Breast tissue characterization based on fractional differencing model of ultrasonic RF echo

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ABSTRACT

A number of researchers have previously shown that the ultrasound RF echo of tissue exhibits $(1/f)^{-\beta}$ characteristics and developed tissue characterization methods based on the fractal parameter β. In this paper we propose Fractional Differencing Autoregressive Moving Average (FARMA) process for modeling RF ultrasound echo and develop breast tissue characterization method based on the FARMA model parameters. This model has been used to capture statistical self-similarity and long-range correlations in image textures, in wide ranging engineering and science applications, including communication network traffic. Here, we present estimation techniques to extract the model parameters, namely features, for classification purposes and tissue characterization.We show the performance of our tissue characterization procedure on several *in vivo* ultrasound breast images including benign and malignant tumors. The area of the receiver operator characteristics (ROC) based on 60 *in vivo* images yields a value of 0.79, which indicates that proposed tissue characterization method is comparable in performance with other successful methods reported in the literature.

Keywords: Fractional differencing, ultrasound, classification, RF echo, autoregressive, moving-average, tissue characterization

1. INTRODUCTION

1.1. Motivations

Breast cancer is currently the leading cause of mortality among women. While X-ray is the primary imaging modality for breast cancer detection, limitations in X-ray mammography have motivated research in other imaging modalities, such as ultrasound, positron emission tomography (PET), and magnetic resonance imaging (MRI). Ultrasound provides several advantages for breast cancer detection and screening as compared to other imaging modalities:

- Ultrasound is safe. It uses low power pulses with very short exposition time. X-ray mammography and PET uses radiation whose adverse effects are cumulative.
- Ultrasound is relatively inexpensive as compared to other imaging modalities. It can be used to complement other noninvasive screening techniques to improve specificity.
- Ultrasound provides texture information based on speckle that is not available from other imaging modalities.
- Modern ultrasound devices are digital and can use computer-aided detection systems very easily.
- Ultrasound works for dense breast unlike X-ray mammography.
- Ultrasound examination is painless compared to X-ray mammography which uses compression.

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Ultrasound imaging is based on acoustic impedance, which is a product of the density of the observed tissue and the ultrasound velocity along the tissue. X-ray mammography imaging on the other hand, is based on accumulated density of the tissue. As a result, mammography looks for microcalcifications while ultrasound looks for shape and texture. Ultrasound speckle often times masks microcalcifications. Nevertheless, it provides relevant information through speckle. Speckle is formed by scattered signals coming from reflectors smaller than the ultrasound wave length. This scattering gives rise to the resulting texture that constitutes important diagnostic information. In this paper, we modeled the RF tissue echo using fractional differencing autoregressive moving average model (FARMA). This is a long-term correlated time series model with $1/f$ behavior that has been extensively utilized to model and classify image textures.[1,2] It has been observed by several researchers that RF echo exhibits $1/f$ characteristics. This observation is consistent with the behavior of image textures.

1.2. Related Work

In most ultrasonic tissue characterization techniques reported in the literature, the ultrasonic data is parameterized via a statistical model and model parameters are utilized for cancer differentiation. Gaussianity assumption and second order statistics[3–7] were used to model RF echo and characterize the behavior of tissue. Wagner[3] and Tuthill[5] proposed Rician distribution to model envelope statistics of ultrasound RF echo. Cohen[6,7] proposed WOLD decomposition of the RF echo to estimate mean scatterer spacing in tissue. Shankar[8,9] proposed K distribution for ultrasound RF echo by observing the deviations from Rayleigh statistics, extracted parameters from this model and utilized these parameters to classify benign, malignant and normal tissue regions in breast. In addition to K distribution, Shankar[10] proposed generalized K distribution, and Dutt[11] proposed homodyned K distribution models for ultrasound RF echo since these distributions covers formerly proposed distributions like Rayleigh and Rician distributions. Instead of using second order statistics, Abeyratne and Petropulu used higher order statistics[12,13] for feature extraction from RF echo. Kutay and Petropulu modeled RF echo based on power law shot noise phenomena.[14,15] Recently Shankar[16,17]and Clifford[18] proposed Nakagami distribution and investigated discrimination of the model parameters for benign and malignant tumors.

1.3. Proposed Method

In this paper we propose to model ultrasound RF echo as a Fractional Differencing Auto-regressive Moving-average (FARMA) process to capture the speckle texture. It has been observed empirically by a number of researchers that RF echo exhibits $1/f$ characteristics.[14,15,19] This is consistent with the $1/f$ behavior of image textures in computer vision.[1,2] Transducer response is modeled as an ARMA (p,q)[20,21] process, where p and q are orders for AR (Auto-regressive) and MA (Moving-average) models respectively, and tissue response is modeled as a fractional differencing process (FDM),[22] leading to a FARMA process for RF echo.

Transducer response, i.e., ARMA parameters, are estimated from water phantom based on the final prediction error (FDE) and residual time series methods. Next, the transducer response is deconvolved from the RF echo and the FD parameter d is estimated from the resulting signal based on a log periodogram technique. The estimation method provides an unbiased, consistent and asymptotically Gaussian estimate of the parameter d. A mean and variance of the parameter d from inside and outside the suspected tumor were estimated using multiple adjacent scanlines. Classification is based on a significance testing algorithm, namely the t-test. Finally, we formed the receiver operator characteristics (ROC) for the proposed method using 60 *in vivo* ultrasound breast images that contain both benign and malignant tumors. The calculated ROC, which has an area of 0.79, shows that the proposed method can be used to differentiate the benign and malignant breast tumors.

1.4. Organization of the Paper

The paper is organized as follows. In Section II, we present the FARMA model of the ultrasound RF echo. In Section III, we present the parameter estimation methods for the FARMA model and experimental results on several ultrasound B-Scan images with benign and malignant tumors. In Section IV, we discuss the hypothesis testing method based on the t-test and demonstrate the performance of the proposed model. Finally, some concluding remarks and future directions are provided in Section V.

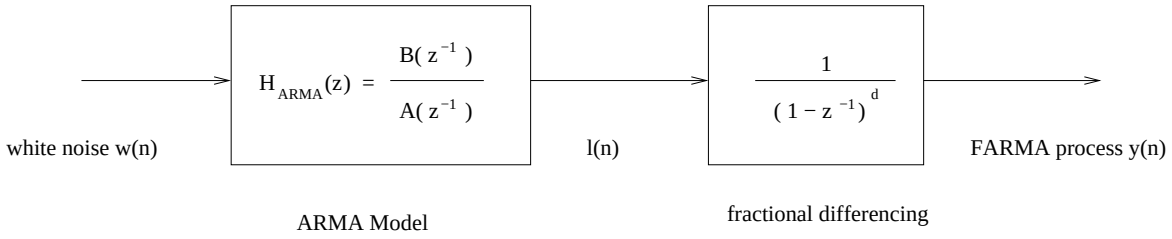


Figure 1. Model of a fractionally differenced ARMA process.

2. FARMA MODEL FOR RF ECHO

In ultrasonic applications, the RF echo scattered from tissue is modeled as a convolution integral of the ultrasonic pulse and the scattering structure as follows :

$$y(n) = h(n) * x(n) \tag{1}$$

where $h(n)$ is the impulse response of the transducer and $x(n)$ is the response from tissue.

It was empirically observed by Onaral et.al.in[19] that the tissue response exhibits $1/f$ characteristics due to the complex structure of tissue scatterers. From the point of view of texture modeling, similar observations were also made for natural terrain and texture in remote sensing imagery.[23, 24] In the later case, self-similar and long-term correlated time series models were successfully used to model and classify image texture. In this paper, we propose to model ultrasonic tissue response as a fractional differencing process.[22] FD model has a number of advantages as compared to other $1/f$ models.[25, 26] FD is a discrete, stationary process with self-similar and long-term correlated structure. It is governed by a long-term correlation parameter d, $0 < d < 0.5$. This parameter was shown to discriminate natural textures successfully in.[1, 2] Recently, FD model was used to capture the self-similar nature of the network traffic.[27]

This process can be compactly represented as follows :

$$x(n) = (1 - z^{-1})^{-d} w(n) \tag{2}$$

Fractional differencing model can be viewed as an infinite order MA process, where MA model parameter is a known function of the self-similarity parameter d, given by :

$$x(n) = \sum_{k=0}^{\infty} f_k(d) w(n-k) \tag{3}$$

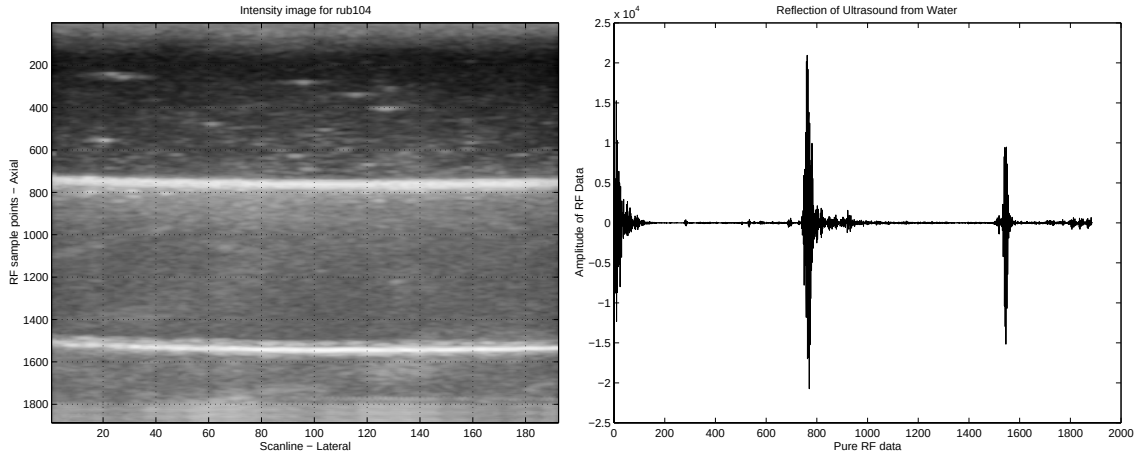
where $w(n)$ is a white Gaussian noise sequence with zero mean and variance and $f_k(d)$ is given by:

$$f_k(d) = \frac{d(1+d)(2+d).....(k-1+d)}{k!} \tag{4}$$

We model the transducer response as an ARMA(p,q) model, which leads to the FARMA modeling of the ultrasonic RF echo. FARMA process can be represented as in Equation (5):

$$A(z^{-1})x(n) = B(z^{-1})(1 - z^{-1})^{-d} w(n)\sqrt{\rho} \tag{5}$$

where $w(n)$ is a white Gaussian noise sequence with zero mean and variance ρ, z^{-1} is back-shift operator, $A(z^{-1})$, and $B(z^{-1})$ are the autoregressive and moving-average polynomials of orders p and q, respectively. A block diagram representation of the FARMA process is given in Figure 1.



(a) (b)

Figure 2. Transducer impulse response: a) B-scan image of ultrasonic RF echo reflected from flat-surface reflector in water. 30 consecutive scanlines of data with length of 1x256 were used to estimate ARMA model orders and model parameters. b) A-scan data sequence of reflection of the ultrasound from flat-surface reflector in water. As a sequence of data portion, indices between 700 and 955 were taken for estimation procedure.

The transfer function of the complete system described in Figure 1 is given by:

$$H(z^{-1}) = \frac{1}{(1-z^{-1})^d} H_{ARMA}(z^{-1}) \tag{6}$$

where $H_{ARMA} = \frac{B(z^{-1})}{A(z^{-1})}$ is the ARMA part of the system that represents the transducer response and $\frac{1}{(1-z^{-1})^d}$ is the FDM part of the system that models the tissue response.

To perform tissue classification, first we have to estimate the order of the ARMA model and the ARMA model parameters from the transducer response and use these estimates to obtain an estimate of the fractional differencing parameter d from the RF echo. We will then use the FD parameters as the characteristic feature vector to discriminate between the malignant and benign tumor regions. In the next two sections, we will address these estimation and classification problems.

3. ESTIMATION OF FARMA MODEL PARAMETERS FOR TISSUE CHARACTERIZATION

3.1. Estimation of ARMA Parameters for Transducer Response

We perform the estimation of FARMA model parameters in two steps: First, ARMA parameters of the transducer response is estimated, and next, the FD parameter of the tissue response is estimated. For the estimation of ARMA parameters we used transducer impulse response data, which was obtained by using pulse-echo measurements from a flat surface reflector in water. B-scan and A-scan measurements of the transducer impulse response are presented in Figure 2 (a) and (b), respectively.

We utilized Final Prediction Error (FPE) criterion in our study to estimate the order of the ARMA type transducer response. Akaikes Final Prediction Error[28] (FPE) is a common statistical measure for the goodness-of-fit of the data to the ARMA(p,q) model. FPE is a function of residuals given by:

$$FPE = \frac{1+n/N}{1-n/N} V \tag{7}$$

where V is the variance of model residuals, N is the length of the time series, and $n = p + q$ is the number of estimated parameters in the ARMA model.

We computed the FPE for various candidate models, and the model with the lowest FPE was selected as the best-fit model. We determined out that best model order is an ARMA (3,1) for our transducer. We utilized this information to estimate ARMA (3,1) parameters using the residual time series model.[29–31]

3.2. Estimation of Fractional Differencing Model Parameter d

After modeling transducer response as an ARMA (p,q) process, fractional differencing model parameter d of the tissue response is estimated from the FARMA process. The FD process is given as:

$$x(n) = (1 - z^{-1})^{-d} w(n)\sqrt{\rho} \tag{8}$$

where d is differencing model parameter and $w(n)$ is white Gaussian noise with zero mean and variance ρ.

The estimation procedure is based on the log-periodogram method[32] that uses linear least square procedure. Using equation (8), the periodogram of $x(n)$ can be rewritten as:

$$f_x(k/N) = |2sin(\pi k/N)|^{-2d} \rho f_w(k/N) \tag{9}$$

Thus,

$$log|X(k)|^2/N = log f_x(k/N) = -2d log|2sin(\pi k/N)| + log\rho + log|f_w(k/N)| \tag{10}$$

where $X(k)$ is the N point DFT of $x(n)$.

The linear least-squares estimator of d and ρ can be obtained by the following standard formula:

$$[d, \rho] = \left[\sum_{k=1}^{N/2} Z(k) Z^T(k)\right] \left[\sum_{k=1}^{N/2} Z(k) log f_x(k/N)\right] \tag{11}$$

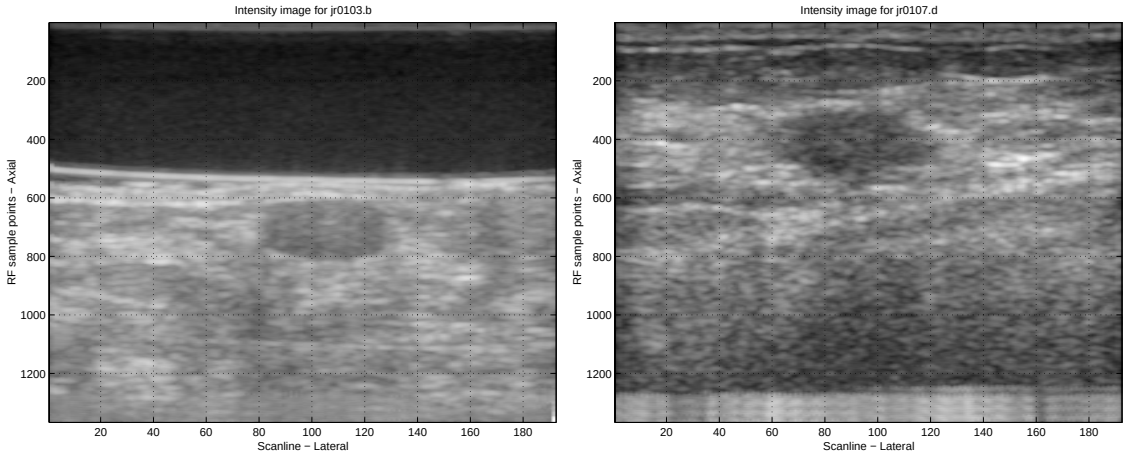
where $Z(k) = [-2log|2sin(\pi k/N)| \ -1]^T$.

It was shown in[32] that this estimator is unbiased, asymptotically Gaussian and consistent since the variance of the estimated parameters go to zero with increasing values of N.

In order to estimate the fractional differencing parameter d, 60 different data sets from 60 different B-scan images were used. 29 of these patients have malignant tumor and 31 of them have a benign breast tumor. The B-scan (grey scale) breast images were obtained from the Radiology Department of Thomas Jefferson University Hospital Philadelphia, PA, and each of them has dimension of 192x1368. The data was sampled at 20 MHz. A sample image from the benign and malignant data sets are presented in Figure 3 (a) and (b), respectively.

Raw RF ultrasonic echo data reflected from tissue was demodulated using base-band conversion techniques. This data set was used for model fitting and estimation procedures.

For each B-scan image, 30 scanlines from inside and outside the tumor region were taken with data lengths of 1x128, and each of these scanlines were used to estimate the fractional differencing parameter d. Hence, we have 30 values of d from inside and 30 values of d from outside the tumor sample. For each B-scan image, mean and variance of the fractional differencing parameter d were calculated for classification purposes. The distribution of the FD parameter d estimated for 30 scanlines (1x128) from inside and 30 scanlines (1x128) from outside the tumor region are given in Figure 4 for a randomly chosen B-scan image. As shown in Figure 4, fractional differencing parameter d is between 0 and 0.5, which meets the desired condition for long-term memory and stationarity, based on the fractional differencing model described by Hosking.[22] In Figure 5, we present the mean values of the parameter d obtained from inside and outside the suspected tumor. Figure 5 (a) shows the values for benign cases and Figure 5 (b) shows the values for the malignant cases. Figure 5 (c) displays the values of d parameter for randomly selected 30 B-scan images.



(a) (b)

Figure 3. Ultrasound B-Scan images for (a) a benign case (b) a malignant case.

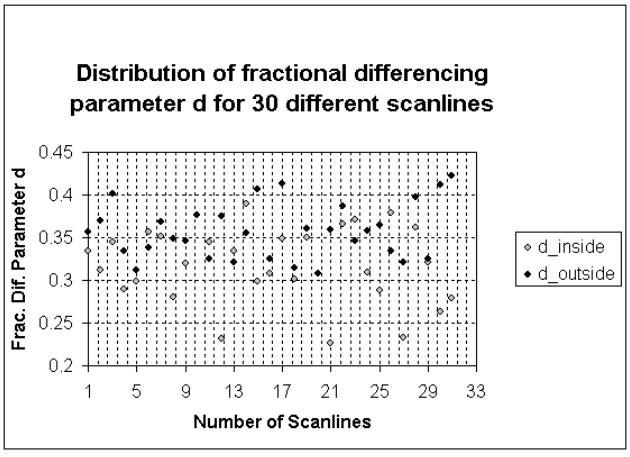
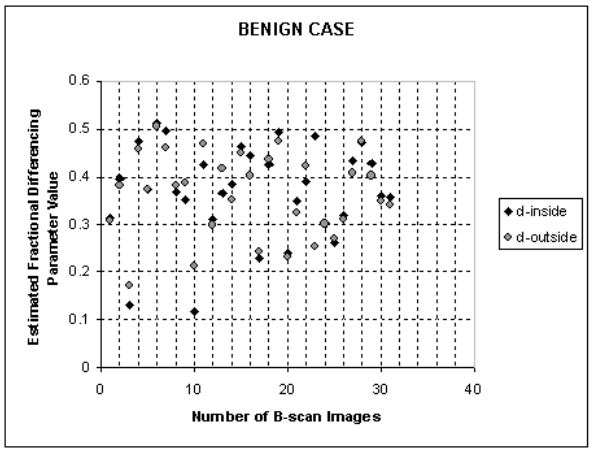
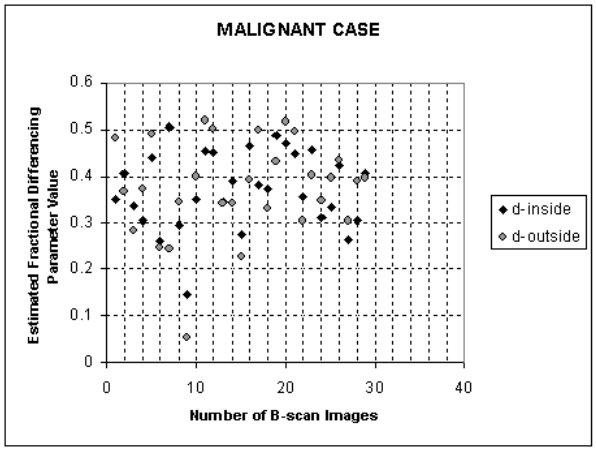


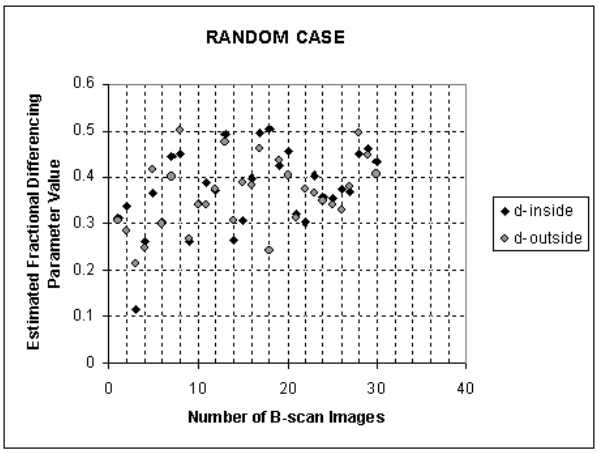
Figure 4. Fractional differencing model parameter d for 30 scanlines from inside and outside of the tumor region for randomly selected B-scan image.



(a)



(b)



(c)

Figure 5. Mean values of fractional differencing parameter d for inside and outside the tumor region for (a) benign, (b) malignant, (c) randomly selected cases

4. CLASSIFICATION FOR TISSUE CHARACTERIZATION USING T-TEST

We perform discrimination of malignant and benign tumors via a hypothesis testing method. Our approach relies on the following assumption. If the texture or speckle characteristics of the tissue for both inside and outside of the tumor are similar, we label the tumor as benign. Otherwise, we label the tumor as malignant. In mathematical terms this means that, if the mean values of the d parameter estimated from inside and outside the tissue are statistically different from each other, then we label tumor as malignant. Otherwise we label the tumor as benign. Since the estimated d values are asymptotically Gaussian distributed, we used t-test for the hypothesis testing problem described above.

The t-test assesses whether the means of the two groups are statistically different from each other with the assumption of normal distributed groups.[30] The formula for the t-test is a ratio given as:

$$\frac{signal}{noise} = \frac{difference\ between\ group\ means}{variability\ of\ groups} = t \tag{12}$$

The numerator is the difference between the mean values and the denominator is a measure of variability that is essentially noise, which makes it harder to see the group difference.

In our case the important point in the t-test is the value of the mean difference of d between inside and outside the tumor regions. In order to differentiate between benign and malignant cases for a fixed value of $t_{boundary}$, we added a value $d_{threshold}$ to the mean differences of d. The boundary value, $t_{boundary}$, can be extracted from the look-up for t-distributions tables. Under this assumption the modified formula for the t-test is given as:

$$t = \frac{d_{outside} - d_{inside} + d_{threshold}}{\sqrt{(\frac{var_{outside}}{n_{outside}-1})(\frac{var_{inside}}{n_{inside}-1})}} \tag{13}$$

where $d_{outside}$ and d_{inside} are the mean values of the fractional differencing model parameter d for $n_{outside}$ and n_{inside}, number of scanlines, and $var_{outside}$ and var_{inside} are variances of these d values, respectively.

Using the formula given in Equation (13), a single t value for each B-scan images was calculated using estimated $d_{outside}$, d_{inside} parameters and $var_{outside}$, var_{inside} values. For a randomly selected B-scan image, mean value of d parameter composed of 30 elements, is 0.3969, and the variance is 0.0317 for inside the tumor region, the values are 0.3829 and 0.0091, respectively for outside the tumor region. For the same B-scan image, using a suitable $d_{threshold}$ value, and the values given above, calculated value for t is 1.1931. The $t_{boundary}$ value used for characterization of tissue is 2 for 95% confidence limits for $n1 + n2 - 2$ degrees of freedom.(For our case $n1 = 30$, $n2 = 30$). According to this boundary value, if calculated t value is greater than $t_{boundary}$, then one may conclude that the B-scan image is malignant, on the other hand, if $t_{boundary}$ is greater than calculated t value then one may conclude that the B-scan image is benign. The characterization process can be formalized as:

$$t > t_{boundary} \quad : \quad malignant \quad tumor$$

$$t < t_{boundary} \quad : \quad benign \quad tumor$$

For the sample B-scan image, it was observed that $t < t_{boundary}$. In this case we may conclude that this patient has a benign breast.

We obtained 29 different t values from the malignant images and similarly 31 different t values from the benign images. Using these calculated t values and the boundary value, $t_{boundary}$, classification of B-scan images was performed.

The ROC curve was obtained by plotting the probability of false alarm versus the probability of detection for different values of $d_{threshold}$ given in Equation (13). Probability of detection is the ratio between the number of correct malignant decisions and total number of malignant cases (29). The probability of false alarm is the ratio between the number of incorrect benign decisions and total number of benign cases (31). Each point in

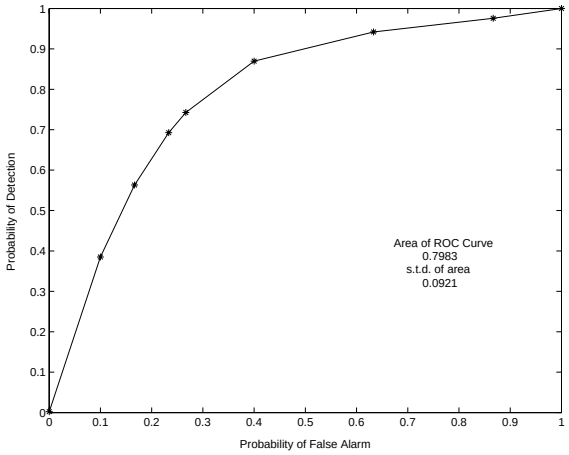


Figure 6. ROC curve for fractional differencing parameter d with different $d_{threshold}$ values. The area under ROC curve and standard deviation of the area is also added to the figure.

the curve is obtained by finding probability of false alarm and the probability of detection for different $d_{threshold}$ values. The area under ROC curve was calculated as 0.7983.

Standard deviation of area σ under the ROC curve, which yields a value of 0.0921, was calculated using the following expression:

$$\sigma = \sqrt{A(1-A)/N} \tag{14}$$

where A is the area under ROC and N is the number of malignant cases. The resulting ROC is shown in Figure 6.

5. CONCLUSION

In this paper, we modeled the RF echo as a FARMA process. We showed that the FARMA model parameters can be used to discriminate between benign and malignant tumors. The ROC analysis based on 60 *in vivo* B-scan images shows that the proposed method yields results that are comparable to, or better than most methods reported in the literature. In our future work, we will include morphological features such as tumor size and smoothness and patient age to improve our ROC results.

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