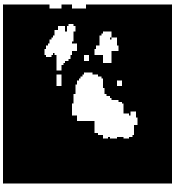
Figure 7. (a) Intensity Mapped Image (b) Boundary region extraction

Thresholded Binarized image



(a)

Morphologically operated Dilated image

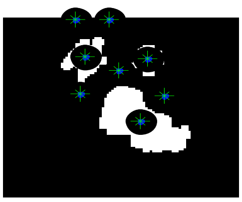


(b)

Figure 8. (a) Threshold binarized image (b) Recurrent morphology image

Region filled Image

(a)



(a) (b)

Figure 9. (a)Region filled image (b) Centroid marked regions

Extracted Region

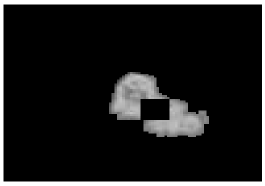


Figure 10. Segmented Mass regions

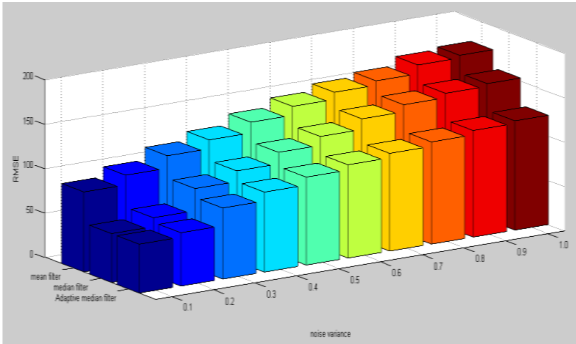


Fig 11 comparative variation of obtained root mean square value over noise variation for the masking length of 3 for the three filters

The Obtained RMSE estimation approach shows that with the increase in noise variance, the obtained root mean square error for the proposed AMF filtration is comparatively lower than the other two conventional approaches. With the increase in the noise variance to the input signal, it is observed that RMSE effectively falls down almost to 1/2 for median filter and double for mean filter.

Table 1: Observation for obtained RMS value over different noise variance for the given sample

Noise variance	**RMSE(mean filter)**	**RMSE(median filter)**	**RMSE(adaptive)**
0.1	90	55	55
0.2	101	65	60
0.3	115	90	80
0.4	125	102	90
0.5	137	115	99
0.6	147	125	105
0.7	155	137	110
0.8	160	145	115
0.9	170	150	120
1.0	173	153	123

N=5.

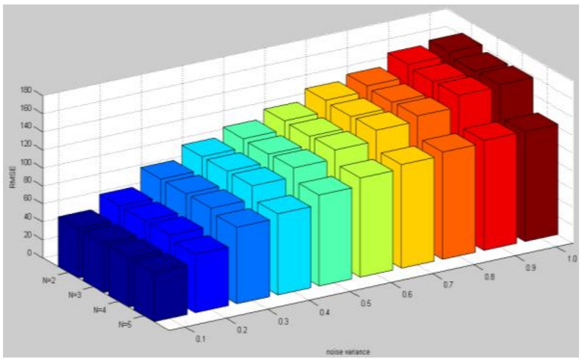


Fig.12 RMS observed for the AMF filter at different block lengths for Noise variance of 0.1 to 1.

The observation made for the RRMSE value at different noise variance with the change in block size (N) is presented in figure 12. The RMSE value for the test MRI sample is observed comparatively very low at N=5 , for high noise variance in the image.

Table 2 Observation of RMS for different noise variance

Noise variance	**RMSE(N=2)**	**RMSE(N=3)**	**RMSE(N=4)**	**RMSE(N=5)**
0.1	55	55	55	55
0.2	70	70	70	65
0.3	90	90	90	85
0.4	105	105	105	90
0.5	115	114	115	101
0.6	125	124	125	110
0.7	138	136	137	115
0.8	144	142	143	119
0.9	158	155	156	122
1.0	162	157	158	122

To evaluate the performance of the developed approach following parameters are used.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (13)$$

Where,

TP = True positive (Correctly identified)
FP = False positive (Incorrectly identified)
TN = True negative (false, Correctly identified)
FN = False negative (false, incorrectly identified)

For the given simulation model, four classes with each class having 5 subjects, forming total of 20 subjects is used for training. During testing process, a query sample is given and the extracted features are passed to SVM classifier.

Along with accuracy, to show the enhancement of propose approach and also to compare the proposed approach with earlier approaches, few more metrics such as sensitivity, specificity, Recall, precision and F-measure was evaluated with following mathematic expressions.

Sensitivity measures the proportion of positives that are correctly identified as such.

$$Sensitivity = \frac{TP}{TP+FN} \quad (14)$$

Specificity measures the proportion of negatives that are correctly identified as such.

$$Specificity = \frac{TN}{TN+FP} \quad (15)$$

Precision is the fraction of identified instances that are correct, while recall is the fraction of correct instances that are identified.

$$Recall = \frac{TP}{TP+FN} \quad (16)$$

$$Precision = \frac{TP}{TP+FP} \quad (17)$$

F-measure or balanced F-score is a measure that combines precision and recall is the harmonic mean of precision and recall.

$$F\_measure = \frac{2*Recall\ .Precision}{Recall\ +Precision} \quad (18)$$

Table 3. Parametric evaluation of the developed system for processing efficiency.

Test sample	DR-method	Accuracy (%)	Sensitivity	Specificity	Recall	Precision	F-Measure	CT
	Mean	55.670	0.220	0.608	0.220	0.680	0.478	0.545
	Median	62.500	0.315	0.752	0.315	0.740	0.523	0.348
Class 1	**Adaptive**	**70.000**	**0.444**	**0.909**	**0.444**	**0.800**	**0.571**	**0.138**
	Mean	49.484	0.432	0.712	0.432	0.508	0.542	0.273
	Median	58.1341	0.458	0.854	0.458	0.666	0. 621	0.143
Class 2	**Adaptive**	**69.500**	**0.524**	**0.946**	**0.524**	**0.820**	**0.652**	**0.137**
	Mean	55.670	0.420	0.762	0.420	0.650	0.569	0.310
	Median	63.824	0.452	0.886	0.452	0.720	0.688	0.139
Class 3	**Adaptive**	**70.840**	**0.484**	**0.924**	**0.484**	**0.795**	**0.690**	**0.132**
	Mean	58.360	0.446	0.738	0.446	0.650	0.583	0.374
	Median	65.420	0.558	0.824	0.558	0.745	0.600	0.183
Class 4	**Adaptive**	**72.820**	**0.582**	**0.908**	**0.582**	**0.810**	**0.680**	**0.132**

The obtained retrieval observations for different test action in the Weizmann dataset were observed through the feature count and the overhead.

VI. CONCLUSION

In this paper two new filters for removing impulse noise from images and shown how they compare to other well-known techniques for noise removal. First, common noise filtering algorithms were discussed. Next, a Spatial Median Filter was proposed based on a combination of work on the Median Filter and the Spatial Median quantile order statistic. Seeing that the order statistic could be utilized in order to make a judgment as to whether a point in the signal is considered noise or not, a Modified Spatial Median Statistic is proposed. The Modified Spatial Median Filter requires two parameters: A window size and a threshold T of the estimated non-noisy pixels under a mask. In the results, the best threshold T to use in the Modified Spatial Median Filter and determined that the best threshold is 4 when using a 3×3 window m ask size. Using these as parameters, this filter was included in a comparison of the Mean, Median, and Spatial Median Noise Filters. In the broad comparison of noise removal filters, it was concluded that for images containing p = 0.15 noise composition, the Modified Spatial Median Filter performed the best and that the Component Median Filter performed the best over all noise models tested.

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