Statistical characterization of ischemic stroke lesions from MRI using discrete wavelet transformation

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ABSTRACT

The segmentation and characterization of lesion structures from brain Magnetic Resonance Imaging (MRI) slices serves to recognize the degree of the influenced tissues for effective diagnosis and planning in the treatment of ischemic stroke. The different portions of the affected tissues might exhibit different properties in the different imaging modalities. Hence, developing a fully-automatic approach for segmentation of these abnormal structures is considered to be a challenging research issue in medical image processing. This research applies the discrete wavelet transformation of different types for characterizing the properties of the lesion structures from MRI images. The wavelet co-efficients were determined for different levels and the statistical parameters were extracted from it for characterizing the texture properties of the brain tissues. The experimental results were presented for both normal and abnormal MRI datasets. Observations indicate that there was a clear demarcation between the range of values in the statistical features obtained for normal and abnormal images.

Keywords: MRI, Ischemic stroke, Lesion, Wavelet, Feature, Characterization.

1. INTRODUCTION

Ischemic stroke is rising as one of the significant causes behind death in both adults and elderly individuals. In the past few years, a new trend has been observed in both developed and developing countries i.e. a transition from diseases influenced by poverty to life style based diseases. In specific, these diseases are more prevalent among the young adults than the elderly population. This result in various complications like depression, stress, seizures and sometimes results in stroke too. Globally, twenty million people experience the effects of stroke every year [1]. The developed countries alone represent 85% of fatal cases due to stroke [2].

Ischemic stroke occurs when a blood vessel is obstructed due to a block. Typically this block is created because of fat deposition inside the blood vessel [3]. Early recognition of this condition could expand the survival rate of the patient. Diagnosis of this disease commonly utilizes scanning procedures like either CT (Computed tomography) or Magnetic Resonance Imaging (MRI). Out of these two modalities, MRI is considered as a suitable technique for visualizing brain tissue structures due to its high differentiation to delicate tissues [4-5].

Several approaches were presented in the past two decades for detecting the stroke lesions using manual and semi-automated segmentation based approaches. Kabir et al. presented a Markov Random Field (MRF) based approach to segment the lesion structures [6]. It was applied to multimodal MRI images for segmenting the lesion structures. But one major consideration with MRF models was that they were computationally complex and thus demands more computations. Ozertem et al. presented an approach for lesion segmentation. It used active contour models to automatically segment the region of interest. Stein et al. presented a deformable snake based approach for delineating the lesion structures. The method assumed that a lesion was a single connected component. This would fail, if there were many disconnected lesions. Also, these snake based methods require user input for initializing the snakes [7].

Once the region of interest was successfully segmented, the next step is to characterize it in order to model its properties. In the last few decades, the texture parameters extracted from the images were utilized for image description and interpretation. The Gray Level Co-Occurrence Matrix (GLCM) is generally used to describe the statistical properties of the texture content of an image in the spatial domain. Hema Rajini et al. developed one such scheme using GLCM for detection of ischemic stroke [8]. The method basically divided the brain CT image into two equal halves and then texture features were determined on each half to detect the lesion area. Gupta et al. proposed a similar kind of approach for MRI images [9]. Oliveira et al. developed a texture analysis scheme to quantify the severity of the lesion regions using GLCM features [10]. As the brain tissues are very complex in nature, these images could be studied well in the frequency domain than the spa-

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tial domain. If these images were decomposed into different scales of frequency and analysed, then the features might be captured as signals of higher variation in their strength [11].

Wavelet transform is one of the widely used frequency domain techniques for feature extraction in MRI images [12-15]. It basically decomposes a signal into different frequency bands based on a dyadic scheme. This kind of partitioning the frequency bands matches the statistical properties of the medical images in an effective way. Ajikumar et al. presented an approach for predicting the early occurrence of brain tumor using wavelet based features [16]. Farias et al. developed an approach for diagnosis of brain tumor using wavelet features and support vector machines [17]. Sajjadi et al. presented a wavelet based filter bank algorithm for early detection of ischemic stroke from brain CT images [18]. All these works presents the efficiency of wavelet transform in medical image analysis. Hence, this research aims at exploring the power of wavelets for characterizing the properties of the normal and abnormal brain tissues from MRI images.

2. METHODOLOGY

At first, the skull-stripping was employed as a preprocessing step to expel the skull portions from the input MRI images. Then, it is subjected to fuzzy based segmentation procedure to identify and extract the lesion portion from the image. From the extracted region of interest, different types of wavelet functions were applied and statistical features were extracted. These features are examined for both normal and abnormal classes. The basic workflow of the proposed approach was presented in Fig.1.

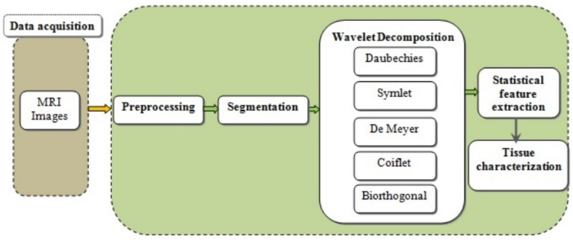
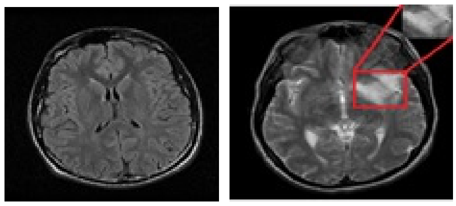


Fig.1: *Architecture of the proposed approach.*

2.1 Data acquisition

The MRI datasets were collected from multiple online and offline sources [19]. The format of the input MRI Slices was in Neuroimaging Informatics Technology Initiative (NIfTI) and Digital Imaging and Communication in Medicine (DICOM). A sample normal and abnormal MRI slice is presented in Fig. 2 (a) and (b) respectively. The lesion part due to ischemic stroke was highlighted in Fig. 2 (b).

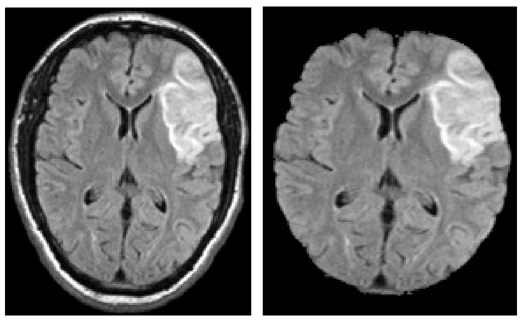


(a) (b)

Fig.2: *(a) Normal MRI slice (b) MRI slice with ischemic stroke lesion.*

2.2 Pre-processing

Pre-processing is generally employed to enhance certain image features or eliminate unwanted details in the input image which are important for further processing. Global thresholding based skull stripping is employed as a pre-processing technique in this work. The skull portion is the largest connected region in the brain image with higher bone density. This information is used as a cue for eliminating the skull portions from the input image. Initially the input image is converted to binary based on the threshold obtained with respect to skull region using global thresholding. i.e. a mask is formed by setting the pixels from the skull region to '0' and the remaining pixels as '1'. This mask is convolved with the input image to remove the skull portion. The corresponding results were presented in Fig. 3.



(a) (b)

Fig.3: *(a) Input MRI slice (b) Skull stripped image after pre-processing.*

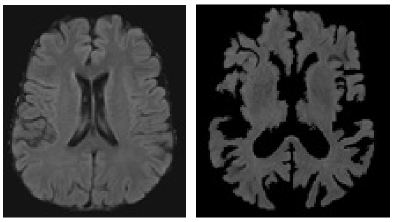
2.3 Segmentation

The fuzzy c-means method was one of the widely utilized approaches for image segmentation. In this method, the cluster groups were formed by repeatedly minimizing a cost function. It basically assigns the pixels of the source image, to the clusters with respect to their fuzzy membership values. The cost function is dependent on the distance of how close it is located to the center of the cluster. This cost function 'J' can be mathematically represented as:

$$J = \Sigma_{j=1}^{N} \Sigma_{i=1}^{C} U_{ij}^{m} \left|\left|x_j - v_i\right|\right|^2 \quad (1)$$

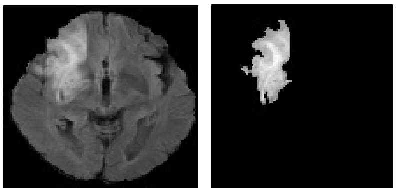
where, 'U_{ij}^{m}' represents the pixel membership x_j to i^{th} cluster $\forall x_j \in K$. Here 'K' indicates the set of points that the actual image is composed. The constants 'N' and 'C' were the no. of the clusters and actual data points in 'K'. The variable 'v_i' represents the centroid of the ith cluster.

This method of segmentation was applied to both normal and abnormal MRI slices and the resultant observations were highlighted in Fig. 4 and 5.



(a) (b)

Fig.4: *(a) Input MRI slice (b) Segmented output.*



(a) (b)

Fig.5: *(a) Input MRI slice (b) Segmented lesion.*

2.4 Wavelet Based Decomposition

The Wavelet transform provides a way for transforming the images into their fundamental constituents across multiple scales. It localizes the energy of the input signal in a joint space-scale domain. In this work, the five different wavelet functions are applied to the input MRI images for characterizing the properties of the lesion structures. The discrete wavelet transform of an image f(x,y) of size [M,N] is given in equation 2 and 3.

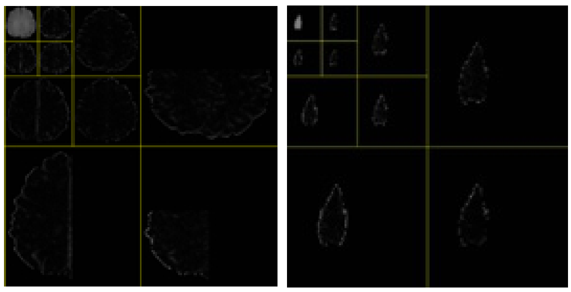
$$\mathrm{W}_{\varphi}\left(\mathrm{j}_0, \mathrm{m}, \mathrm{n}\right) = \frac{1}{\sqrt{\mathrm{MN}}} \Sigma_{\mathrm{x}=0}^{\mathrm{M}-1} \Sigma_{\mathrm{y}=0}^{\mathrm{N}-1} \mathrm{f}\left(\mathrm{x}, \mathrm{y}\right) \varphi_{\mathrm{j}_0, \mathrm{m}, \mathrm{n}}\left(\mathrm{x}, \mathrm{y}\right) \quad (2)$$

$$\mathrm{W}_{\gamma}^{\mathrm{i}}\left(\mathrm{j}, \mathrm{m}, \mathrm{n}\right) = \frac{1}{\sqrt{\mathrm{MN}}} \Sigma_{\mathrm{x}=0}^{\mathrm{M}-1} \Sigma_{\mathrm{y}=0}^{\mathrm{N}-1} \mathrm{f}\left(\mathrm{x}, \mathrm{y}\right) \gamma_{\mathrm{j.m,n}}^{\mathrm{i}}\left(\mathrm{x}, \mathrm{y}\right), \quad \mathrm{i} = \{\mathrm{H}, \mathrm{V}, \mathrm{D}\} \quad (3)$$

where 'j_0' is the starting scale, '$W_{\varphi}(j_0, m, n)$' coefficients defines an approximation of f(x,y) at scale 'j_0', $W_{\gamma}^{i}(j, m, n)$ coefficients add horizontal 'H', vertical 'V' and diagonal 'D' details for scales $j \geq j_0$.

The wavelet transform correlates the image being analysed with the model wavelet function. Hence the choice of the model wavelet function influences the performance of the wavelet decomposition process. Also, the choice of the model wavelet function is highly critical, as it directly influences the description of texture contents in an image. Hence in this research, five different wavelet functions namely Daubechies, symlet, de-Meyer, coiflet and biorthogonal were applied to the input images. The capability of each wavelet function for discriminating the normal brain tissues from abnormal lesions was studied as part of this research.

The level of decomposition was varied from '2' to '5' and the results were analysed. It was inferred that increasing the level of decomposition beyond '3' did not result in producing significant results. Hence the level of decomposition was maintained to be '3' for all the wavelet functions. The wavelet decomposition for Daubechies wavelet function was presented in Fig.6. From these images, It could be observed that the approximation co-efficients were able to describe the lesion tissues. Hence statistical measures namely mean, median, standard deviation, kurtosis and skewness were computed from approximation coefficients of three levels.



(a) (b)

Fig.6: *Daubechies wavelet based decomposition (a) For Normal MRI slice (b) For Segmented lesion.*

2.5 Feature extraction

Statistical features namely mean, median, standard deviation, kurtosis and skewness were computed from the segmented region for evaluating the texture properties of it. The relations for all these parameters were presented in Eq. 4 to 7.

$$Mean\ \mu = \sum_{i=0}^{G-1} i * p\left(i\right) \quad (4)$$

$$Standarddeviation \sigma = \sqrt{\sum_{i=0}^{G-1} \left(i - \mu\right)^2 * p\left(i\right)} \quad (5)$$

$$Kurtosis = \frac{\sum_{i=0}^{G-1} \left(i - \mu\right)^3 * p\left(i\right)}{\sigma^3} \quad (6)$$

$$Skewness = \frac{\frac{1}{N}\sum_{i=0}^{G-1}(i-\mu)^4 * p(i)}{\sigma^4} \quad (7)$$

Where 'G' refers to the total number of grey levels, $p(i)$ is the first order histogram of the images which is given as: $p(i) = (N(i))/m, N(i)$ is the number of pixels having intensity 'r_i' and 'm' is the total number of pixels in the image.

2.6 Tissue Characterization

The proposed approach is applied to all datasets and the observations were presented in table 1. It could be inferred that there was a clear demarcation between the range of values in the statistical features obtained for normal and abnormal images. While the mean, median and kurtosis parameters were higher for the normal brain tissues, the standard deviation and skewness parameters are higher for the abnormal lesions. Hence, this information could be taken into account for differentiating the brain tissues.

3. RESULTS AND DISCUSSION

The dataset employed in this work, consists of 40 different sets of MRI slices, out of which 22 sets were abnormal. These experiments are carried out on Intel core i5 processor and 4 GB RAM. Five different wavelets namely daubechies, symlet, de-meyer, coiflet and biorthogonal were applied to the input images. Statistical measures namely mean, median, standard deviation, kurtosis and skewness were computed for each wavelet function across different scales. The collective interpretation obtained based on the feature statistics for different wavelet functions were presented in Fig. 7 to 10.

3.1 Comparison based on the type of wavelet function.

Out of the five different wavelet functions, the daubechies and de-meyer wavelet functions exhibited higher differentiation in discriminating the normal brain tissues from the abnormal lesion patterns. With respect to the daubechies wavelet function, the mean, median, standard deviation and skewness of the wavelet coefficients were comparatively higher for the lesion structures than the normal brain tissues. Interestingly, for de-meyer wavelet function, the mean, median and standard deviation parameters were higher for the normal brain tissues than the lesion structures.

3.2 Comparison based on the type of feature extracted

Five different statistical measures namely mean, median, standard deviation, kurtosis and skewness were computed for each wavelet function across different scales. On observing the feature statistics across multiple levels, it could be inferred that the mean, median and kurtosis parameters were higher for the normal brain tissues than the lesion structures. Interestingly, the standard deviation and skewness parameters were lower for the normal brain tissues than the lesion structures.

4. CONCLUSION

The segmentation of lesion regions from MRI images is one of the crucial and time consuming step in the automation of medical imaging diagnosis systems. The extent of the tissue damage due to the blood clot should be clearly analyzed and characterized for effective diagnosis and treatment. Hence this research presents a comprehensive analysis on normal and abnormal brain tissues with different types of wavelet functions to understand the nature of its statistical properties. Five different wavelet functions namely daubechies, symlet, de-meyer, coiflet and biorthogonal wavelets were applied to the segmented structures and the significant statistical measures were extracted from it. It could be inferred that there was a clear demarcation between the range of values in the statistical features obtained for normal and abnormal images. Out of the five wavelet functions, the Daubechies and de-Meyer functions exhibited maximum distinction between the normal and abnormal brain tissues. In future, this research could be further extended by categorizing the severity of stroke into different levels.

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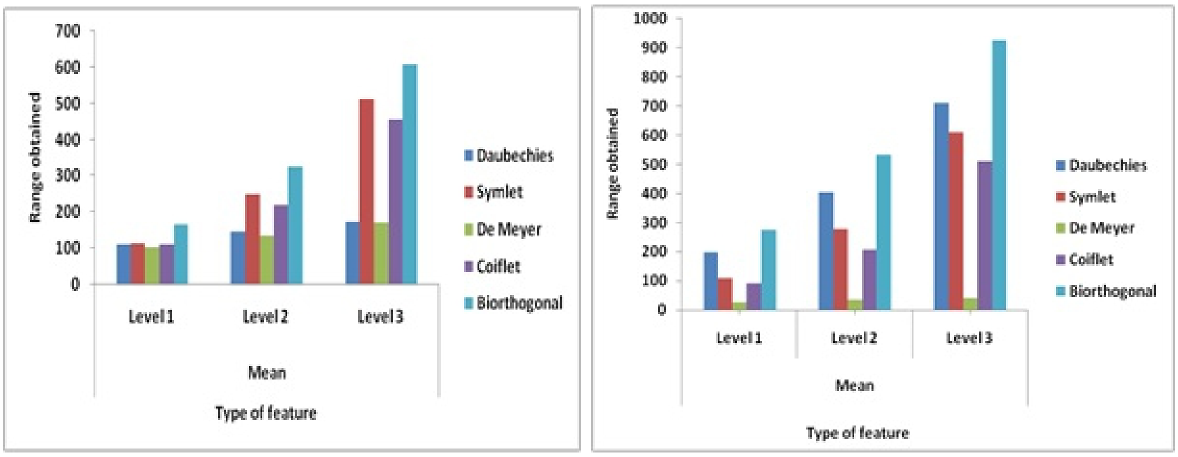
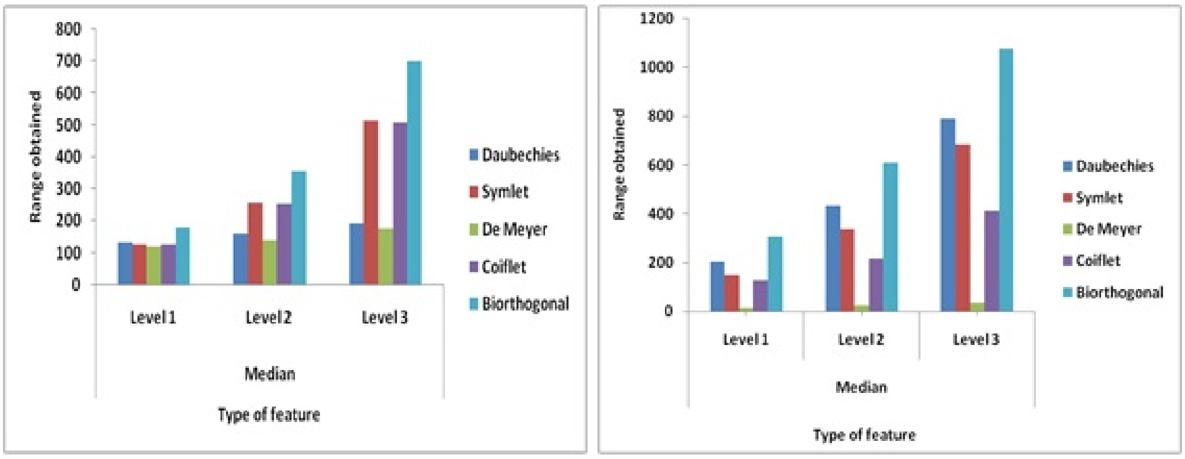


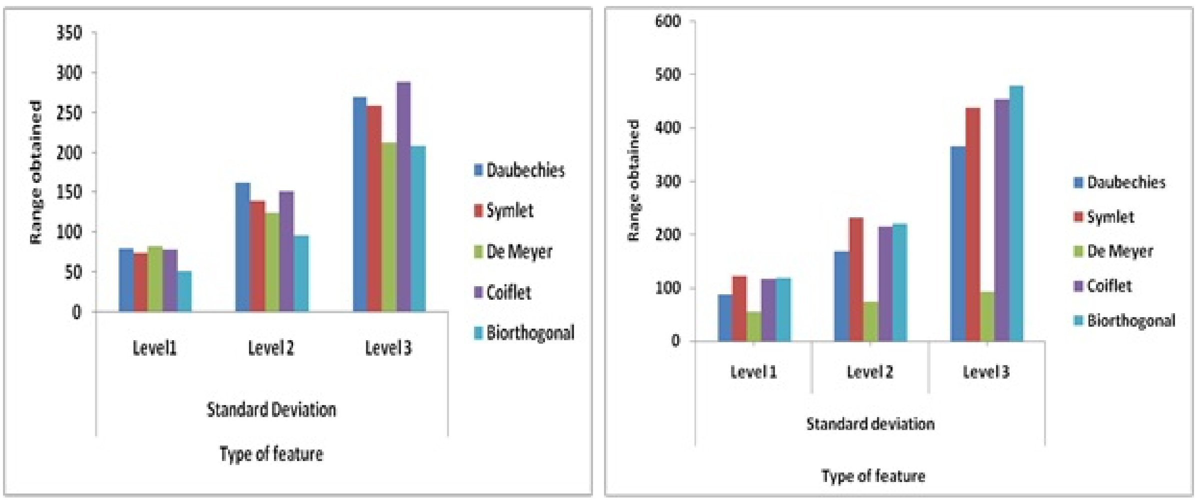
(a) (b)

Fig. 7: *Performance comparison for different wavelets based on mean (a) normal datasets (b) abnormal datasets.*



(a) (b)

Fig. 8: *Performance comparison for different wavelets based on median (a) normal datasets (b) abnormal datasets.*



(a) (b)

Fig. 9: *Performance comparison for different wavelets based on standard deviation (a) normal datasets (b) abnormal datasets.*

Table 1: *Cumulative summary for all the wavelet based methods*

Type		Mean			Median		
		Level 1	**Level 2**	**Level 3**	**Level 1**	**Level 2**	**Level 3**
Normal	Daubechies	110.023	147.407	172.366	132	162.5	190.75
	Symlet	114.412	248.86	511.722	128.064	258.018	515.721
	De Meyer	103.991	135.558	169.85	120.455	140.954	178.09
	Coiflet	112.593	221.115	456.5	126.166	252.957	508.629
	Biorthogonal	165.865	325.175	607.316	179.2	356.8	699.375
Abnormal	Daubechies	198.521	403.442	711.817	202.8	433.5	790.85
	Symlet	109.487	277.443	610.29	148.525	336.712	683.316
	De Meyer	26.441	33.884	40.51	14.787	25.03	33.65
	Coiflet	91.013	205.269	509.961	127.737	215.286	412.612
	Biorthogonal	276.432	532.099	924.824	307.3	607.6	1074.55

Table 2: *Cumulative summary for all the wavelet based methods*

Type		Standard Deviation			Kurtosis		
		Level 1	**Level 2**	**Level 3**	**Level 1**	**Level 2**	**Level 3**
Normal	Daubechies	80.21	162.71	270.04	7.9	6.75	5.39
	Symlet	74.56	139.64	259.56	2.69	3.41	4.13
	De Meyer	83.27	124.57	213.07	1.64	1.31	2.62
	Coiflet	78.66	151.45	289.45	2.05	2.18	2.76
	Biorthogonal	51.801	96.11	208.6	7.538	5.914	3.793
Abnormal	Daubechies	88.27	168.26	365.38	3.64	3.08	1.85
	Symlet	122.88	232.79	439.09	1.51	1.37	1.61
	De Meyer	55.67	74.07	92.31	14.62	33.62	91.46
	Coiflet	117.01	214.94	454.07	2.11	1.59	1.49
	Biorthogonal	118.04	220.35	479.72	4.623	2.454	1.566

Table 3: *Cumulative summary for all the wavelet based methods*

Type		Skewness		
		Level 1	**Level 2**	**Level 3**
Normal	Daubechies	-2.04	-1.87	-1.7
	Symlet	-1.12	-1.33	-1.5
	De Meyer	-0.59	0.33	1.16
	Coiflet	-0.85	-0.91	-1.12
	Biorthogonal	-2.301	-1.918	-1.401
Abnormal	Daubechies	-1.27	-0.99	-0.44
	Symlet	0.35	0.09	-0.2
	De Meyer	3.54	5.49	8.82
	Coiflet	0.8	0.54	0.1
	Biorthogonal	-1.817	-0.938	-0.142

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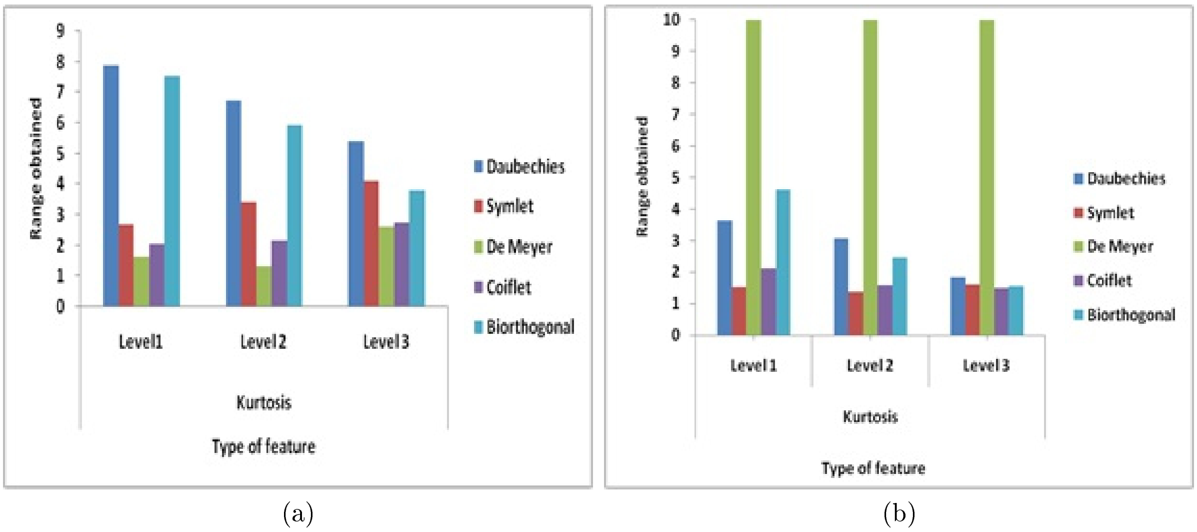

Fig.10: *Performance comparison for different wavelets based on kurtosis (a) normal datasets (b) abnormal datasets.*

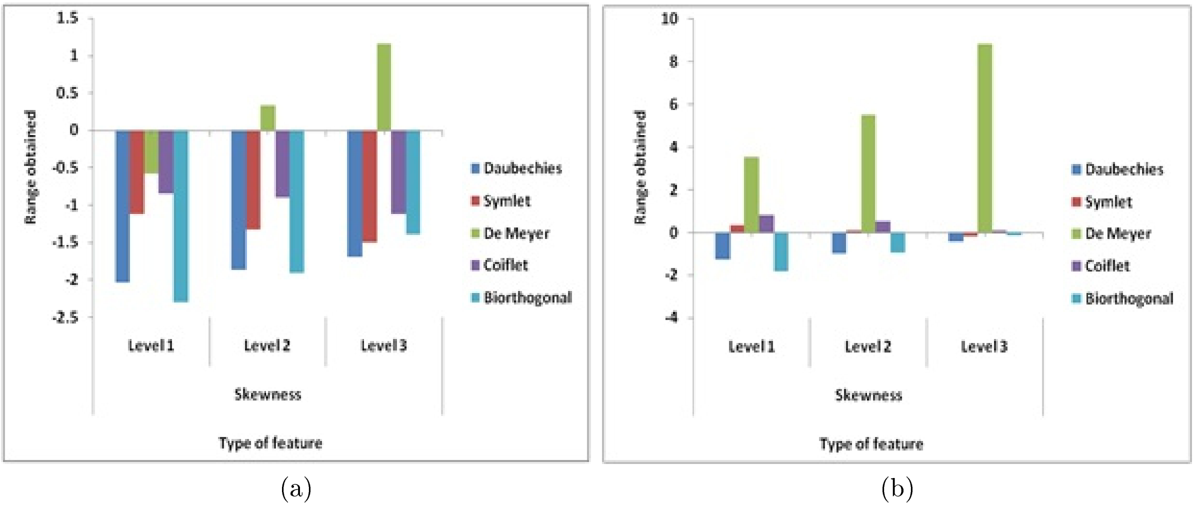

Fig.11: *Performance comparison for different wavelets based on Skewness (a) normal datasets (b) abnormal datasets.*

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