Maximum Likelihood Deconvolution of Ultrasonic Signals for Biological Tissue Classification

I. Diouf, K. L. Watkin

Departments of Obstetrics and Gynecology and Biomedical Engineering
McGill University

Introduction- A model for the backscattered signal consists of a convolution of components representing the contributions of a measuring system impulse response, the input signal and the medium or structure to be classified [3]. In order to perform such a classification, the impulse response of the medium needs to be extracted. Techniques such as homomorphic processing [4], fourier deconvolution [2], have been used to perform this task. Homomorphic processing is computationally expensive, it involves two fourier transforms and a filtering operation. The fourier deconvolution technique is unstable when zero's are present in the system transfer function. Whereas the result of the maximum likelihood deconvolution method (MLD) is an efficient estimator of the tissue impulse response in the Cramer-Rao sens. The purpose of this work was to develop a robust and efficient estimator of the insonified tissue structure in order to achieve a good classification in the presence of noise. The classification problem was to identify the tissue type based on the observation data $r_1, r_2, ..., r_N$ where N is the number of samples in one insonification experiment. We have assumed stationarity of the backscattered signal. It was also assumed that under hypothesis H_i the observation sample was the sum of the true underlying nonrandom sample value and a noise term. Thus, all observations were corrupted with an additive zero-mean white Gaussian noise with variance σ_n^2. The noise samples at various instants were independent random variables and were independent of the source output.

Deconvolution Method-The return echo from a target medium can be represented as a convolution of the impulse response $h_s[n]$ of the measuring system, the input signal $i[n]$ and the impulse response $M_i[n]$ due to the structure of the medium as shown in equation (1). The contributions of the impulse response of the measuring system as well as that of the input signal were fixed throughout the experiment.

$$y_i[n] = i[n] * h_s[n] * M_i[n] = s[n] * M_i[n] \quad (1)$$

$$r_i[n] = y_i[n] + noise[n] \quad (2)$$

where i represents the tissue under investigation and n represents the time index of the window used as the analysis frame for each insonification experiment. In order to perform the deconvolution, the received waveform $\mathbf{r}$ was passed through a filter matched to the system response $\mathbf{s}$ to give a set of numbers $a[k]$. The measuring system autocorrelation coefficients $b[k]$ and the noise at the matched filter output $ns[k]$ were computed:

$$a[k] = \sum_{n=1}^{N} r[n]s[n-k] \quad k = 1, 2...N \quad (3)$$

$$b[k] = \sum_{n=1}^{N} s[n]s[n-k] \quad k = 1, 2...N \quad (4)$$

$$ns[k] = \sum_{n=1}^{N} noise[n]s[n-k] \quad k = 1, 2...N \quad (5)$$

The $a[k]$'s form a set of sufficient statistics in the estimation of the M_i's. Values of $s[n-k]$ outside the window of analysis were padded with zero's. The problem was reduced to an estimation of the $M_i[k]$'s given a set of relations:

$$a[k] = \sum_{n=1}^{N} M_i[j]b[k-j] + ns[k] \quad k = 1, 2...N \quad (6)$$

Using suitable notation, the solution of the above equation can be written in matrix form as:

$$\mathbf{a} = \mathbf{B} \times \mathbf{M_i} + \mathbf{ns} \quad (7)$$

where $\mathbf{B}$ is a symmetric non singular NxN matrix formed by the autocorrelation coefficients $b[k]$'s.

Classification Method-The classification method was treated as a M-hypotheses testing problem. We hypothesized that different structures will generate different trends in the signal and consequently similar media or structures will influence the signal the same way. For each tissue class, a vector formed by the MLD estimate for each insonification position was computed. The power spectrum pow_i of this MLD vector $\mathbf{M_i}$ was then computed. This was repeated for different insonification positions for each class of tissue. Within any given tissue class, there is a degree of variability. This variability was modelled as an additive white Gaussian noise. Therefore the computed power spectrum was composed of the true underlying power spectrum representing a given class and an additive zero-mean white Gaussian noise term with variance σ_n^2. A general Gaussian problem formulation is then used together with the Bayes criterion with cost $C_{ij} = 0$ if $i = j$ and $C_{ij} \neq 0$ otherwise to perform the classification [5]. The test reduces to choosing H_i for:

$$P_i P(R|H_i) \geq P_j P(R|H_j) \quad \forall j \quad (8)$$

where R is a random vector computed in the same way as pow_i from an unknown tissue to be identified and H_i is an hypothesis representing a given tissue type. The equivalent test was to compute $P_i P(R|H_i)$ for all H_i and choose the largest. Since log is a monotonically increasing function of its argument, taking the log of each likelihood and eliminating the constant term yields the sufficient statistic:

$$l_i(R) = logP_i - 1/2log|K_i| - 1/2(R^T - m_i^T)K_i^{-1}(R - m_i) \quad (9)$$
$$K_i = E[(R - m_i)(R^T - m_i^T)|H_i)] \quad (10)$$

where m_i is the expected value of the random variable pow_i and K_i is the covariance matrix. E is the expectation operator. In order to simplify equation 9, we represent R in a new coordinate system in which the components are statistically independent random variables. The new coordinate system is computed by the Gram-Schmidt orthogonalization method using the set of power spectrum vectors formed from each class of tissue as the initial coordinate system [1]. It was assumed that all the hypotheses have equal *a priori* probabilities and that the statistics of the observations were only due to the statistics of the additive white Gaussian noise. Thus we have $K_i = \sigma_n^2 I$ in the new coordinate system. After eliminating constant terms, the sufficient statistic reduces to :

$$l_i'(R) = (-1/2\sigma_n^2)(R'^T - m_i'^T)(R' - m_i') = (-1/2\sigma_n^2)d^2 \quad (11)$$

The largest of $l_i'(R)$ corresponds to the minimum of distance d. Therefore, the processor of the classification is a minimum-distance decision rule.

Computer generated data simulating the backscattered ultrasonic signal were used to test the reliability of the MLD and the classification algorithms. The probability of correct decision was found to be influenced by the following factors: the data size and the noise variance. As the number of sample points was increased so was the correct decision percentage. It was also possible to increase arbitrarily the level of the noise variance. Such increases caused the performance of the classifier to degrade to the point where it was unable to extract any information from the data.

In-Vitro Experiments and Results with Biological Tissues-The classification technique was used to identify 3 tissues types: liver, kidney and pancreas. The experiments were conducted using a Panametrics broadband transducer with 5 MHz center frequency and a 3-dB bandwidth of 2.75 MHz. A Matec pulser and receiver were also used to excite the transducer and receive the backscattered echo signal. A Tektronix digital oscilloscope was used to digitize the echo signal with a sampling rate of 25 MHz.

The maximum likelihood estimate vector of the underlying signature of a tissue at a given position was computed from 60 A-scans data. The power spectrum of the MLD vector was then computed. A set of 20 power spectrum vectors was computed for a given tissue at different positions. Half of the set was used to construct the minimum distance processor and the remaining 10 vectors were used for the classification test. Figure 1 shows

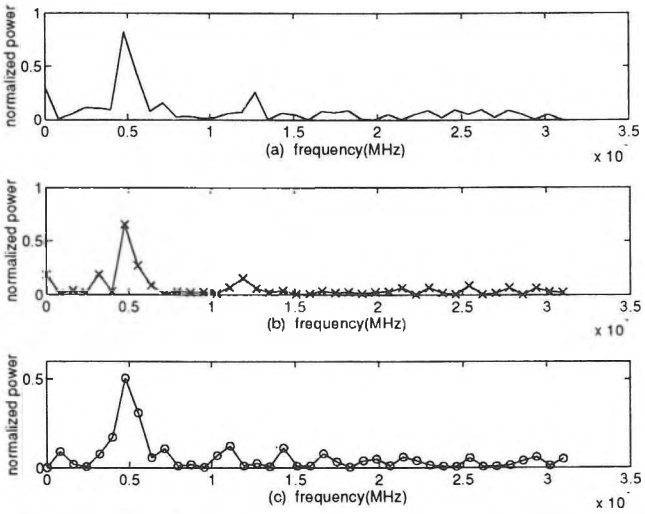

Figure 1: Power spectrum samples of the 3 tissue types: (a) liver, (b) kidney, (b) pancreas.

power spectrum vectors for each class of tissue. The result of the classification yielded a percentage of correct decision of 90%.

Conclusion-We implemented a backscattered echo signal classifier using a minimum distance processor. The decision was based of the nearest neighbor rule. Results obtained from both computer simulation and in-vitro biological tissue resulted in a probability of correct classification of about 90%. Further improvement can be achieved by applying this technique at different scales and combining the results of all the scales into one probability of correct decision.

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