BREAST CANCER DETECTION USING TIME REVERSAL

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Abstract

Breast cancer is the second leading cause of cancer death after lung cancer among North American women. Mammography and magnetic resonance imaging (MRI) have known limitations in detecting breast cancer especially during its early stage of development. A number of studies have shown that the microwave array imaging has the potential to become a successful clinical complement to conventional X-ray mammography in early-stage breast cancer detection. Microwave array imaging is performed by illuminating the breast tissues with an electromagnetic waveform and recording its reflections (backscatters) emanating from variations in the normal breast tissues and tumour cells, if present, using an antenna array. These backscatters, referred to as the overall (tumour and clutter) response, are processed to estimate the tumour response, which is applied as input to array imaging algorithms used to estimate the location of the tumour. Due to changes in the breast profile over time, the commonly utilized background subtraction procedures used to estimate the target (tumour) response in array processing are impractical for
breast cancer detection. The thesis proposes a new tumour estimation algorithm based on a combination of the data adaptive filter with the envelope detection filter (DAF/EDF), which collectively do not require a training step. After establishing the superiority of the DAF/EDF based approach, the thesis shows that the time reversal (TR) array imaging algorithms outperform their conventional counterparts in detecting and localizing tumour cells in breast tissues at SNRs ranging from 15 to 30dB.
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Preface
Abbreviations
1 Introduction

Breast cancer is the second leading cause of cancer death after lung cancer among women in North America [4]. Each year more than 200,000 new cases of invasive breast cancer are diagnosed and more than 40,000 women die from the disease in US and Canada alone [5]. The standard computing approaches for detecting breast cancer based on mammography and magnetic resonance imaging (MRI) have proven limitations especially in early stage breast cancer patients. False negative results (i.e., the failure in detecting tumours) are fairly common for patients with a palpable mass not visible with ultrasound or mammography. Likewise, false positive results (i.e., the failure in differentiating benign masses from invasive tumours) are equally common especially for younger patients with higher proportion of fatty tissues in their breast. Unnecessary biopsy and additional costly imaging are consequence of false positive results, while false negative results frequently lead to delay in cancer diagnosis and possible death of the untreated patients.

In the last decade, a number of studies [6–8] have shown that microwave breast
cancer detection has the potential to become a successful clinical complement to conventional X-ray mammography. Microwave imaging utilizes non-ionizing electromagnetic radiation to detect cancerous tumours in the human body by exploiting differences between the dielectric properties of normal and malignant tissues. Active microwave imaging, in which an external source illuminates the breast tissues, may broadly be classified into two different categories: (i) Tomographic methods, and; (ii) Backscatter methods, which are differentiated based on how observations are collected from the underlying modalities used in the two approaches. The tomographic methods are based on microwave radiation measurements recorded on the other side of the patient as the probing signal travels through the breast, while backscatter methods use reflections (backscatter) from the tumour tissues recorded on the same side as the transmitting source. Both categories impose their own sets of challenges. The problem with microwave tomography is the computationally complexity of the algorithms used to solve the ill-conditioned, non-linear, inverse scattering problem of determining the dielectric profile for the breast tissues from sound speed and attenuation measurements [9–11]. Another challenge is its high vulnerability to noise resulting from observations and experimental uncertainties. A third challenge comes from the need of accurate modeling of the antenna array configuration used for signal transmission / detection in tomography. Such inaccuracies adversely affect the performance of the tomographic-based localization
algorithms.

In backscatter imaging, several microwave emitters illuminate the breast and the resulting backscatter (i.e., reflection) is measured at multiple detectors on the same side of the human body as the transmitting array. Malignant breast tumours have electrical properties that are significantly different from those of healthy breast tissues \([10,11]\). Consequently, a cancerous tumour produces a stronger electromagnetic backscatter compared to the returns from normal tissues. In principle, it is then possible to locate the tumours from these backscatters. However, unlike X-rays, which are non-diffractive and travel in straight lines, electromagnetic microwave propagation in breast tissues is characterized by refraction and multipath effects, i.e., the backscattered cancer signature signal reaches the detector via two or more paths. As a result, conventional signal processing algorithms do not perform well due to multipath propagation and are, therefore, unable to accurately identify or locate the cancer tumours with accuracy. Most backscatter approaches, therefore, attempt to reduce the multipath component of the received signal.

In this thesis, I introduce a different backscatter imaging paradigm based on time reversal (TR) signal processing that uses multipath propagation to its advantage for finding the exact spatial locations of malignant tumours \([4,12–14]\). I will illustrate the superiority of the application of the proposed TR approach \([12]\) over conventional breast cancer detection approaches by running finite difference
time domain (FDTD) based electromagnetic simulations run on a close-to-reality model of the human breast. A major issue in applying TR based detection and localization algorithms stems from the difficulty in isolating the target (breast tumour) response from the overall response containing backscatter reflections from both target and clutter. Background subtraction typically used for estimating the target response assumes a linear system and requires knowledge of the clutter only response. It is, therefore, necessary to have a priori knowledge of response of the normal breast tissue (without tumour) of the patient in an environment identical to the one in which the examination for finding anomalies is later conducted. This is not possible even in screening situations because of the variations in the normal tissues and their growth over time. The main focus of the thesis is on the development of an adaptive filter, envelope detection (AFED) algorithm capable of isolating the target response from the overall (target plus clutter) response without the need of a training stage.

To summarize, the thesis makes three important contributions. First, the thesis proposes an AFED based target response estimation algorithm that isolates the target response from the overall response containing both the reflections from the background as well as tumour. The second contribution is the generation of a close-to-reality 2D electromagnetic breast model from a recorded MRI. This enables us to develop a computational technique for breast cancer detection, which
is non-intrusive and does not require any further testing. Third, the performance of the TR-based localization algorithms is compared with the performance of the conventional algorithms in the context of breast cancer detection by running FDTD based electromagnetic simulations.

The thesis is organized as follows. In Chapter 2, I provide a literature review of the commonly used time reversal (TR) and conventional array imaging algorithms suitable for breast cancer detection. In Chapter 3, my focus is on two underlying concepts used in the experimental simulations: (i) Generating a realistic electromagnetic (EM) breast model using an MRI, and; (ii) Estimating the target response from the overall (clutter and target) response. In Chapter 4, I present the simulation results to quantify the performance of the TR and conventional algorithms in estimating the location of the tumour from real MRI data. In addition, the outputs of target response estimators are also compared for their usefulness to breast cancer detection in this chapter. Finally, Chapter 5 summarizes the thesis and presents some directions for possible future work.
2 Time Reversal Array Imaging Algorithms

2.1 Introduction

In an array imaging system, a set of sensors (collectively referred to as an antenna array) is used to observe a region of interest for a prespecified physical phenomena. Depending on the application and type of sensors used in the antenna array, the frequency content and other characteristics of the probing signal used to illuminate the channel may vary considerably. In medical sonar imaging, for example, a beam of mechanical energy, e.g., ultrasound, illuminates the tissues of a human organ under observation and reflections (backscatters) from its tissues are captured by special microphones. An image is formed by processing the observed backscatters into a pseudospectrum that describes certain characteristics of the human organ. In this thesis, my focus is on active array imaging system, where the target is passive. Consequently, an array of transmitters artificially illuminate the medium by transmitting a set of probing signals. Their backscatter reflections are recorded by an observation array. This chapter introduces array imaging processing with
special emphasis on breast cancer detection using raw data from magnetic resonance imaging (MRI). In such passive imaging system, two arrays (one for transmission of the probing signal and the other one for the reception of the resulting backscatters) are used with an electromagnetic signal probing the channel.

The Chapter is organized as follows. Further details on the array imaging setup are described in Section 2.2. Next, the mathematical formulation of the array imaging framework used to derive array imaging algorithms is presented in Section 2.3. Conventional imaging algorithms (direct subtraction beamforming (DSBF) and direct subtraction multiple signal classification (DS/MUSIC)) and their limitations are discussed in Section 2.4. Section 2.5 focuses on the time reversal (TR) array imaging algorithms. Finally, Section 2.6 concludes the chapter with a summary of important results.

## 2.2 Array Imaging Setup

An array imaging setup is illustrated in Fig. 2.1, where an array of $N$ transceivers probes a medium containing $M$ embedded targets and record the backscatters from the medium. As previously described, the signal type may be mechanical, e.g., ultrasound, or electromagnetic, e.g., microwaves. In order for the array of transceivers to capture sufficient spatial samples, the distance between the array elements is kept at or less than $\lambda/2$, where $\lambda$ is the wavelength corresponding to the central
frequency of the probing signal [15]. This distance also guarantees minimum interference between neighboring transceivers [16]. The backscatters of the probing signal is processed by an array imaging algorithm to detect and estimate the locations of the targets. Although Figure 2.1 illustrates the array imaging setup used for target localization based on two antenna arrays, one used for transmitting the probing signal and the other used to record the observations, but in many applications, such as radar systems, only one antenna array is sufficient to both probe the channel and to capture the resulting backscatters. The output of the imaging algorithm is typically a pseudospectrum, which shows the spatial locations of the potential targets in terms of high intensity pixel values in an image. The next section describes the notation used in the array imaging framework, which is used
to describe common target detection algorithms.

2.3 Notation

In terms of Figure 2.1, the probing array (Array A) is assumed to contain \( P \) elements, while the observing array (Array B) contains \( N \) elements. Each element in Array A probes the channel sequentially with signal \( f(t) \), \( 0 \leq t \leq T \). The discrete time Fourier transform (DTFT) of the probing signal is denoted by \( F(\omega_q) \), where \( \omega_q = \omega_0 + q\Delta\omega \), for \( 1 \leq q \leq Q \). The antennas in Array B record the backscatters as each transducer element in Array A probes the channel. This results in a \((P \times N)\) matrix, referred to as multistatic matrix \( K(t) \), in the time domain. Transformed to the frequency domain, the multistatic response matrix is denoted by \( K(\omega_q) \) and is represented by \( Q \) blocks of dimensions \((N \times P)\). Each block corresponds to a particular frequency \( \omega_q \). Note that the entry \((n, p)\) in \( K(\omega_q) \) corresponds to the observation recorded by the \( n^{th} \) element \( B_n \) in Array B when the \( p^{th} \) element \( A_p \) in Array A probes the channel. Let \( k(\omega_q; A_p \rightarrow B_n) \) be the channel response at frequency \( \omega_q \) between elements \( A_p \) and \( B_n \). For a single target, therefore, element \( [K(\omega_q)]_{n,p} \) is

\[
[K(\omega_q)]_{n,p} \triangleq k(\omega_q; A_p \rightarrow B_n) = G(r_{B_n}, r_m; \omega_q) \tau(r_m; \omega_q) G(r_{A_p}, r_m; \omega_q) F(\omega_q).
\]

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In deriving Eq. (2.1), only the line of sight’s (LOS) path (referred to as the direct path) is considered between $A_p$ and $B_n$. Notation $\tau (r_m; \omega_q)$ is the complex reflectivity of the point target at location $r_m$ and $G (r, r'; \omega_q)$ is the Green’s function of the background medium between sites $r$ and $r'$ at frequency $\omega_q$. The Green’s function is the channel response recorded at location $r$ to a probing impulse $\delta(t)$ emitted from location $r'$. In reciprocal channels, the Green’s function satisfies the reciprocity property

$$G (r, r'; \omega_q) = G (r', r; \omega_q), \quad (2.2)$$

i.e., the Green’s function stays the same if the transmitter and observation sites are interchanged. When secondary reflections or/multipath are negligible, the free-space Green’s function $[12, 17]$ is given by

$$G (r, r'; \omega_q) = \frac{1}{4j} H_0^2 (k_q |r - r'|) \approx -\frac{1}{8\pi k_q} \frac{e^{-jk_q|r - r'|}}{|r - r'|}, \quad (2.3)$$

where $H_0^2 (\cdot)$ denotes the zeroth-order Hankel function of the second kind, $k_q = \omega_q / v$ is the wave number of a propagating wave with angular frequency $\omega_q$, and $v$ is the medium propagation velocity. For a medium with relative permittivity $\epsilon_r$ and relative permeability $\mu_r$, the propagating velocity $v = \frac{1}{\sqrt{\epsilon_r \mu_r}} c$, where $c$ is the speed of light. For a single target $m$, the Green’s function vector is formed by collecting all scalar Green functions between target $m$ and the spatial locations of the $N$
receiving antenna as follows

\[ g_B(r_m; \omega_q) = [G(r_{B1}, r_m; \omega_q), \ldots, G(r_{BN}, r_m; \omega_q)]^T, \tag{2.4} \]

where \( r_{Bi} \) is the spatial location of element \( i \) in Array B and \( r_m \) is the spatial location of the \( m^{th} \) target. Similarly, the Green’s vector for Array A with respect to the target location \( r_m \) is given by

\[ g_A(r_m; \omega_q) = [G(r_{A1}, r_m; \omega_q), \ldots, G(r_{AN}, r_m; \omega_q)]^T. \tag{2.5} \]

Based on Eq. (2.1), the \((N \times P)\) multistatic response matrix \( K(\omega_q) \) can be represented in terms of the Green’s functions vectors \( g_A \) and \( g_B \) as follows

\[ K(\omega_q) = \tau(r_m; \omega_q) g_B(r_m; \omega_q) g_A^T(r_m; \omega_q) F(\omega_q). \tag{2.6} \]

For \( M \) well resolved targets, the individual multistatic matrices are added together to determine the overall multistatic matrix. This leads to

\[ K(\omega_q) = \sum_{m=1}^{M} \tau(r_m; \omega_q) g_B(r_m; \omega_q) g_A^T(r_m; \omega_q) \tag{2.7} \]

\[ = G_B(\omega_q) \Pi G_A(\omega_q) \]

where \( \Pi \) is the \( M \times M \) diagonal matrix with target reflectivities \( \tau(r_m; \omega_q) \) as its diagonal entries, \( G_B(\omega_q) \) is an \((N \times M)\) matrix that collects \( g_B \), and \( G_A(\omega_q) \) is an
(\(M \times P\)) that collects \(\mathbf{g}_A\) vectors for all \(M\) targets as defined below

\[
\Pi = \text{diag}[\tau(r_1; \omega_q), \cdots, \tau(r_M; \omega_q)], \quad (2.8)
\]

\[
\mathbf{G}_B(\omega_q) = [\mathbf{g}_B(r_1; \omega_q), \cdots, \mathbf{g}_B(r_M; \omega_q)], \quad (2.9)
\]

and

\[
\mathbf{G}_A(\omega_q) = [\mathbf{g}_A(r_1; \omega_q), \cdots, \mathbf{g}_A(r_M; \omega_q)]. \quad (2.10)
\]

Recall that in deriving Eq. (2.6), only direct paths between target \(m\) and antenna arrays are considered. In a rich multipath environment, the structure of the multistatic matrix is much more complicated and is difficult to be modeled by an analytical expression. In addition, the multistatic matrix \(\mathbf{K}(\omega_q)\) is contaminated with reflections from the target and undesired scatters (clutter). We refer to the multistatic response matrix containing both clutter and target responses as the overall multistatic matrix and denote it by \(\mathbf{K}_{c+t}(\omega_q)\). Assuming that the whole system is linear and secondary reflections between targets and clutters are negligible, the reflected energy from the targets can be derived using the following expression

\[
\mathbf{K}_t(\omega_q) = \mathbf{K}_{c+t}(\omega_q) - \mathbf{K}_c(\omega_q), \quad (2.11)
\]

where \(\mathbf{K}_t(\omega_q)\) corresponds to the target response and \(\mathbf{K}_c(\omega_q)\) corresponds to the clutter response. Based on the target multistatic matrix \(\mathbf{K}_t(\omega_q)\), the goal of array imaging is to derive a pseudospectrum that specifies the spatial of the targets within the medium. If the number \(M\) of targets is known, then the first \(M\) peaks in the output pseudospectrum correspond to the \(M\) locations of the targets. In Section
2.4, I describe the conventional array imaging approaches, while Section 2.5 covers the time reversal approaches.

2.4 Conventional Array Imaging

Because of the large number of applications where array imaging is used, a range of target localization algorithms have been developed. Broadly speaking, these algorithms can be divided into three categories based on the bandwidth of the probing signal and the signal processing approach used to derive the pseudospectrum.

(i) Time-domain, broadband methods: The most famous algorithm in this category is the synthetic aperture radar (SAR) imaging algorithm [18–20]. In the simplest form of SAR, the area of the interest is first mapped to a 2D pixels or 3D voxels image. Before modeling any observation, a preprocessing step is run where the time delay between the sites corresponding to the mapped pixels (or voxels) and the antenna array is calculated. An antenna array typically located on an airborne plane probes the region of the interest and records the time for the received backscatters. Each pixel or voxel is then voted as a likely possible target location by comparing the actual and estimated time delays between the probing signal and its backscatter. A thresholding binary decision can be used to identify the location of the target at each pixel or voxel. In a more complicated version, other properties of the observed signals
such as frequency shift, amplitude, phase, and/or polarization may be used for voting. Note that the preprocessing step, where the time delays are calculated, is completed in the time domain. Also the probing signal used in these algorithms has a wide bandwidth to cover frequency shifts. Such techniques are suitable for detecting a broad range of targets with different frequency responses and frequency shifts, e.g., in military applications.

(ii) Frequency-domain, narrowband methods: The localization algorithms belonging to this category can be further classified into two groups: (i) Beamforming, and; (ii) MUltiple SIgnal Classification (MUSIC). Beamforming algorithms [19, 20] consist of two steps: training and imaging. In the first step, the Green’s functions between the probing site and the discretized medium are either measured or computed. The result of this step is the differential phase information for all sites in the medium in the frequency domain. In the second step, backscatters recorded at the antenna array are matched in the frequency domain with the differential phase information obtained from the first stage to compute a pseudospectrum. If a target exists in the reference medium, the phase match process yields a peak in the pseudospectrum. MUSIC imaging algorithm [21, 22], on the other hand, uses subspace projection of the recorded signals in the frequency domain to identify targets within a channel. The subspace projection separates the target subspace from the
background noise. Any of the two subspaces can be used to derive the pseudospectrum providing information on the targets’ locations. Because both groups of algorithms employ a broadband probing signal, therefore, the approaches are bounded to special types of targets with narrowband frequency responses and no significant frequency shifts. Further details of these algorithms are presented in Sections 2.4.1.1 and 2.4.2.

(iii) Incoherent methods: In some applications, there is considerable fluctuations in the characteristics of the reference channel over time. As a result, the recorded backscatters when transformed to the frequency domain are statistically unstable. This precludes the application of the MUSIC algorithm because the observations can no longer be separated into the target subspace and the background noise subspace. Random fluctuations in the reference medium over time change the differential phase information such that these can no longer be matched to the one obtained during the training step. These fluctuations result in false positive spots appearing as ghost targets in the pseudospectrum. For such applications, incoherent methods [15, 23] have been developed. They use both time domain observations and the frequency domain transformations to construct the pseudospectrum. Theoretical analysis show that the algorithms are statistically stable.
The choice of a particular localization algorithm is based on a priori knowledge of the channel and target characteristics. Category (i) assumes a stationary channel with known statistical properties and is applicable to a broad range of targets with unknown frequency responses. Category (i), therefore, uses broadband techniques and is applicable to long range target detection as in military and satellite telemetry. Category (iii) algorithms are used in applications where the reference medium is nonstationary (i.e., the medium is changing rapidly over time as in human heart sonography), as is also the case for Category (i), but where the frequency characteristics of the target are known. Finally, Category (ii) assumes a stationary channel with known target response. A possible application for category (ii) algorithms is breast cancer detection. In this application, the channel under investigation does not fluctuate statistically during examination and the frequency response of the malignant tumour cells is known. In other words, we expect only one kind of targets (breast cancers) within the reference medium (breast tissues). As such, category (ii) algorithms are of interest to me. One drawback with these algorithms is degradation in their performance in rich multipath environments. In this thesis, I propose to combine the localization algorithms in Category (ii) with time reversal (TR) to compensate for multipath. In the next section, I provide a step-by-step introduction of two conventional algorithms: direct subtraction beamforming (DSBF) and direct subtraction MUSIC (DS/MUSIC) [12, 13] and explain how their performances are
affected by multipath. Other limitations of these algorithms are also discussed.

2.4.1 Direct Subtraction Beam Forming (DSBF) Imaging Algorithm

In a real life situation, as in biomedical array imaging applications, the recorded multistatic matrix at Array B with Array A probing the channel is the combined clutter and target response, denoted by $K_{c+t}(\omega_q)$. Before applying an imaging algorithm the target response $K_t(\omega_q)$ is typically estimated from the overall response $K_{c+t}(\omega_q)$. As previously described, one way of doing so is background subtraction or direct subtraction (DS) based on Eq. (2.11). The target response $K_t(\omega_q)$ obtained from direct subtraction is not precise because Eq. (2.11) assumes that the reference medium is linear and there are no secondary reflections between the target and clutter. Once the target response is estimated, any of the imaging techniques can be applied to estimate the location of the target. In the following section, I describe one such DSBF approach. Although the beamforming approach is described in conjunction with direct subtraction but the initial step of estimating the target response $K_t(\omega_q)$ from mixed response $K_{c+t}(\omega_q)$ can be replaced with a more elaborate target response estimation scheme.
2.4.1.1 Beamforming

Beamforming is a technique used for converging the probing signal on to a target. In array imaging, this technique can be applied at either the probing or imaging step. While beamforming at the probing step is used in radar or sonar systems, array imaging algorithm uses beamforming at the imaging step by maximizing the pseudospectrum at likely locations where targets may be present. This is accomplished by two weight vectors, \( \{ w_B(x; \omega_q), w_A(x; \omega_q) \} \) corresponding to the two transducer arrays and expressing the beamforming step in terms of the maximization problem

\[
\max |w_B(x; \omega_q) K_t(\omega_q) w_A(x; \omega_q)|^2 \quad (2.12)
\]

subject to \( \| w_B(x; \omega_q) \|^2 = \| w_A(x; \omega_q) \|^2 = 1. \quad (2.13) \)

Assuming only one target exists in the medium, we can represent the target response \( K_t(\omega_q) \) based on the model defined in (2.6) as

\[
K_t(\omega_q) = \tau(x; \omega_q) g_B(x; \omega_q) g_T^A(x; \omega_q), \quad (2.14)
\]

where \( x \) is the spatial coordinates of the target. Substituting Eq. (2.14) in (2.12) and applying the Cauchy-Schwartz inequality, we get

\[
|w_B(x; \omega_q) \tau g_B(x; \omega_q) (x; \omega_q) g_T^A(x; \omega_q) w_A(x; \omega_q)|^2 \leq
\]

\[
|\tau(x; \omega_q)|^2 \left| w_B(x; \omega_q) g_B(x; \omega_q) \right|^2 \left| g_T^A(x; \omega_q) w_A(x; \omega_q) \right|^2 \quad (2.15)
\]
Each term on the right hand side of Eq. (2.15) is maximized separately. Based on the Cauchy-Schwartz inequality, Term 1 maximizes if $w_B(x; \omega_q) = c g_B(x; \omega_q)$. Given that $|g_B(x; \omega_q)| = 1$, the above equation reduces to

$$w_B(x; \omega_q) = \frac{g_B^H(x; \omega_q)}{\|g_B(x; \omega_q)\|}. \quad (2.16)$$

Similarly, Term 2 maximizes when

$$w_A(x; \omega_q) = \frac{g_A^*(x; \omega_q)}{\|g_A(x; \omega_q)\|}. \quad (2.17)$$

Substituting Eq. (2.16) and (2.17), Expression (2.12) reduces to

$$I_{DSBF}(x; \omega_q) = \left| \frac{g_B^H(x; \omega_q) K_t(\omega_q) g_A^*(x; \omega_q)}{\|g_B(x; \omega_q)\| \|g_A(x; \omega_q)\|} \right|^2, \quad (2.18)$$

which is the pseudospectrum plotted to determine the target location $x$ at frequency $\omega_q$. Combining the resulting pseudospectrum for all frequencies $\omega_q$, $1 \leq q \leq Q$, the overall pseudospectrum is given by

$$I_{DSBF}(x) = \sum_{q=1}^{Q} \left| \frac{g_B^H(x; \omega_q) K_t(\omega_q) g_A^*(x; \omega_q)}{\|g_B(x; \omega_q)\| \|g_A(x; \omega_q)\|} \right|^2. \quad (2.19)$$

Table 2.1 summarizes the steps involved in the DSBF algorithm. Although the derivation of the algorithm is based on a single target but it is applied in the same format to multiple $M$ targets with the first $M$ peaks in the overall pseudospectrum corresponding to the $M$ locations of the targets.
Algorithm DSBF ([in] $K_{c+t}$, $K_c$, [out] $I_{DSBF}$)

Initialization: $I_{DSBF}(x) = 0$

For all $1 \leq q \leq Q$:

$\omega_q = \omega_0 + q\Delta\omega$

Calculate $K_t(\omega_q) = K_{c+t}(\omega_q) - K_c(\omega_q)$

For all image pixels $x$

Calculate $g_B(x, \omega_q)$ and $g_A(x, \omega_q)$ for pixel $x$

Calculate $I_{DSBF}(x) = I_{DSBF}(x) + \left| \frac{g_B^H(x, \omega_q)K_t(\omega_q)g_A^*(x, \omega_q)}{\|g_B(x, \omega_q)\|\|g_A(x, \omega_q)\|} \right|^2$

End For

End For

Table 2.1: The Direct Subtraction Beamforming (DSBF) algorithm
2.4.2 DS/MUSIC Imaging Algorithm

The MUSIC algorithm, listed under Category (ii), was originally used in signal processing to separate different frequency components of a composite signal. Devaney [21] used the orthogonality principle to extend the MUSIC algorithm to array imaging applications. Suppose that the number of elements in both Array A and B (shown in Fig. 2.1) is equal, given by \( N \), and is greater than the number \( M \) of targets, i.e., \( M < N \), and the medium is homogeneous with no scatterers. In comparison with the central wavelength \( \lambda \) of the probing signal, the dimensions of the targets are assumed to be small. In such cases, the targets are referred to as well resolved targets and have negligible secondary reflections. The observed target response \( K_t \) in Array B is then modeled as

\[
K_t(\omega_q) = S_1(\omega_q) + S_2(\omega_q) + \cdots + S_M(\omega_q) + W(\omega_q)
\]  

(2.20)

where \( S_i(\omega_q) \), \( (1 \leq i \leq M) \), is the reflected signal from the \( i^{th} \) target and \( W(\omega_q) \) is the additive Gaussian noise with variance \( \sigma^2 \) at frequency \( \omega_q \). Eq. (2.20) implies that reflections from targets are independent from each other and the noise is independent of the target’s response. For a reciprocal medium, model (2.7) ensures that channel response \( K_t(\omega_q) \) is Hermitian symmetric. Also, \( K_t(\omega_q) \) has a signal space with rank of \( M \) significant eigenvectors (corresponding to nonzero eigenvalues) resulting from the target. The noise \( W(\omega_q) \) defines the null space for \( K_t(\omega_q) \).
In other words, the eigenvector decomposition of $K_t(\omega_q)$ yields

$$K_t(\omega_q) = U(\omega_q) \Sigma U^H(\omega_q), \quad (2.21)$$

where $U(\omega_q)$ contains eigenvectors

$$U(\omega_q) = \begin{bmatrix} u_1(\omega_q), \ldots, u_M(\omega_q), u_{M+1}(\omega_q), \ldots, u_N(\omega_q) \end{bmatrix}$$

Signal space Null space

and $\Sigma(\omega_q)$ is a diagonal matrix

$$\Sigma(\omega_q) = \begin{pmatrix} \Lambda_t(\omega_q) & 0 \\ 0 & \Lambda_n(\omega_q) \end{pmatrix}. \quad (2.23)$$

The diagonal block $\Lambda_t(\omega_q)$ contains $M$ non-zero eigenvalues corresponding to the target subspace, while $\Lambda_n(\omega_q)$ is a zero matrix corresponding to the null subspace.

By finding a break point in the ordered eigenvalues sequence, the targets subspace and the noise subspace are separated. In this way, the first $M$ eigenvectors corresponding to nonzero eigenvalues are selected as targets subspace and the rest of the eigenvectors span the null subspace. In the MUSIC algorithm, the number of targets is determined by performing a SVD of the target response matrix $K_t(\omega_q)$. The number of non zero (significant) eigenvalues provides an estimate of the number of targets embedded in the medium. The locations of the targets are determined by noting that the noise subspace is the orthogonal complement of the target subspace.
This leads to the expression

\[ \frac{1}{\| u_m^H(\omega_q)U_n(\omega_q) \|} = \infty, \]  

(2.24)

where \( u_m^H(\omega_q) \) is a vector corresponding to the \( m^{th} \) target and \( U_n(\omega_q) \) is the null subspace. Eq. (2.24) is used to localize targets using the target response \( K_t(\omega_q) \).

Recall that the target reflections are modeled by Green’s vectors \( g_B(x;\omega_q) \) and \( g_A(x;\omega_q) \). Replacing \( U_t(\omega_q) \) in (2.24) with \( g_B(x;\omega_q) \) and \( g_A(x;\omega_q) \), we get

\[ \Upsilon_B(x;\omega_q) = \frac{1}{\| g_B^H(x;\omega_q)U_n(\omega_q) \|}, \]  

(2.25)

\[ \Upsilon_A(x;\omega_q) = \frac{1}{\| g_A^H(x;\omega_q)U_n^*(\omega_q) \|}. \]  

(2.26)

Again, using the Cauchy-Schwartz inequality for (2.25) and (2.26) and then applying the unit norm constraint, gives

\[ \Upsilon_B(x;\omega_q) = \frac{1}{\| g_B^H(x;\omega_q)U_n(\omega_q) \|^2 / \| g_B(x;\omega_q) \|^2}, \]  

(2.27)

and \( \Upsilon_A(x;\omega_q) = \frac{1}{\| g_A^H(x;\omega_q)U_n^*(\omega_q) \|^2 / \| g_A(x;\omega_q) \|^2}. \)  

(2.28)

The pseudospectrum in MUSIC algorithm is then formed by

\[ I_{MUSIC}(x) = \frac{1}{Q} \prod_{q=1}^{Q} \Upsilon_A(x;\omega_q) \Upsilon_B(x;\omega_q), \]  

(2.29)

where the first \( M \) peaks in the pseudospectrum are the estimated locations of the targets. If, like the DSBF algorithm, \( K_t(\omega_q) \) is determined from the overall clutter and target response using direct subtraction (Eq. (2.11)) then the overall algorithm
is called DS/MUSIC. Other variants of the MUSIC algorithm can be obtained by using a different scheme for estimating the target response $K_t(\omega_q)$. The DS/MUSIC algorithm is summarized in Table 2.2.

### 2.4.3 Limitations of Conventional Array Imaging Algorithms

Both beamforming and music algorithms successfully localize targets in a stable and homogeneous medium but perform poorly if the received backscatters are contaminated with multipath reflections, as is the case for inhomogeneous environments with rich clutter. Since most real applications such as ground penetrating radar, biomedical imaging, and underwater acoustic deals with random and non-static media, these algorithms perform poorly. In addition, the MUSIC algorithm has its own limitation. It requires the number $N$ of receivers be greater than number $M$ of all backscatters including targets and other scattering elements. Recall that the eigenvalue space in MUSIC is divided into two subspaces: target subspace and noise subspace. In an inhomogeneous medium, such as human tissues, there are many backscatters due to normal variations in the medium and the number of backscatters does exceed the number of receivers. To overcome the multipath problems, time reversal can be used. For relaxing the limitation on the number of receivers, a beamforming clutter cancellation step can be introduced to eliminate the effect of backscatters introduced by clutter. Both these modifications are introduced in
Algorithm DS/MUSIC ([in] $K_{c+t}$, $K_c$, [out] $I_{DS/MUSIC}$)

$I_{DS/MUSIC}(x) = 0$

For all $1 \leq q \leq Q$:

$\omega_q = \omega_0 + q \Delta \omega$

Calculate $K_t(\omega_q) = K_{c+t}(\omega_q) - K_c(\omega_q)$

For all image pixels $x$

Calculate $g_B(x, \omega_q)$ and $g_A(x, \omega_q)$ for pixel $x$

Calculate $[U \Sigma U^*] = SVD(K_t(\omega_q))$

Number of targets = Number of nonzero eigenvalues in $\Sigma$

Find the break point in $\Sigma$ and separate the null space $U_n(\omega_q)$ in $U$

Calculate $\Upsilon^B = \frac{1}{\|g_B(x; \omega_q)U_n(\omega_q)\|/\|g_B(x; \omega_q)\|^2}$

Calculate $\Upsilon^A = \frac{1}{\|g_A(x; \omega_q)U_n(\omega_q)\|/\|g_A(x; \omega_q)\|^2}$

$I_{DS/MUSIC}(x) = I_{DS/MUSIC}(x) + (\Upsilon^A \Upsilon^B)$

End For

$I_{DS/MUSIC}(x) = \frac{I_{DS/MUSIC}(x)}{Q}$

End For

Table 2.2: The Direct Subtraction MUSIC (DS/MUSIC) algorithm.
Section 2.5.

As a final note to our discussion on beamforming and MUSIC, we observe that the performance of these algorithms depend on the quality of the target response \( K_t(\omega_q) \). The direct background subtraction is a crude method of determining \( K_t(\omega_q) \). Consequently, both beamforming and MUSIC do not perform well with background subtraction. Later in the thesis, I present alternative techniques for determining \( K_t(\omega_q) \) from the overall response.

### 2.5 Time Reversal Array Imaging Algorithms

Time reversal (TR) has been employed in many different applications in areas as diverse as radar, communications, geophysics, and medicine. In electromagnetic radar systems, TR has been used for locating targets in highly cluttered environments [24, 25]. Geophysicists have used TR to estimate the epic-centers for earthquakes [26]. TR methods have also been employed in both underwater and air communication systems to get rid of multipaths [27–29]. In medicine, TR has been employed for therapeutic applications including transcranial ultrasonic therapy [30,31], lithotripsy [32], and hyperthermia therapy [33]. Medical imaging using TR is an attractive and rather new area. In this field, we are looking for a target in an obscured medium. Because of its positive treatment of multipath arising from channel inhomogeneities and strong clutter in the medium, TR offers an alternate
paradigm for medical imaging [4, 14, 17, 34]. The second half of this chapter deals with TR array imaging techniques.

2.5.1 TR Background

Though the exact schematics of the TR configuration depend upon the application under consideration, most existing TR techniques exploit the phenomena of super-resolution focusing observed by following the steps outlined below.

(i) Forward Probing: An active target or scatterer, embedded in an unknown medium, generates a signature pulse $f(t)$ into the random medium. If the target is passive, then a transducer array illuminates the unknown medium with a probing pulse such that reflections from the target constitutes the signature pulse $f(t)$.

(ii) Forward Backscatter Observations: The transducer array, placed either within or outside the medium, records the waveforms at each of its transducer elements. For passive targets (as is the case for breast tumours), the backscatters of the probing pulse form the observations used later during the TR steps. At this stage the recordings at antenna element $i$ at location $r_i$ from source $s$ at location $r_s$ is given by

$$z = f(t) \otimes h_{r_s r_i}(t)$$  \hfill (2.30)
where \( h_{r_s r_i}(t) \) is the channel impulse response between location \( r_i \) and \( r_s \).

(iii) TR Probing: Each transducer element time reverses its recorded waveform (i.e., \( f(T_0 - t) \ast h_{r_s r_i}(T_0 - t) \)). This is equivalent to phase conjugation in the frequency domain. The energy normalized time-reversed waveform is retransmitted into the medium in conjunction with other elements of the antenna array at the same time. The time reversed signal experiences the same changes such as multiple scattering, reflections, and refraction that the forward probing signal underwent during forward propagation. The received signal at source \( r_s \) is given by

\[
\begin{align*}
\begin{split}
z'_i(r_s, t) = k_i &\left( f(T_0 - t) \ast \left( h_{r_s r_i}(T_0 - t) \ast h_{r_s r_i}(t) \right) \right)
\end{split}
\end{align*}
\]  

(2.31)

where \( k_i \) is the energy normalization constant. Note that Term 1 corresponds to a matched filter, namely a time-correlator, and has the maximum value of \( \int |h_{r_s r_i}|^2\, dt \) at \( t = T_0 \). The phenomena is referred to as the temporal super-resolution focusing. Eq. (2.31) also illustrates spatial super-resolution focusing. Assume that we observe the backscatters of TR signal at \( r_x \), which is not at the same location as the location of the source \( r_s \). Since \( h_{r_s r_i}(T_0 - t) \) and \( h_{r_s r_i}(T_0 - t) \) are different terms, \( z_i(t) \) is not maximized at location \( r_x \). The super-resolution phenomenon is amplified if all transceivers time reverse and send back their observations simultaneously. In this case, Eq. (2.31) can
be expressed as

\[ z_i'(r_s, t) = \sum_{i=1}^{N} k_i(f(T_0 - t) \ast h_{r_ir_i}(T_0 - t) \ast h_{r_is}(t)) . \]  

(2.32)

(iv) TR Observations: The backscatters of time reversed probing, \( z_i'(r_s, t) \), is observed at the transducer array and are used as inputs to the TR array imaging algorithms.

In physical TR, Steps (iii) and (iv) are performed in real, while in computational TR (frequently used in array imaging), Steps (iii) and (iv) are implemented using computational simulations. TR offers an alternative to traditional detectors, e.g., the matched filter in one dimensional signal processing and the matched field processing (MFP) in multidimensional signal processing. The difficulty with MFP is that the Green's function used to model the channel is not known and, therefore, has to be computed numerically. By its inherent nature, TR intrinsically derives the Green's functions of the channel as long as the receiving transducer array provides an adequate sampling of the channel. The second advantage of TR lies in the productive treatment of the channel multipaths. As is generally known, multipath significantly affects the performance of traditional detectors and is considered to be detrimental and a negative whose effect should be minimized. TR presents the opposite opportunity: multipath as a positive effect, the more the better.
2.5.2 TRAIC/TRBF Imaging Algorithm

Based on the super-resolution phenomenon in TR (Eq. (2.32)), the backscatters focus both temporarily and spatially at the locations of the scatterers (targets and clutter included). Time reversal adaptive interface canceler (TRAIC) algorithm [12] differentiates between the desired targets and undesired clutter. It attempts to eliminate the effect of clutter by performing TR computationally in two steps: One to cancel the effect of the clutter and the other to focus the TR signal on the targets. In the first step, TR is used to mitigate backscatters from the clutter. In the second step, TR is used a second time to focus on targets only. The result of focusing in the second step is used finally in the time reversal beamforming (TRBF) algorithm to form a pseudospectrum. The TRAIC/TRBF consists of five distinct steps described below. We assume that the number $N$ of elements in Array A and B are equal though the algorithm is generalizable for the general case with $N \neq P$.

(i) *Clutter Channel Probing from Array A to B* ($A \rightarrow B$): In this step, the clutter response $K_c(\omega_q)$ is estimated between all elements in Array A and Array B. This step involves some initial training when no target is present in the medium. Because we assume that the media is reciprocal, probing from $(A \rightarrow B)$ is the same as $(B \rightarrow A)$. Assume that the media is illuminated by the $p^{th}$ element in Array A, namely $A_p$, and backscatters are recorded by all
elements in Array B for all frequencies $\omega_q, q = 0, \ldots, Q - 1$. In this case, an $N$ element vector $r(\omega_q)$ whose $n^{th}$ entries corresponds to $n^{th}$ element in Array B is formed for each frequency $\omega_q$. To make the estimation more robust, the measurement is performed multiple ($1 \leq l \leq L$) times through Monte Carlo repetitions. For each noisy measurement $l$ recorded by element $A_p$ in Array A,

$$r_{p,l}(\omega_q) = K_c(\omega_q)e_pF(\omega_q) + n_l(\omega_q) \quad (2.33)$$

where $e_p$ is the vector whose $p^{th}$ entry is 1 and 0 elsewhere and $n_l(\omega_q)$ is additive white Gaussian noise. Assuming $F(\omega_q) = 1$ and taking the average of $L$ measurements yields

$$\hat{K}_c(\omega_q)e_p = \frac{1}{L} \sum_{l=1}^{L} r_{p,l}(\omega_q) \simeq K_c(\omega_q)e_p. \quad (2.34)$$

Thus for all elements in Array A, we get

$$\hat{K}_c(\omega_q) \simeq K_c(\omega_q). \quad (2.35)$$

In some applications, the resulting $K_c(\omega_q)$ in (2.35) is precise enough to form the input for the later steps. For breast cancer detection, however, this estimation of $K_c(\omega_q)$ can not be used because breast examinations are typically conducted over time and the reference medium (i.e., breast tissues) may vary significantly in size and density. In Chapter 3, I present a practical alternative to estimating $K_c(\omega_q)$ without any prior training.
(ii) *Waveform Reshaping for Clutter Cancellation:* Before describing Step (ii), I define the time reversal matrix in frequency domain for Array A as

\[
T_{c}(\omega_{q}) = K_{c}^{T}(\omega_{q}) K_{c}^{*}(\omega_{q})
\]

(2.36)

where the multistatic clutter matrix is assumed to be Hermitian symmetric based on Eq. (2.7). Since no target is present during the training step used to estimate \( K_{c}(\omega_{q}) \), \( T_{c}(\omega_{q}) \) focuses on the clutter. The main goal of this step is to take advantage of this focusing to nullify the effect of the clutter. Given the channel response \( K_{c}(\omega_{q}) \) from the training step, backscatters from the clutter recorded at Array B is given by

\[
x_{p}(\omega_{q}) = K_{c}(\omega_{q}) e_{p} F(\omega_{q}).
\]

(2.37)

when element \( p \) on Array A probes the medium. The time reversed version of \( x_{p}(\omega_{q}) \) is given by

\[
x_{p}^{*}(\omega_{q}) = K_{c}^{*}(\omega_{q}) e_{p} F^{*}(\omega_{q}).
\]

(2.38)

A reshaping filter \( W(\omega_{q}) \) is designed to minimize the reflected energy from the clutter and applied before \( x_{p}^{*}(\omega_{q}) \) is transmitted into the medium. In this case, the nullified clutter signal recorded at Array A is given by

\[
y_{p}(\omega_{q}) = K_{c}^{T}(\omega_{q}) W(\omega_{q}) K_{c}^{*}(\omega_{q}) F^{*}(\omega_{q}) e_{p}
\]

(2.39)
where \( \mathbf{W}(\omega_q) \) in Eq. (2.39) is a \((N \times N)\) matrix. In order to design \( \mathbf{W}(\omega_q) \), the nullified signals \( \mathbf{y}(\omega_q) \) are organized in the form an array

\[
\mathbf{y}(\omega_q) = [\mathbf{y}_1(\omega_q), \ldots, \mathbf{y}_P(\omega_q)]^T.  
\]  

(2.40)

Ordering \( \mathbf{y}(\omega_q) \) for all frequencies \( \omega_q \), in a \((PQ \times 1)\) vector

\[
\mathbf{y} = [\mathbf{y}(\omega_1), \ldots, \mathbf{y}(\omega_Q)]^T 
\]  

(2.41)

transfer function \( \mathbf{W}(\omega_q) \) is evaluated by minimizing the total energy in \( \mathbf{y} \).

Expressed as a minimization problem gives

\[
\text{arg min}_{\mathbf{W}(\omega_q)}: ||\mathbf{y}||_F^2 = \sum_{q=1}^{Q} \left( ||\mathbf{K}_c^T(\omega_q) \mathbf{W}(\omega_q) \mathbf{K}_c^*(\omega_q)||_F^2 |\mathbf{F}^*(\omega_q)|^2 \right) 
\]  

(2.42)

where \( \cdot || \cdot F \) represent the Frobenius norm. Assuming \( |\mathbf{F}^*(\omega_q)| = 1 \), the minimization problem is reduced to

\[
\mathbf{W}(\omega_q)_{opt} = \text{arg min}_{\mathbf{W}(\omega_q)}: ||\mathbf{K}_c^T(\omega_q) \mathbf{W}(\omega_q) \mathbf{K}_c^*(\omega_q)||_F^2, 
\]  

(2.43)

which results in the following equation [12]

\[
\mathbf{W}(\omega_q)_{opt} = k_q \left[ \mathbf{K}_c^*(\omega_q) \mathbf{K}_c^T(\omega_q) \right]^{-1} 
\]  

(2.44)

where

\[
k_q = \left( \frac{\sum_{i=1}^{N} 1}{\lambda_{q,i}} \right)^{-1} = \left( \left| \mathbf{F}^*(\omega_q) \right|^2 \right)^{-1} 
\]  

(2.45)
and \( \lambda_{q,i} \) are eigenvalues of \( K_c(\omega_q) \). As a result, when the number of elements in Array A and B are equal,

\[
K^T_c(\omega_q) W(\omega_q) K^*_c(\omega_q) = k_q I_N
\]  

(2.46)

where \( I_N \) is an identity matrix. Eq. (2.46) shows that by using \( W(\omega_q) \), the backscatters from the clutter are suppressed in the TR matrix presented in (2.36).

(iii) **Target channel monitoring** \((B \rightarrow A)\): In this step, we assume that a single target is present in the medium. Antenna element \( k \) probes the channel. The recorded backscatter \( x_p \) at Array B is filtered with the clutter cancellation filter, and then energy normalized, time reversed, and retransmitted back to the medium. Based on Eqs. (2.38) and (2.44), the received signal at the \( p^{th} \) element in Array A is given by

\[
z_p(\omega_q) = (K_t(\omega_q) + K_c(\omega_q))^T W(\omega_q) x^*_p(\omega_q) \\
= (K_t(\omega_q) + K_c(\omega_q))^T k_q [K^*_c(\omega_q) K^T_c(\omega_q)]^{-1} K^*_c(\omega_q) e_p F^*(\omega_q) \\
= k_q (K_t^T(\omega_q) K_c^{-T}(\omega_q) + I_N) e_p F^*(\omega_q) \\
= k_q K_t^T(\omega_q) K_c^{-T}(\omega_q) e_p F^*(\omega_q) + k_q I_N e_p F^*(\omega_q)
\]

(2.47)

is received. In Eq. (2.47), \( \xi \) is the clutter component and can be subtracted
out using Eq. (2.11). Thus, for all elements in Array A, the matrix

\[
Z(\omega_q) = k_q K_t^T(\omega_q) K_c^{-T}(\omega_q) F^*(\omega_q)
\]  

(2.48)

denotes the signal received at Array A.

(iv) Time Reversal Target Focusing (A → B): The backscatters received in the
previous step at Array A contains backscatters from the target plus noise.
The reflections from the clutter are eliminated by applying the reshaping
filter. Applying time reversal on \(Z(\omega_q)\) and retransmitting them from Array
A, the focusing happens on the target only. Thus, the final observations made
at Array B is given by

\[
r_p(\omega_q) = [K_t(\omega_q) + K_c(\omega_q)] [z_p(\omega_q)]^*
\]

(2.49)

\[
= [K_t(\omega_q) + K_c(\omega_q)] \left[ k_q K_t^H(\omega_q) K_c^{-H}(\omega_q) e_p F(\omega_q) \right]
\]

\[
= k_q K_t(\omega_q) K_t^H(\omega_q) K_c^{-H}(\omega_q) e_p F(\omega_q)
\]

\[
+ k_q K_c(\omega_q) K_t^H(\omega_q) K_c^{-H}(\omega_q) e_p F(\omega_q).
\]

Note that Term 2 is the clutter component and can be subtracted out. Therefore,
the target component is given by Term 1 as

\[
r_p^{(t)}(\omega_q) = k_q K_t(\omega_q) K_t^H(\omega_q) K_c^{-H}(\omega_q) e_p F(\omega_q),
\]  

(2.50)
Organizing \( r_p^t (\omega_q) \) for all antennas in Array A, \((p = 1, \ldots, P)\), in an \( N \times N \) matrix \( M^B \), yields

\[
M^B (\omega_q) = [r_1^t (\omega_q), \ldots, r_P^t (\omega_q)] = k_q K_t (\omega_q) K^H_t (\omega_q) K^{-H}_c (\omega_q).
\]  

(2.51)

which contains the reflected focused energy from the target received at Array B. Note that Eq. (2.51) is the result of two time reversal steps (Step 3 and 4), which initially started at Array B and also ended at Array B. By changing the order of antennas with Step 3 starting at Array A and Step 4 ending at Array A, the processing yields

\[
M^A (\omega_q) = k_q K^T_t (\omega_q) K^*_t (\omega_q) K^{-*}_c (\omega_q),
\]

(2.52)

provided the medium is reciprocal with \( K_c (\omega_q) \) observed at Array A equal to \( K_c (\omega_q) \) observed at Array B.

(v) **Image Formation**: Unlike DSBF and DS/MUSIC imaging algorithms, the TRAIC algorithm has two beams \( M^B (\omega_q) \) and \( M^A (\omega_q) \). Using the beamforming concept for array imaging, two weighing vectors are defined for \( M^B (\omega_q) \) and \( M^A (\omega_q) \) each during the transmission and receiving steps. For location \( x \), the focused beams are, therefore, given by

\[
Y^B (x; \omega_q) = w_{rB}^H (x; \omega_q) M^B (\omega_q) w_{tB} (x; \omega_q)
\]

(2.53)

\[
Y^A (x; \omega_q) = w_{rA}^H (x; \omega_q) M^A (\omega_q) w_{tA} (x; \omega_q)
\]

(2.54)
where $w_{rB}(\omega_q)$ and $w_{rA}(\omega_q)$ are, respectively, the receiving weight vectors for $M^B(\omega_q)$ and $M^A(\omega_q)$ beams. Similarly, $w_{tB}(\omega_q)$ and $w_{tA}(x;\omega_q)$ are the transmittinf weight vectors for $M^B(\omega_q)$ and $M^A(\omega_q)$, respectively. Using triangulation, the pseudospectrum expression for each pixel, i.e. spatial location $x_i$, is defined as

$$I_{TRAIC/TRBF}(x_i) = \sum_{q=1}^{Q} |Y^A(x;\omega_q) Y^B(x;\omega_q)|^2. \quad (2.55)$$

Expanding Eqs. (2.51) and (2.52), and using the Cauchy-Schwartz inequality for maximizing (2.53) in terms of the weighting vectors, gives

$$w_{rB}(x;\omega_q) = \frac{g_B(x;\omega_q)}{\|g_B(x;\omega_q)\|}.$$ \quad (2.56)

$$w_{tB}(x;\omega_q) = \frac{K_{c}^{-1}(\omega_q) g_B(x;\omega_q)}{\|K_{c}^{-1}g_B(x;\omega_q)\|}.$$ \quad (2.57)

$$w_{rA}(x;\omega_q) = \frac{g_A(x;\omega_q)}{\|g_A(x;\omega_q)\|}.$$ \quad (2.58)

and

$$w_{tA}(x;\omega_q) = \frac{K_{c}^{-T}(\omega_q) g_A(x;\omega_q)}{\|K_{c}^{-T}g_A(x;\omega_q)\|}.$$ \quad (2.59)

Based on the aforementioned description, the main steps involved in the TRAIC/TRBF algorithm are summarized in Table 2.3.

### 2.5.3 TRAIC/MUSIC Array Imaging Algorithm

Recall that the MUSIC algorithm requires the number of receivers to be greater than the number of backscatters (targets plus clutter sources) embedded in the
Algorithm TRIAC/TRBF ([in] $K_{c+t}$, $K_c$, [out] $I_{TRAIC/TRBF}$)

$I_{TRAIC}(x) = 0$

For all $1 \leq q \leq Q : \quad \omega_q = \omega_0 + q\Delta\omega$

Calculate $K_t(\omega_q) = K_{c+t}(\omega_q) - K_c(\omega_q)$

Calculate $k_q = \left(\| \left( K_c^T(\omega_q) K_c(\omega_q) \right)^{-1} \right)_F^{-1}$

Calculate $M_B(\omega_q) = k_q K_t(\omega_q) K_c H(\omega_q) K_c^{-H}(\omega_q)$

Calculate $M_A(\omega_q) = k_q K_t^T(\omega_q) K_c^*(\omega_q) K_c^{-*}(\omega_q)$

For all image pixels $x$

Calculate $g_B(x, \omega_q)$ and $g_A(x, \omega_q)$ for pixel $x$

Calculate $w_{rB}(x; \omega_q) = \frac{g_B(x; \omega_q)}{\|g_B(x; \omega_q)\|}$

Calculate $w_{tB}(x; \omega_q) = \frac{K_c^{-1}(\omega_q) g_B(x; \omega_q)}{\|K_c^{-1}g_B(x; \omega_q)\|}$

Calculate $Y^B(x; \omega_q) = w_{rB}(x; \omega_q) M_B(\omega_q) w_{tB}(x; \omega_q)$

Calculate $w_{rA}(x; \omega_q) = \frac{g_A(x; \omega_q)}{\|g_A(x; \omega_q)\|}$

Calculate $w_{tA}(x; \omega_q) = \frac{K_c^{-T}(\omega_q) g_A(x; \omega_q)}{\|K_c^{-T}g_A(x; \omega_q)\|}$

Calculate $Y^A(x; \omega_q) = w_{rA}(x; \omega_q) M_A(\omega_q) w_{tA}(x; \omega_q)$

$I_{TRAIC}(x) = I_{TRAIC}(x) + \left| Y^A Y^B \right|^2$

End For

End For

Table 2.3: The TRAIC/TRBF algorithm.
reference medium. Satisfying this condition is almost impossible in an inhomogeneous medium. Since the TRAIC algorithm removes the effect of the clutter, it can, therefore, be applied before the MUSIC algorithm thus relaxing the condition on the number of elements in the receiver array. The resulting algorithm is referred to as the TRAIC/MUSIC array imaging algorithm, where the number of receiving array elements should only exceed the number of targets. The number of clutter sources are no longer significant. The TRAIC/MUSIC algorithm uses the outputs $M^B(\omega_q)$ and $M^A(\omega_q)$ of Step 4 instead of $K_t(\omega_q)$ as input to the MUSIC algorithm. Performing an eigenvalue decomposition on $M^B(\omega_q)$ and $M^A(\omega_q)$ on Eq. (2.21), yields

$$M^B(\omega_q) = \begin{pmatrix} U^B_t(\omega_q) & U^B_n(\omega_q) \end{pmatrix} \begin{pmatrix} \Gamma^B_t(\omega_q) & 0 \\ 0 & \Gamma^B_n(\omega_q) \end{pmatrix} \begin{pmatrix} V^B_t(\omega_q) \\ V^B_n(\omega_q) \end{pmatrix}$$

and

$$M^A(\omega_q) = \begin{pmatrix} U^A_t(\omega_q) & U^A_n(\omega_q) \end{pmatrix} \begin{pmatrix} \Gamma^A_t(\omega_q) & 0 \\ 0 & \Gamma^A_n(\omega_q) \end{pmatrix} \begin{pmatrix} V^A_t(\omega_q) \\ V^A_n(\omega_q) \end{pmatrix},$$

where the signal space (spanned by $U^A_t(\omega_q)$ and $U^B_t(\omega_q)$) and the nullspace (spanned by $U^A_n(\omega_q)$ and $U^B_n(\omega_q)$) are determined by looking at the nonzero eigen values. As in Eqs. (2.25) and (2.26), two beams are formed as follows

$$\Im^B(x; \omega_q) = \frac{1}{\| g^H_B(x; \omega_q) U^B_n(\omega_q) \|^2 / \| g_B(x; \omega_q) \|^2}$$

(2.62)
Based on Eqs. (2.62) and (2.63), the pseudospectrum at location $x$ is given by

$$I_{TRAIC/MUSIC} (x) = \frac{1}{Q} \prod_{q=1}^{Q} \Xi^B (x; \omega_q) \Xi^A (x; \omega_q),$$

where the first $M$ peaks correspond to the locations of the targets. The TRAIC/MUSIC algorithm is summarized in Table 2.4.

### 2.6 Summary

In this chapter, I covered two categories (Conventional and TR) of array imaging localization algorithms. For each category, I presented two representative algorithms.

For conventional array imaging, DSBF and DS/MUSIC were described. As representative of the TR approaches, TRAIC and TRAIC/MUSIC were covered. I showed that the conventional array imaging algorithms are applicable when the medium under investigation is uniform and stable, i.e., there is minimal multipath effect. If the medium is inhomogeneous and random, TR approaches have advantages over conventional approaches used to localize targets because of the super resolution focusing phenomena of TR. In Chapter 4, I show the superiority of TR algorithms over conventional algorithms in the context of localizing breast cancer tumours by running different electromagnetic simulations. To run these simulations, I will require an electromagnetic (EM) model of the human breast. The EM
Algorithm TRAIC/MUSIC ([in] $K_{c+t}$, $K_c$, [out] $I_{TRAIC/MUSIC}$)

$I_{TRAIC/MUSIC}(x) = 0$

For all $1 \leq q \leq Q$ : $\omega_q = \omega_0 + q\Delta\omega$

Calculate $K_t(\omega_q) = K_{c+t}(\omega_q) - K_c(\omega_q)$

For all image pixels $x$

- Calculate $g_B(x, \omega_q)$ and $g_A(x, \omega_q)$ for pixel $x$
- Calculate $[U\Sigma V^*] = SVD(M_B(\omega_q))$
- Find the break point in $\Sigma$ and separate the null space $U_n^B(\omega_q)$ in $U$
- Calculate $[U\Sigma V^*] = SVD(M_A(\omega_q))$
- Find the break point in $\Sigma$ and separate the null space $U_n^A(\omega_q)$ in $U$
- Calculate $\mathcal{A}^B = \frac{1}{\|g_B(x, \omega_q)U_n^B(\omega_q)\|^2 + \|g_B(x, \omega_q)\|^2}$
- Calculate $\mathcal{A}^A = \frac{1}{\|g_A(x, \omega_q)U_n^A(\omega_q)\|^2 + \|g_A(x, \omega_q)\|^2}$

$I_{TRAIC/MUSIC}(x) = I_{TRAIC/MUSIC}(x) + (\mathcal{A}^A\mathcal{A}^B)$

End For

$I_{TRAIC/MUSIC}(x) = \frac{I_{TRAIC/MUSIC}(x)}{Q}$

End For

Table 2.4: The TRAIC/MUSIC algorithm.
model is derived using finite difference time domain (FDTD) discretization, which is described in the next chapter. Although TR approaches are more sophisticated, they are not directly applicable for breast cancer detection. These algorithm assumes that the clutter multistatic matrix $K_c(\omega_q)$ can be estimated from a training step. In breast cancer prognostics, which typically covers months if not years, estimating $K_c(\omega_q)$ is difficult since the medium (breast tissues) changes over time. In the next chapter, I present a new algorithm to predict $K_c(\omega_q)$ directly from $K_{c,t+\ell}(\omega_q)$ without requiring a training step.
3 Estimating Tumor Response

3.1 Introduction

Microwave breast array imaging is a promising procedure for detecting breast cancer tumours [4,17,34–38]. The procedure involves illuminating the patient’s breast with an electromagnetic wave referred to as the probing signal. Generally, when an electromagnetic wave passes through a lossless medium, it undergoes changes due to four different phenomena: refraction, reflection, diffraction, and scattering. Most electromagnetic array imaging algorithms rely on the differences between the dielectric properties of the tumour cells and its surrounding normal tissues. Consequently, the probing signal undergoes a different set of changes when it propagates through the tumour cells as compared to the propagation in the healthy tissues. In X-ray imaging, for example, electromagnetic waves are blocked by the tumour cells. The tumour can, therefore, be identified as a white spot observed in the output image. Microwave imaging uses the phenomena of scattering instead. As a probing signal propagates through a medium, it may collide to an object whose
dimensions are considerably less than its wavelength. In such cases, the probing signal changes its trajectory by an angle that does not follow the rules of reflection [39, 40]. In optics, this phenomena is referred to as scattering. For different media, the source of scattering may be different. In human tissues, for example, the source of scattering is related to the inhomogeneity of the tissue. Inhomogeneity in physical terms means having different dielectric constants within the medium. In other words, different tissues within an organ have different dielectric constants and they are the cause of a scattering once an electromagnetic wave travels through the medium. The breast malignant tumour is a strong source of scattering for microwave signals because its dielectric constant is significantly different from that of the normal breast tissues in the human breast. These scattering waves bounce of other inhomogeneities as well and the resulting backscatters are recorded by the receivers. Consequently, the drawback of scattering is multipath reception at the receivers. As discussed in the previous chapter, time reversal takes advantage of the multipath phenomena to focus the probing signal and is, therefore, useful for breast cancer detection.

In order to run the TR algorithms for breast tumour detection, the breast tissue is illuminated with a probing pulse. A receiving array records the backscatters resulting from tumour and other inhomogeneities in the breast. Ideally, this process is completed on the patient with a real antenna array illuminating the patient’s
breast. Because of the intrusive nature of the procedure, the thesis proposes electromagnetic simulations based on the MRI of the breast as discussed next. First, the MRI is used to derive the electromagnetic properties of a patient breast. A simulated antenna array probes the breast with an electromagnetic signal and the backscatter observations recorded at the antenna array are used to estimate the location of the tumour. Since the propagation of the electromagnetic waves is based on the Maxwell equations, I use finite difference time domain (FDTD) approximation to simulate the electromagnetic propagation. The backscatters observed at the antenna array contains both the tumour response as well as the response from inhomogeneities such as the skin. In terms of our notation, the backscatter observed at the antenna array is given by $K_{c+t}(ω_q)$ and includes both the tumour and clutter (other inhomogeneities including skin) responses. In order to run an array imaging algorithm, we need to isolate the tumour response $K_t(ω_q)$ and the clutter response $K_c(ω_q)$ from the mixed response $K_{c+t}(ω_q)$. In this chapter, I discuss three different algorithms (matched filter algorithm, the data adaptive filter algorithm, and a new algorithm, the data adaptive filter/envelope detection filter (DAF/EDFF)) to estimate the multistatic clutter response $K_c(ω_q)$ and the multistatic tumour $K_t(ω_q)$ from the mixed response. Comparing the performance of the three algorithms, I show that the proposed DAF/EDF algorithm can successfully separate the two components from the mixed backscatter observation.
This chapter is organized as follows. Section 3.2 reviews the FDTD procedure used to simulate electromagnetic propagation in the human breast. The section also discusses the method used to derive the electromagnetic properties of the patient’s breast from a magnetic resonance image (MRI) taken from a real patient. In Section 3.3, the matched filter, the data adaptive filter, and the DAF/EDF algorithms are used to derive the target and clutter response from the mixed response are discussed. Finally, Section 3.4 concludes the chapter.

3.2 Electromagnetic Model for the Human Breast

In Subsection 3.2.1, I introduce the FDTD approach used to discretize the Maxwell equations for numerical solutions. In addition, I present a procedure used to derive realistic 2D electromagnetic properties of a human breast from an MRI of a real patient. The electromagnetic properties used in the FDTD simulations are the permeability, permittivity, and conductivity of the breast tissues defined on a 2D discretized domain.

3.2.1 Finite Difference Time Domain (FDTD) method

The Maxwell equations [1,41,42] are a set of four fundamental equations governing the behaviour of electric and magnetic fields including their propagations in matter and space. In a linear, isotropic, and nondispersive media, (i.e., materials having
Figure 3.1: The Yee cell [1] used in the FDTD simulations.
field-independent, direction-independent, and frequency independent electric and magnetic properties), the Maxwell equations are given by

\[ \frac{\partial \vec{B}}{\partial t} = -\nabla \times \vec{E} - \vec{J}_m, \]  
\[ \frac{\partial \vec{D}}{\partial t} = \nabla \times \vec{H} - \vec{J}_e, \]  
\[ \vec{B} = \mu \vec{H}, \]  
and \[ \vec{D} = \epsilon \vec{E}, \]

where \( \vec{B} \) is the magnetic field density in Webers per square meter, \( \vec{E} \) is the electric field intensity in Volts per meter, \( \nabla \) is the curl operator, \( \vec{D} \) is the electric displacement field in dielectric (flux density in free space), \( \vec{H} \) is the magnetic field intensity in Amperes per meter, \( \vec{J}_m \) is the equivalent magnetic conduction current density in Volts per square meter, \( \vec{J}_e \) is the current density in Amperes per square meter, and \( \mu \) and \( \epsilon \), respectively, denote the permeability in Henry per meter and permittivity in Farad per meter of the medium. Note that both \( \mu \) and \( \sigma \) are functions of space, time, and frequency. The current density \( \vec{J}_e \) is calculated using the expression

\[ \vec{J}_e = \sigma \cdot \vec{E}, \]

where \( \sigma \) denotes the electrical conductivity in Siemens per meter of the discretized medium at a specific frequency.

The discretized grid at site \((i, j, k)\) used in the FDTD simulations is shown in Fig. 3.1, which is commonly referred to as the Yee cell. The three components
\{H_x, H_y, H_z\} of the magnetic fields are defined at the center of the cube, while the electric fields components \{E_x, E_y, E_z\}, are defined along the edges. For the Yee cell, the curl operator is defined as

\[
\frac{\partial H_x}{\partial t} = \frac{1}{\mu} \left( \frac{\partial E_y}{\partial z} - \frac{\partial E_z}{\partial y} - J_{m,x} \right), \tag{3.6}
\]

\[
\frac{\partial H_y}{\partial t} = \frac{1}{\mu} \left( \frac{\partial E_z}{\partial x} - \frac{\partial E_x}{\partial z} - J_{m,y} \right), \tag{3.7}
\]

\[
\frac{\partial H_z}{\partial t} = \frac{1}{\mu} \left( \frac{\partial E_x}{\partial y} - \frac{\partial E_y}{\partial x} - J_{m,z} \right), \tag{3.8}
\]

\[
\frac{\partial E_y}{\partial t} = \frac{1}{\varepsilon} \left( \frac{\partial H_z}{\partial x} - \frac{\partial H_x}{\partial y} - \sigma E_x \right), \tag{3.9}
\]

\[
\frac{\partial E_x}{\partial t} = \frac{1}{\varepsilon} \left( \frac{\partial H_y}{\partial z} - \frac{\partial H_z}{\partial x} - \sigma E_y \right), \tag{3.10}
\]

and

\[
\frac{\partial E_z}{\partial t} = \frac{1}{\varepsilon} \left( \frac{\partial H_x}{\partial y} - \frac{\partial H_y}{\partial x} - \sigma E_z \right). \tag{3.11}
\]

My electromagnetic FDTD simulations of the human breast makes the following realistic assumptions.

(i) The magnetic current density components \( J_{m,x} = J_{m,y} = J_{m,z} = 0 \) within the human breast. In my experiments, the probing signal results from an electric current in an element of the antenna array. The current induces a magnetic field that propagates through the tissues. Because tissues are dielectric in nature, the strength of the conduction current induced by the magnetic field is extremely small and negligible. This assumption simplifies Eqs. (3.6)-(3.8).

(ii) A 2D model is used in the FDTD simulations. A consequence of the 2D sim-
ulation is that only three equations (depending on the mode of the simulation as described later) completely define the model. The functions \( \mu, \epsilon, \) and \( \sigma \) are also reduced to two dimensions.

(iii) The probing signal occupies a frequency band in which the electromagnetic constants, \( \mu, \epsilon, \) and \( \sigma, \) of the human breast tissues are relatively constant. As a result, the electromagnetic constants are frequency independent in our model.

(iv) Although the human breast tissues change significantly with time, the electromagnetic properties of the human breast are assumed to be statistically invariant. Thus \( \mu, \epsilon, \) and \( \sigma \) vary spatially but do not vary in time such that their partial derivatives with respect to time are zero.

Based on these realistic assumptions, three 2D models representing the values of \( \mu, \epsilon, \) and \( \sigma \) across the breast tissues are sufficient to describe the electromagnetic properties of a human breast.

A 2D FDTD simulation can be run in one of the two modes: (i) Transverse Electric (TE) mode, or, (ii) Transverse Magnetic (TM) mode. Each of the mode is described next with respect to Fig. 3.1. In the TE mode, the probing signal is in a form of magnetic field \( \mathbf{H}_z \) along the \( z \) axis inducing the electric field components \( \mathbf{E}_x, \mathbf{E}_y \) within its cell. The induced components in turn induce a magnetic field \( \mathbf{H}_z \)
in the neighboring cells. The process repeats itself leading to the propagation of
electromagnetic wave. In the TE mode, Maxwell equations are reduced [41] to

\[
\frac{\partial E_x}{\partial t} = \frac{1}{\epsilon} \left( \frac{\partial H_z}{\partial y} - \sigma E_x \right), \quad (3.12)
\]
\[
\frac{\partial E_y}{\partial t} = \frac{1}{\epsilon} \left( -\frac{\partial H_z}{\partial x} - \sigma E_y \right), \quad (3.13)
\]
and
\[
\frac{\partial H_z}{\partial t} = \frac{1}{\mu} \left( \frac{\partial E_x}{\partial y} - \frac{\partial E_y}{\partial x} \right). \quad (3.14)
\]

Note that the above representation of the Maxwell equations in the TE mode is
valid only if the stationary assumption (item 4) and the frequency independence
assumption (item 3) are valid.

In the TM mode, the probing signal takes the form of electrical current \( E_z \) along
the \( z \) direction. Electromagnetic components \( H_z = E_x = x_y = 0 \) and, therefore,
the Maxwell equations are reduced to

\[
\frac{\partial H_x}{\partial t} = \frac{1}{\mu} \left( -\frac{\partial E_z}{\partial y} \right), \quad (3.15)
\]
\[
\frac{\partial H_y}{\partial t} = \frac{1}{\mu} \left( \frac{\partial E_z}{\partial x} \right), \quad (3.16)
\]
and
\[
\frac{\partial E_z}{\partial t} = \frac{1}{\epsilon} \left( \frac{\partial H_y}{\partial x} - \frac{\partial H_x}{\partial y} - \sigma E_z \right). \quad (3.17)
\]

A simulation may choose either of the two modes to simulate the electromagnetic
wave propagation through a medium. In my simulations, I used the TM mode
for simulating propagation of an electromagnetic field through an electromagnetic
breast model since it is easier to generate and control an electrical current as the
probing signal. The resulting magnetic field propagates through the breast tissues. Backscatters of the magnetic field resulting from inhomogeneities and tumour reach the receiving antenna array and are induce electrical currents in the elements of the receiving antenna array, which are recorded as observations. In other words, I model the cross section between the transmitters and receivers from an MRI, excite the medium with an electrical current, which induces a magnetic field in the breast. Finally, we note that the permeability $\mu$ is almost constant throughout the breast tissues, therefore, the TM equations can be further simplified if needed.

### 3.2.2 Building an Electromagnetic Human Breast Model

In this subsection, we describe a procedure [4, 14, 17, 34] to derive an EM model from an MRI of the human breast. Based on the TM mode (Eqs. (3.15)-(3.17)) and Assumptions 1-4, presented in Subsection 3.2.1, the electromagnetic parameters, $\mu$, $\epsilon$, and $\sigma$ are all spatial functions and time independent. To model a cross section of the human breast based on Fig. 3.2, these functions should be defined for every anatomical location (disretized site) in the breast model. A 2D EM human breast model, therefore, consists of three metrics: the relative permeability $\mu_r$, relative permittivity $\epsilon_r$, and electrical conductivity $\sigma$. Since $\mu$ and $\epsilon$ are numerically very small, they are usually compared with their corresponding free space constants $\mu_0$ and $\epsilon_0$. By dividing $\mu$ and $\epsilon$ with $\mu_0$ and $\epsilon_0$, respectively, relative permeability $\mu_r$
and relative permittivity $\varepsilon_r$ are calculated.

For a 2D anatomical representation of the human body, one of the several different cross sections: sagittal, cronal, and transverse, may be used. Either of these anatomical cross sections can be used as a reference for the EM human breast model. Having selected a cross section, multiple 2D models at different depths are developed to cover the entire breast. In this thesis, I use the sagittal cross section. An example illustration of the sagittal cross section is included in Fig. 3.2. The advantage of using the sagittal cross section is that it shows the strong backscatter elements including skin and chest wall in one cross section. The drawback is that it results in the worst case multipath scenario, which is close to the scattering situation in real life. To make the EM model realistic, an MRI of a real patient taken in the sagittal cross section is used. The MRI technique depicts the density of Hydrogen atoms due to water concentration in tissues and their resonance frequencies as pixel intensity values [43]. We also know [44] that the density of the Hydrogen atoms and the resonance frequencies of tissues are directly related to the dielectric constant $\varepsilon$ and conductivity $\sigma$ of the human tissues (Fig. 3.3), where bright pixels represent higher permittivity $\varepsilon$ and conductivity $\sigma$ compared to the surroundings. Thus an MRI can be used for a one to one relationship for both permittivity $\varepsilon$ and conductivity $\sigma$. Although an MRI shows the variability of permittivity and conductivity in a human tissue, the actual values for these electromagnetic proper-
Figure 3.3: An example MRI of a normal human breast.
Figure 3.4: Variations in the values of: (a) the average relative permittivity, and; (b) the average conductivity of normal and malignant tissue in the frequency range 0.5 GHz to 30 GHz as reported in [3].
ties for each anatomical location is not revealed by the MRI. Several investigations
have been done for determining the actual values for electromagnetic properties of
the human breast tissues and malignant tumours at different frequencies [3,45–48].
These investigations show that the average relative permeability $\mu_r$ of the human
breast tissues and malignant tumours are both equal to 1. As a result, the matrix
representing relative permeability $\mu_r$ is 1 for all sites in the discretized cross section.
Values for average relative permittivity and conductivity shown in Fig. 3.4 are used
to build the EM model. In my experiments, the selected bandwidth for the probing
signal is 8GHz to 10GHz where the relative permittivity $\epsilon_r$ and conductivity $\sigma$ are
both constant in normal and as well as malignant tissues, but the absolute difference
between the permittivity of the normal and malignant tissues is at is maximum.
Since the source of scattering in the breast tissues is the variability of permittivity,
differences in the permittivity of the normal and malignant tissues enables us to
differentiate the malignant tumour from the normal cells. As a result, both $\epsilon_r$ and
conductivity $\sigma$ are defined spatially and assumed to be independent of frequency.
Table 3.1 summarizes the main steps involved in computing the electromagnetic
properties of the human breast based on an MRI. We assume that the space out-
side of the breast tissue is filled with a lossless fluid with a relative permittivity
values equal to the average relative permittivity $\bar{\epsilon}_r$ in the selected bandwidth in the
EM model. Because the relative permittivity $\epsilon_r$ values of the skin and chest wall
are not represented clearly in MRI, the above procedure successfully produces an EM model for the breast tissues only. The corresponding values for the skin and chest wall are introduced manually based on their anatomical position represented in Fig. 3.2. The values for relative permittivity and the conductivity of the skin and chest wall are based on [49].

3.2.3 Building a Perfectly Matched Layer (PML)

In a real world situation, an EM wave continues to propagate across a large distance until it is completely absorbed by the environment. The EM breast model contains a finite 2D medium. If the EM field is terminated outside the medium, the propagating waves at the border of the 2D EM model are reflected back into the medium and introduce unwanted interferences with the backscatter reflected from the tumour. We introduce absorbing boundary conditions (ABC) in the EM breast model to simulate an infinite propagation of the EM wave. Numerous algorithms [1, 42] have been proposed to define the ABC. One of the best method to implement the ABC is the perfectly matched layer (PML) approach [50, 51] for EM waves. The design of the algorithm is based on the reflection parameter

\[ \Gamma = \frac{\eta_A - \eta_B}{\eta_A + \eta_B} \]  

(3.18)

where \( \eta_A \) and \( \eta_B \) are the impedances of medium A and B, respectively, across their boundary. In terms of the permeabilities \{\mu_A, \mu_B\} and permittivities \{\epsilon_A, \epsilon_B\}, the
Given an MRI \( I(m, n) \) of a human breast with \( N \) pixels \( (m, n \in \mathbb{N}) \).

1. Calculate sum \( S \) of the intensity values of the \( N \) pixels within the breast.

2. Select signal with bandwidth over which the relative permittivity \( \epsilon_r \) and conductivity \( \sigma \) are fairly constant.

3. Using Fig. 3.4, calculate the average relative permittivity \( \bar{\epsilon}_r \) and conductivity \( \bar{\sigma} \) in the selected bandwidth for normal breast tissues.

4. Calculate the transformation coefficients for both relative permittivity \( \epsilon_r \) and conductivity \( \sigma \) as follows

\[
k_{\epsilon_r} = \frac{N \bar{\epsilon}_r}{S}, \quad k_{\sigma} = \frac{N \bar{\sigma}}{S}.
\]

5. Compute the relative permittivity matrix \( P(m, n) \) and conductivity matrix \( C(m, n) \) for the breast tissues \( m, n \in \mathbb{N} \) based on the transformations

\[
P(m, n) = k_{\epsilon_r} \times I(m, n) \quad \text{and} \quad C(m, n) = k_{\sigma} \times I(m, n).
\]

6. For matrix \( \epsilon_r \) outside of the breast tissue, set all values to \( \bar{\epsilon}_r \).

7. For matrix \( \sigma \) outside of the breast tissue, set all values to 0.

8. Insert manually the values of the relative permittivity and conductivity corresponding to the skin and chest wall in both matrices \( P \) and \( C \).

**Table 3.1:** Procedure used to derive the EM properties for the human breast from an MRI. The EM breast model is used in our FDTD simulations.
impedances are given by
\[ \eta_A = \sqrt{\frac{\mu_A}{\epsilon_A}}, \quad \text{and} \quad \eta_B = \sqrt{\frac{\mu_B}{\epsilon_B}}. \] (3.19)

To prevent reflections from the boundaries, $\Gamma$ is kept at zero 0 implying that the impedances of two medium should be the same. In other words, we introduce a new medium at the boundaries by increasing the relative permeability $\mu_B$ and permittivity $\epsilon_B$ such that its ratio is constant and equal to $\eta_A$. In this situation, no EM wave is reflected back into the medium defined by the breast model. But still some EM waves may propagate into the new medium introduced at the boundary. By gradually increasing the conductivity $\sigma$ in medium B, the EM wave is absorbed gradually with no reflections from the boundaries.

### 3.3 Estimating the Tumor Response without Training

The backscatter observations recorded at the antenna array contains reflections from both target (tumour) and clutter (skin and other inhomogeneities present in the breast). As previously discussed, one method useful for removing the effect of clutter in the mixed response is based on background subtraction

\[ k_t[n] = k_{c+t}[n] - k_c[n]. \] (3.20)

In Eq. (3.20), the clutter response $k_c[n]$ is obtained by introducing a training step where the target is not present and the mixed (clutter and target) response $k_{c+t}[n]$ is
recorded at the examination time. Assuming a linear system, the target response is then obtained by subtracting the clutter response from the mixed response. Fig. 3.5 illustrates the background subtraction step through a real example of a patient diagnosed with breast cancer.

For human breast examinations, successive MRIs are typically separated by days, if not months. Over time, not only the breast tissues change in composition but keeping the breast shape same for two MRIs is impossible. Therefore, the background subtraction procedure introduces unwanted distortions in the target response. In such cases where the training step is not useful, e.g., in breast cancer detection, the clutter response $k_c[n]$ is unknown. A possible solution to this problem is to design a filter $h[n]$ that isolates the target and clutter responses from the overall response. The ultimate goal of a filter is to extract the target response $k_t[n]$ from the mixed response $k_{c+t}[n]$ because the target response can be estimated relatively easily than the clutter response. If the filter successfully extracts the target response, Eq. (3.20) can be used to calculate the background response to be used if needed. To decompose the mixed response $k_{c+t}[n]$ to the target response $k_t[n]$ and the clutter response $k_c[n]$ without a training step, I present three different filtering algorithms, namely the matched filter, data adaptive filter, and data adaptive filter/envelope detection filter (DAF/EDFF), which are discussed next.
Figure 3.5: An example of the direct subtraction procedure for the breast model shown in Fig. 3.11a: (a) Waveform for the mixed response; (b) Waveform for the clutter response obtained during the training step, and; (c) Estimated target response derived by subtracting subplot (b) from subplot (a) based on Eq. (3.20).
3.3.1 The Matched Filter

In signal processing, a matched filter is used to detect the presence (or absence) of a known signal within a noisy observation. My experiments show that the shape of the target response in the time domain, specially around the peak in a particular temporal window, is very much alike the initial clutter response resulting due to skin (Fig. 3.5). This observation complies with the results reported in [52]. As such, the signature response for the tumour can be identified by extracting the mixed portion of the mixed response due to skin. Following the Matlab notation, assume $k_{c+t}[n]$ represent the mixed signal recorded at element $i$ of the receiving antenna array (Array B), then the target signature signal (TSS) used to identify the target response within the mixed response and is given by

$$\vartheta = [a, b] \land r[n] = k_{c+t}^{(i)}[a : b], \quad (3.21)$$

where $\vartheta$ is a defined window around the peak of the mixed recorded signal $k_{c+t}^{(i)}$. Within the time index ($a \leq n \leq b$), it resembles the target response. Generally,
the best candidate for selecting $k_{c,t}^{(i)}$ is the middle receiver but ultimately the selection is dependent on the geometry of receivers. The window parameters, $a$ and $b$, are derived experimentally. Note that the TSS may instead be estimated using other approaches. For example, a tumour can be modeled and inserted into a homogeneous breast tissue without skin and chest wall. In this case, the recorded backscatter may be used as the TSS.

Without loss of generality, the following steps describe the algorithm used to extract the tumour response from a received backscatter in Array B while one of the elements in Array A probes the human breast tissue. Because the $i^{th}$ receiver is chosen as the reference signal, there are $N - 1$ unknown signals. For each received signal, a matched filter is run to find the optimum match for the tumour response. The matching process for the reference signal may be expressed in terms of two parameters: scaling factor $\alpha$ and delay $\tau$ [52]. Assume a tumour exists in the breast tissue, therefore, each receiver in Array B receives the backscatters from the tumour with a different scaling factor $\alpha$ and delay $\tau$. Using TSS, the tumour signal $s_j[n]$ applied as input to the matched filter at the $j^{th}$ receiver is given by

$$s_j[n] = \alpha_j r[n - \tau_j].$$

(3.22)

The scaling factor $\alpha_j$ and time delay $\tau_j$ are dependent on the relative position of the tumour with respect to the transmitters and receivers and the size of the tumour and can be considered as random variables. Given an observation $x_j[n]$ at $j^{th}$ receiver
with no target present in the breast tissues, observations \( x_j[n] \) are different at all other receivers due to the variability in the skin and inhomogeneity of the breast tissue. The disparity \( \theta_j \) between all receivers is considered to be random and is given by

\[
\theta_j[n] = x_j[n] - x_0^j[n],
\]

(3.23)

where \( x_0^j[n] \) is a deterministic signal which corresponds to an estimation of the clutter response for the \( j^{th} \) receiver. Aligning and averaging over recorded backscatters is a crude solution for estimating \( x_0^j \). Thus, \( x_0^j[n] \) is the average of the random variable \( \theta_j[n] \). Making an assumption that \( \theta_j[n] \) has normal distribution, i.e., with \( \theta_j[n] \sim \mathcal{N}[x_0^j[n], \sigma^2 I_M] \), where \( M \) is number of samples in observation \( x_0^j[n] \), the probability density function (PDF) of \( \theta_j[n] \) is given by

\[
f(\theta_j[n]) = \prod_{n=1}^{M} \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_j[n]-x_0^j[n])^2}{2\sigma^2}}.
\]

(3.24)

Now assume that there is a tumour in the breast tissue. The tumour signal \( s_j[n] \) adds its own variability to observation \( x_j[n] \) and produces another random variable \( \theta_j'[n] \) given by

\[
\theta_j'[n] = x_j[n] - (x_0^j[n] + s_j[n]).
\]

(3.25)

Note that the average of random variable \( \theta_j'[n] \) is \( (x_0^j[n] + s_j[n]) \), which is assumed
to have a normal distribution \( (\theta_j'[n] \sim \mathcal{N}[x_j^0[n] + s_j[n], \sigma^2 I_M] ) \) with the PDF

\[
f(x_j[n], s_j[n]) = \prod_{n=1}^{M} \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x_j[n]-x_j^0[n]-s_j[n])^2}{2\sigma^2}}. \tag{3.26}
\]

Conditional probability is used to estimate the probability of the presence of the tumour signal \( s_j[n] \) in observation \( x_j[n] \) using

\[
f(s_j[n]|\theta_j[n]) = \frac{f(\theta_j[n], s_j[n])}{f(\theta_j[n])}, \tag{3.27}
\]

where \( f(s_j[n]|\theta_j[n]) \) is the posterior PDF of \( s_j[n] \) given observation \( \theta_j[n] \), \( f(\theta_j[n]) \) is the PDF of the clutter backscatter in the absence of a target observed at the \( j^{th} \) element, and \( f(\theta_j[n], s_j[n]) \) is the PDF of the mixed response containing both the clutter and tumour backscatters. In other words,

\[
f(\theta_j[n], s_j[n]) = f(\theta_j'[n]). \tag{3.28}
\]

Substituting (3.28) in (3.27) and taking the natural logarithm of both sides in Eq. (3.27), yields

\[
\ln f(s_j[n]|\theta_j[n]) = \ln f(\theta_j'[n]) - \ln f(\theta_j[n]). \tag{3.29}
\]

Maximizing Eq. (3.29) is known as the maximum a posterior probability (MAP) estimate of \( s_j \) [53]. Replacing (3.24) and (3.26) in (3.29) yields the log-likelihood ratio as

\[
\max_{(\alpha_j, \tau_j)} L(x_j[n], s_j[n]) = \frac{1}{2\sigma^2} \sum_{n=1}^{M} (x_j[n] - x_j^0[n])^2 - (x_j[n] - x_j^0[n] - s_j[n])^2. \tag{3.30}
\]
Expanding (3.30) gives

\[
\max_{(\alpha_j, \tau_j)} L(x_j[n], s_j[n]) = \frac{1}{2\sigma^2} \sum_{n=1}^{M} 2s_j[n] \left( x_j[n] - x_j^0[n] \right) - s_j^2[n].
\] (3.31)

Note that \( L(x_j, s_j) \) is a correlation-type operation where \( \theta_j[n] \) is correlated with the tumour signal \( s_j[n] \). If the estimation of \( x_j^0[n] \) is optimum, \( \theta_j[n] \) in Eq. (3.31) has the most correlation with the tumour response \( s_j[n] \). Thus the algorithm is reduced to an optimization problem based on maximizing (3.31) over two parameters \( \alpha_j \) and \( \tau_j \) in \( s_j[n] \).

To maximize Eq. (3.31) first the delay \( \tau_j \) is found for an arbitrary scaling factor \( \alpha_j \) over the \( M \) sample space. For finding optimum scaling factor \( \alpha_j \) in a given expected range which is determined experimentally, the found optimum delay \( \tau_j \) is used in Eq. (3.31). Given optimum values for the delay \( \tau_j \) and scaling factor \( \alpha_j \), the target response is given by

\[
k_t^{(j)}[n] = \alpha_j k_{c+t}[n - \tau_j].
\] (3.32)

The algorithm is summarized in Table 3.2. Although (3.31) is designed to match the peak of \( L(x_j, s_j) \) with the the tumour response, it is possible that it also matches with the clutter. One way to eliminate this problem is to use the temporal correlation of the established peak with peaks of the observations made in the neighboring receivers. If the established peak is off the expected delay, the peak is ignored and the search for maximizing \( L(x_j, s_j) \) is continued. By comparing
Figure 3.7: The matched filter approach used to estimate the target response from the overall response for the $j^{th}$ receiver. The target signature signal is based on the $i^{th}$ receiver, where ($i \neq j$).
The Matched Filter Algorithm \( \left( [\text{in}]k_{c+t}[n], x^0[n] \right) [\text{out}] k_t[n] \)

1. For each transmitter do
2. Define \( a \) and \( b \), and then define the temporal window \( \vartheta = [a, b] \)
3. Select the \( i^{th} \) recorded response as the reference signal and define
   \[
   r[n] = k^{(i)}_{c+t}[a : b]
   \]
4. For each element \( j \) in Array B (using aligning, scaling, and averaging operations)
5. Define the target template signature as \( s_j[n] = \alpha_j r[n - \tau_j] \)
6. Maximize
   \[
   L(x_j[n], s_j[n]) = \frac{1}{2\sigma^2} \sum_{n=1}^{M} 2s_j[n] \left( x_j[n] - x^0_j[n] \right) - s^2_j[n]
   \]
   to find \( \alpha_j \) and \( \tau_j \)
7. If \( \alpha_j \) and \( \tau_j \) are not in the expected range, go to line 6
8. Calculate \( k^{(j)}_t[n] = \alpha_j k^{(i)}_{c+t}[n - \tau_j] \)
9. Calculate \( k^{(j)}_c[n] = \alpha_j k^{(j)}_{c+t}[n] - k^{(j)}_t[n] \)
10. End For
11. End For

Table 3.2: The matched filter approach used to estimate the tumour response from the mixed response.
the values of the scaling factor and delay for the neighboring receivers because of non-accurate clutter estimation $x_j^0$, the estimated $k_t^{(j)}[n]$ is not precise enough as an input for an array imaging algorithm. In addition, the size of the windows $\vartheta$ is depended on the location, size, and shape of the tumour and in a real life situation they can not be defined accurately without a training step.

3.3.2 The Data Adaptive Filter

The data adaptive filter (DAF) [36] provides another way to extract the tumour response $k_t[n]$ from the mixed response $k_{c+t}[n]$ in the discrete time domain. Generally, adaptive filters use their outputs as feedback to optimize their filter coefficients. The data adaptive filter is designed such that for every mixed recorded responses, it estimates the clutter response $k_c[n]$ due to skin, breast inhomogeneities, and chest wall using from the mixed response $k_{c+t}[n]$ (Fig. 3.8). The target response $k_t[n]$ can be obtained by subtracting the estimated clutter response $\hat{k}_c[n]$ from the mixed response $k_{c+t}[n]$.

Recall that one crude method [52] to estimate the clutter response in the matched filter algorithm was aligning, scaling and averaging all received signals recorded at different elements of the receiving array. To calculate a better estimate of the clutter response, the filter coefficients of DAF are calculated using the least mean square (LMS) method. Since the tumour backscatters as compared to the
skin responses have significantly lower energy, the LMS method is employed to minimize the difference among all the mixed responses. The algorithm for computing the filter coefficients from the mixed response is described next.

Assume that we want to remove the effect of clutter from the first mixed recorded response \( k_{c+t}[n] \) recorded at element 1 of the receiving array when the first transmitter probes the reference medium. To estimate the clutter response for element \( k \), the remaining responses \( k_{c+t}, \ldots, k_{c+t}^{(N)} \) are used. The data adaptive filter approach assumes a delay of \( J \) samples between the probing signal and clutter response recorded at the neighboring elements of the receiving array. The actual value of the delay \( J \) is determined experimentally. To estimate the clutter response in sample \( n \) of \( k_{c+t}[n] \), i.e. \( k_{c+t}^{(1)}[n] \), the following \( (N - 1) \) vectors of length \( (2J + 1) \) are defined as follows

\[
\forall \ 2 \leq i \leq N : \quad b_i[n] = \left[ k_{c+t}^{(i)}[n - J], \ldots, k_{c+t}^{(i)}[n], \ldots, k_{c+t}^{(i)}[n + J] \right]^T.
\] (3.33)

By concatenating all vectors \( b_i[n], 2 \leq i \leq N \), we get

\[
b_{2N}[n] = \left[ b_2^T[n], \ldots, b_N^T[n] \right]^T,
\] (3.34)

of length \( (N - 1)(2J + 1) \). By selecting the value of \( n \) appropriately, \( b_{2N} \) can be constructed such that it includes the clutter response primarily. The filter coefficients
of the DAF are obtained by solving the following minimization problem

$$\min_{\mathbf{q}_{2N}} \sum_{n=n_0}^{n_0+m-1} \left| \mathbf{k}_{c+i}^{(1)}[n] - \mathbf{q}_{2N}^T[n] \mathbf{b}_{2N}[n] \right|^2,$$

(3.35)

where \( \mathbf{q}_{2N}^T[n] \) for \((0 \leq n \leq (N - 1)(2J + 1) - 1)\), is the filter coefficient filter vector of the DAF. Note that the applied window \((n_0 \leq n \leq (n_0 + m - 1))\) is picked from a region within the mixed response, which constitute primarily of the clutter response. The duration of the window corresponds to the length of clutter response which is determined experimentally through a training step. The LMS solution [36] to the minimization problem is given by

$$\mathbf{q}_{2N} = \mathbf{R}^{-1}\mathbf{p},$$

(3.36)

where

$$\mathbf{R} = \frac{1}{m} \sum_{n=n_0}^{n_0+m-1} \mathbf{b}_{2N}[n] \mathbf{b}_{2N}^T[n],$$

(3.37)

and

$$\mathbf{p} = \frac{1}{m} \sum_{n=n_0}^{n_0+m-1} \mathbf{b}_{2N}[n] \mathbf{k}_{c+i}^{(1)}[n].$$

(3.38)

Since the recorded backscatters \( \mathbf{k}_{c+i}^{(1)}[n] \) with the selected range, \((n_0 \leq n \leq n_0 + m - 1)\), are very much alike at all receivers, matrix \( \mathbf{R} \) is ill-conditioned and, therefore, non-singular. The inverse of \( \mathbf{R} \) is computed from its \( s \) significant eigenvalues \( \lambda_i \) and the corresponding eigenvectors \( \mathbf{u}_i \) as follows

$$\mathbf{R}^{-1} = \sum_{i=1}^{s} \frac{1}{\lambda_i} \mathbf{u}_i \mathbf{u}_i^T.$$

(3.39)
The clutter artifacts due to skin, breast inhomogeneities, and chest wall can be removed from the $n^{th}$ sample in $k_{c+t}^{(1)}$ using

$$
\hat{k}^{(1)}_t[n] = k_{c+t}^{(1)}[n] - q_2^T[n]b_{2N}[n].
$$

Eq. (3.40) is applied to the entire mixed response $k_{c+t}^{(1)}[n]$ to extract the tumour response $\hat{k}^{(1)}_t[n]$. Note that the filter coefficients $q_2[n]$ are used for the entire mixed response.

The above algorithm is repeated for all mixed responses $k_{c+t}^{(i)}[n]$ recorded at different elements of the receiving array when successive elements of the transmitting array probes the medium. Likewise, the algorithm is repeated for all other transmitters-receivers pairs to estimate the target response for all pairs. Note that theoretically all filter coefficients $q_{2N}$ are calculated based on a temporal window $[n_0, \cdots, n_0 + m - 1]$ in which there is no tumour response. But practically the tumour backscatters have interfaces with clutter in the overall sample space and there is no distinct region where only the tumour backscatters is present. As a result, the filter coefficients $q_{2N}$ are fit on both the clutter and tumour backscatters. The level of disparity between the actual tumour backscatters $k_t^{(i)}[n]$ and its primary estimate $\hat{k}_t^{(i)}[n]$ depends on the relative energy of the clutter and the tumour backscatters in the defined temporal window $[n_0, \cdots, n_0 + m - 1]$. Based on this
fact, we decompose $k_{\text{c}+t}[n]$ and $b_{2N}[n]$ as

$$k_{\text{c}+t}[n] = k_{\text{c}}^{(1)}[n] + k_{t}^{(1)}[n] \quad (3.41)$$

and

$$b_{2N}[n] = b_{2N}[n] + b_{2N}[n], \quad (3.42)$$

where $k_{\text{c}}^{(1)}$ and $b_{2N}[n]$ are the clutter component and $k_{t}^{(1)}[n]$ and are target components of the respective signal. Substituting (3.41) and (3.42) in (3.40) yields

$$\hat{k}_{t}^{(1)}[n] = k_{c}^{(1)}[n] - q_{2N}^{T}b_{2N}[n] + k_{t}^{(1)}[n] - q_{2N}^{T}b_{2N}[n]. \quad (3.43)$$

If the temporal window $[n_0, \ldots, n_0 + m - 1]$ is chosen from some part that is related to the clutter and contains enough samples, the designed filter can successfully eliminate the effect of the clutter (i.e., Term 1 in (3.43) is nulled) and Eq. (3.43) is reduced to

$$\hat{k}_{t}^{(1)}[n] \approx k_{t}^{(1)}[n] - q_{2N}^{T}b_{2N}[n]. \quad (3.44)$$

As a result, $\hat{k}_{t}^{(1)}[n]$ is contaminated with the term $q_{2N}^{T}b_{2N}[n]$.

Although the design of this algorithm is sophisticated, there are some drawbacks with the proposed approach. Without a training step there is no way to define the temporal window $[n_0, \ldots, n_0 + m - 1]$ such that it corresponds only to clutter.

If the geometry of receivers related to the breast tissue is changed as is normally the case with a new patient being tested, we need to redo the training step. The second drawback is illustrated in Eq. (3.44), where the estimated target response
is contaminated due to the inability of the DAF approach to isolate a true clutter region. The authors [36] of the approach have suggested an additional step to eliminate these contamination but in our experiments, the results were not much improved. Blow I describe my approach based on data adaptive filter/envelope detection for isolating the target response from the mixed response.

### 3.3.3 The DAF/EDF algorithm

We have two ultimate goals for designing a filter. First, extract the tumour response $k_t$ from mixed response. Second, precise enough for array imaging algorithm to detect the location of the target and no need to have a training step. Note that training step is impractical in the case of breast cancer detection because of the size, shape and different variabilities in the breast tissues over time. Although the structure of the matched and data adaptive filters are mathematically well designed, the matched and data adaptive filters do not satisfy these constraints as explained above.

In the matched filter, the training step estimates the clutter waveform $x_0^j[n]$, which is use as the input signal by the matched filter. This is accomplished by applying a temporal window $\vartheta$ is the mixed response but the location and length of the window need to be determine. With real patients, the location and length of the window varies from one patient to another. Keeping the window (length and
Figure 3.8: The Data Adaptive Filter.
The Data Adaptive Filter Algorithm \((\text{in} k_{c+t}[n] \rightarrow \text{out} \hat{k}_t[n])\)

For each transmitter do

Define a temporal window delay with length of \((2J + 1)\).

For each element \(j\) in Array B

Define \(1 \leq i \leq N\) where \(i \neq j\)

Form \(b_i[n] = \left[k_{c+t}^{(i)}[n - J], \ldots, k_{c+t}^{(i)}[n], \ldots, k_{c+t}^{(i)}[n + J]\right]^T\)

Define \(b_{2N}[n] = [b_i^T[n], \ldots, b_j^T[n], b_{j-1}^T[n], b_{j+1}^T[n], \ldots, b_N^T[n]]^T\)

where \(1 \leq i \leq N\)

Define the temporal window \([n_0, \ldots, n_0 + m - 1]\)

Define matrix \(R = \frac{1}{m} \sum_{n=n_0}^{n_0+m-1} b_{2N}[n]b_{2N}^T[n]\)

Calculate pseudoinverse \(R_s^{-1} = \sum_{i=1}^{s} \frac{1}{\lambda_i} u_i u_i^T\) for \(s\) significant eigenvalues

Calculate \(p = \frac{1}{m} \sum_{n=n_0}^{n_0+m-1} b_{2N}[n]k_{c+t}^{(j)}[n]\)

Calculate \(q_{2N}[n] = R^{-1} p\)

For all samples in \(k_{c+t}^{(j)}\)

\[\hat{k}_t^{(j)}[n] = k_{c+t}^{(j)}[n] - q_{2N}[n]^T b_{2N}[n]\]

End For

Table 3.3: The data adaptive filter approach used to estimate the tumour response from the mixed response.

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location) constant for all patients results in poor performance. Also, the clutter response is different for each patient so defining a general estimate of the clutter response $x^0_j[n]$ for all patients is impractical. Our experiments show that estimating the clutter response using aligning, scaling, and averaging of recorded responses introduces high degree of noise as suggested in [52]. The reason is that channel response is different for each receiver antenna due to difference in the spatial locations of the elements. In other words, each antenna element receives a different form of backscatters compared to other non-neighboring. Using LMS algorithm is another method to estimate the clutter response in the matched filter approach. Although this method gives a better estimate for the clutter but the result is still not close enough to the actual clutter response due to variabilities in the recorded responses.

Another problem with the matched filter approach is in the computation of scaling factor $\alpha$ and delay $\tau$. As illustrated in Table 3.2, the estimated $\alpha$ and $\tau$ may be related to the clutter and not to the tumour. Unfortunately, this method is not practically feasible where there is no certainty for $\alpha$ and $\tau$ among all receivers which is the case for breast cancer detection.

The data adaptive filter also has its own set of limitations. There are three supervised parameters in the data adaptive filter: (i) The starting index $n_0$, length $m$ of the temporal window $[n_0, \ldots, n_0 + m - 1]$, and, (ii) Number of significant the number of eigenvalues $s$ corresponding to the clutter response. The optimum
temporal window is based on a region which contains only the clutter response. In other words, correct selection of $n_0$ and $m$ is important. The values of $n_0$ and $m$ vary from one patient to another and also on the geometry of Arrays A and B with respect to each other and the breast. In the design of the data adaptive filter, this issue is an open question. Suppose we blindly select a part of the signal as the temporal window. During the computation of pseudoinverse matrix $R_s^{-1}$, the $s$ significant eigenvalues may be due to both the clutter and tumour in such a scenario. The reason is related to principal component analysis (PCA). According to PCA, because the clutter response and the tumour response are dependent, the eigenvalue decomposition on autocorrelation matrix $R$ creates eigenvectors that are uncorrelated but yet dependent. In other words, the result of SVD contains components which are not independent and there is no clear break point in the sequence of ordered eigenvalues. As a result, the number of eigenvalues may over-fit or under-fit. If they over-fit, the filter suppresses the tumour response too. If they under-fit, the filter can not cancel the effect of skin and other clutters effectively.

In addition, selecting $(N - 1)$ receivers to estimate the clutter response using the LMS approach is not an effective approach due to the significant channel response difference even if the temporal window contains only the clutter response.

**Design of the DAF/EDF algorithm:** In this section, I propose a new algorithm namely data adaptive filter/Envelope Detection (DAF/EDF) for extracting the
tumour response from the mixed response. The algorithm is unsupervised and does not require a learning step and is more in extracting the tumour response from the mixed response. All steps involving the DAF/EDF algorithm for extracting the tumour response $k_t$ for a pair of transmitter and a receiver are described as follows.

(i) Defining a General Unsupervised Temporal Window $[n_0, \cdots, n_0 + m - 1]$:

My simulation experiments show that the starting location of the tumour response $k_t[n]$ in a mixed response $k_{c+t}[n]$ depends on the geometry of Array A and Array B with respect to the chest wall and the location of the tumour. For example when both Array A and Array B are parallel to the chest wall (Fig. 3.11a) and the tumour location is in the middle of the breast tissues, the starting response of the tumour signal $k_t[n]$ is after the peak of the clutter reflection (Fig. 3.5). Although the separation of these two signals using parallel geometry provides the best situation to select the starting index $n_0$ of the temporal window, but the relative magnitude order of the tumour response compared to the clutter response is very low such that it is not recognizable by any algorithm even if we know the starting index $n_0$ and length $m$ of the window. Further, since the location of the tumour is unknown, we can not define the end of the temporal window $m$ without prior knowledge. I propose another geometry for Array A and B which is diagonal to the chest wall and close to the breast tissue (Fig. 3.11b). Using this configuration makes
the magnitude order of tumour response comparable to the clutter response. However, this results in an overlap between the tumour response and the clutter responses (Fig. 3.10). My simulations show that there is a delay between the clutter \(k_c[n]\) response and tumour \(k_t[n]\) response to calculate FIR filter coefficients. Based on my simulations, the delay is never less than 50 samples which implies \(m = n_0 + 50\). Note that estimating this value does not require any training because the value is based on the the sampling frequency used during discretization by the measuring instrument. In order to find starting index \(n_0\), all mixed responses \(k_{c+i}[n]\) are passed through a low pass filter to derive the envelope of the signals (Fig. 3.12). An envelope of a signal (connecting absolute values of peaks) shows the exact sample where the energy of the signal starts to grow. Since we expect the primary portion of this rise to be related to the clutter, the starting index \(n_0\) is given by sample corresponding to the rise (Fig. 3.12). I use Hilbert algorithm implemented by Kolmogorov [54] for envelope detection.

(ii) For the \(i^{th}\) receiver, \((2 \leq i \leq N - 1)\), align and scale two recorded responses \(k_{c+i}^{(i-1)}\) and \(k_{c+i}^{(i+1)}\) with respect to the peak in \(k_{c+i}^{(i)}\). Note that aligning and scaling only removes the disparity of the channel response for the peak sample for receivers \((i - 1, i, i + 1)\) but other samples are still not matched. If the receiver \((i - 1)\) and \((i + 1)\) are close enough to the \(i^{th}\) receiver, the least mean
square (LMS) algorithm can estimate the clutter response for the $i^{th}$ receiver in the temporal window $[n_0, \ldots, n_0 + m - 1]$ by finding the best fit for the delay $J$ and magnitude of the clutter. The delay $J$ is an independent variable and is related to the inter antenna space and the sampling frequency which are instrumental parameters in the DAF/EDF algorithm. Note that delay $J$ in data adaptive filter implementation is not independent of experiments and it is experimental. Based on delay $J$, the input of the LMS algorithm for finding FIR filter coefficients, which is called the clutter signature for the $i^{th}$ receiver $b_{i-1}^{(i+1)}[n]$, is given by

$$\forall 2 \leq i \leq N - 1 :$$

$$b_{i-1}^{(i+1)}[n] = [k_{c+t}^{(i-1)}[n - J], \ldots, k_{c+t}^{(i-1)}[n + J],$$

$$k_{c+t}^{(i+1)}[n - J], \ldots, k_{c+t}^{(i+1)}[n + J]]^T. \quad (3.45)$$

(iii) The coefficients of the filter are then given by

$$q_{2i} = R^{-1} p, \quad (3.46)$$

$$R = \frac{1}{m} \sum_{n=n_0}^{n_0 + m - 1} b_{i-1}^{(i+1)}[n]b_{i-1}^{(i+1)T}[n], \quad (3.47)$$

$$\text{and} \quad p = \frac{1}{m} \sum_{n=n_0}^{n_0 + m - 1} b_{i-1}^{(i+1)}[n]k_{c+t}^{(i)}[n]. \quad (3.48)$$

Since $R$ contains only the clutter response, the pseudoinverse is calculated based on nonzero eigenvalues and is given by Eq. (3.39).
Apply filter coefficients to calculate the tumour response from

\[ k_t^{(i)}[n] = k_{c+1}^{(i)}[n] - q_{2i}[n]b_{(i-1)}^{(i+1)}[n]. \]  

(3.49)

Because \( R \) contains only the clutter response, there is no need to add additive steps to remove artifacts due to the tumour response in \( R \) as is required by the data adaptive filter.

Table 3.4 summarizes the steps involved in the DAF/EDF algorithm.

### 3.4 Summary

In this chapter, I developed a realistic electromagnetic (EM) breast model from an MRI and proposed the DAF/EDF algorithm to extract the tumour response from the mixed response without any prior training. My FDTD simulations are done in the 2D mode because 2D simulations are less computationally intensive. Constructing an EM breast model in the 2D is easier than in 3D. By combining results of the 2D simulations, it is possible to produce a 3D simulation of the breast. I used 2D Maxwell equations in the TM mode for my FDTD simulations. Using appropriate frequency band for the probing signal, the relative permeability \( \mu_r \), relative permittivity \( \epsilon_r \), and conductivity \( \sigma \) are independent of frequency and consist of three different matrices. Relative permeability \( \mu_r \) for the breast EM model is constant and is 1 for all entries. Relative permittivity \( \epsilon_r \) and conductivity
Figure 3.9: The data adaptive filter/envelope detection filter (DAF/EDF).
The DAF/EDF Algorithm ((in) $k_{c+t}[n]$  [out] $k_t[n]$))

For each transmitter do

Define a temporal window delay with length of $(2J + 1)$.

For each element $i$ in Array B where $2 \leq i \leq N - 1$

Align and scale two signals $k_{c+t}^{(i-1)}[n]$ and $k_{c+t}^{(i+1)}[n]$ respect to the peak of $k_{c+t}^{(i)}[n]$

Run Hilbert transformation on $k_{c+t}^{(i)}[n]$ to find $n_0$

$m = n_0 + 50$ (for my experiment settings)

Form $b_{(i-1)}^{(i+1)}[n] = [k_{c+t}^{(i-1)}[n - J], \ldots, k_{c+t}^{(i-1)}[n + J], k_{c+t}^{(i+1)}[n - J], \ldots, k_{c+t}^{(i+1)}[n + J]]^T$.

Define $R = \frac{1}{m} \sum_{n=n_0}^{n_0+m-1} b_{(i-1)}^{(i+1)}[n]b_{(i-1)}^{(i+1)}^T[n]$

For all samples in $k_{c+t}^{(i)}[n]$ calculate

$k_t^{(i)}[n] = k_{c+t}^{(i)}[n] - a_{2t}[n]b_{(i-1)}^{(i+1)}[n]$

End For

End For

Table 3.4: The data adaptive filter/envelope detection filter (DAF/EDF) to estimate the tumour response from the mixed response.
Figure 3.10: An example of direct subtraction in the time domain when Arrays A and B are diagonal relative to the chest wall and the tumour is in the middle of the breast tissue and close to Array B (the worst case scenario in terms of defining $n_0$ and $m$) (Fig. 3.11b).
Figure 3.11: Two different antenna geometries ‘×’ in Array A transmitters and ‘*’ in Array B are receivers. (a) Parallel to the chest wall, and; (b) diagonal to the chest wall.
Figure 3.12: Using a low pass filter to select the best fit for $n_0$ where Arrays A and B are geometrically diagonal relative to the chest wall and the tumour is in the middle of the breast tissue and close to Array B as shown in Fig. 3.11b.
σ are based on a linear transformation of the MRI pixels. To make the EM breast model more realistic, the values for relative permittivity $\epsilon_r$ and conductivity $\sigma$ for skin and chest wall are introduced manually in both matrices.

Two goals are identified for algorithms used in estimating tumour reflections. First, the algorithm should not require a training step. Second, they are accurate enough for an array imaging algorithm. Fundamentally, the training step is not practically feasible for breast cancer detection because of the variabilities in the breast tissue among patients and variabilities of breast tissue for an individual over time. Three different filters, namely matched filter, data adaptive filter, and data adaptive filter/envelope detection filter (DAF/EDF), for estimating the tumour reflections are introduced in this chapter. The matched filter algorithm requires an estimation of clutter $x^0$ as an input. The estimation is independent of the algorithm and it needs a training step. In addition, the matched filter uses a tumour template signal, which can be estimated using a mixed response $k_{c+t}[n]$ or again estimated by a training step. If it is estimated from the mixed response $k_{c+t}[n]$, it is required to define a temporal window which again depends on a training step. Such a step is practically infeasible. The data adaptive filter, on the other hand, has better structure and does not required a training step. However, the design of the algorithm contains three different variables: starting index $n_0$ of the clutter response, length $m$ of the clutter signal, and number $s$ significant eigenvalues related to the
clutter. The data adaptive algorithm does not provide a clear solution to estimate these parameters accurately without a training step. In addition, estimation of the filter coefficients for each received signal is based on all other receivers that makes the filter coefficients inaccurate because of the high degree of disparity among the receivers. Ultimately, an additional step is added to the algorithm to improve accuracy which add more inconsistency to the estimated tumour response $k_t[n]$.

To compensate for these drawbacks, I introduced a new algorithm based on data adaptive filter namely the data adaptive filter/envelope detection filter (DAF/EDFF). My experiments show that the scaling factor $\alpha$ and delay $\tau$ are closely related to the geometry of Arrays A and B with respect to each other and the breast tissues, and they are closely related to $n_0$ and $m$. The best geometry to receive a strong backscatter from a small tumor from any location in breast tissue is illustrated in Fig. 3.11b. Although this setup can produce more interleaves of the clutter and tumour response, fortunately there is always a sufficient (guaranteed) delay (in my experiments, the delay $m$ is 50 samples) between the start of the clutter and tumour response which completely separates the clutter response from the tumour response. The actual value of $m$ is independent of patients and it is an instrumental parameter. The worst case delay occurs when the tumour is close to the receiver array (Array B) (Figs. 3.11b and 3.12). Since the guaranteed delay is very small, determination of the starting index $n_0$ accurately is very important. I use the en-
velope detection approach to detect \( n_0 \) precisely. To estimate the filter coefficients, the DAF/EDF algorithm employs only two spatially closest neighboring receivers, which contain less disparity in their responses. Given \( n_0 \) and \( m \), the number of significant eigenvalues \( s \) can be determined easily because the autocorrelation matrix \( R \) is guaranteed to have only the clutter response. In the next chapter, I couple the proposed DAF/EDF approach to array imaging algorithms (namely, direct subtraction beamforming (DSBF), direct subtraction/multiple signal classification (DS/MUSIC), time reversal adaptive interface canceler/time reversal beamforming (TRAIC/RBF), and time reversal adaptive interference canceler/multiple signal classification (TRAIC/MUSIC)) and quantify the performance for each of these algorithms.
4 Simulations and Results

4.1 Introduction

In a practical setup, breast cancer detection using array imaging algorithms consists of two different stages: (i) Instrumentation Stage: Immersing the breast in a lossless fluid, transmitting a probing signal physically from an antenna array, and recording the resulting backscatters from the breast tissues, and; (ii) Array Processing Stage: Processing the recorded backscatters by an array imaging algorithm to estimate the location of the tumour. In this thesis, stage (i) is completed using the FDTD simulations on an EM breast model developed from the patient’s MRI. Whether completed physically or using a computational simulation, the output of stage (i) is the mixed response $k_{c+t}[n]$, from which the tumour response $k_t[n]$ and the clutter response $k_c[n]$ need to be separated before the tumour location can be estimated. This can be accomplished by one of the following three setups.

**Setup 1:** involves a training step where the clutter response $k_c[n]$ is measured
from the EM breast model before the tumour is introduced. After introducing the tumour, the mixed response $k_{c+t}[n]$ is measured followed by background subtraction ($k_{c+t}[n] - k_c[n]$) to determine the target response. Note that Setup 1 is not practical and is included to provide the ground truth against which the proposed algorithm can be compared.

**Setup 2:** is similar to Setup 1 except for the clutter response, which is obtained from a second EM breast model derived from the MRI of a different and a healthy patient.

**Setup 3:** is the proposed setup that does not require a training step. After estimating the mixed response $k_{c+t}[n]$, the proposed DAF/EDF algorithm is applied to isolate the clutter and target responses. To illustrate the superiority of the DAF/EDF algorithm, the output of the DAF/EDF algorithm is compared with the outputs of other target response estimation algorithms reviewed in the previous chapter.

After separating the clutter and target responses, the four array imaging algorithms (DSBF, DS/MUSIC, TRAIC/TRBF, and TRAIC/MUSIC) as presented in Chapter 2 are applied to estimate the location of the breast tumour.

The organization of the chapter is as follows. In Section 4.2, I derive the EM profile of the patient’s breast based on the EM algorithm introduced in Chapter 3.
Section 4.3 compares the results of the target response estimation algorithms as described in Setups 1, 2, and 3. I show that the DAF/EDF algorithm used in Setup 3 is better than the current state of art. Section 4.4 compares the results of the array imaging algorithms in terms of their precision in estimating the tumour location. Finally, Section 4.5 summarizes the main contributions of the chapter.

4.2 Experimental Setup

Fig. 4.1(a) plots a reference MRI as a monochrome image with its equivalent electromagnetic profile plotted in Fig. 4.1(b). The electromagnetic profile is derived using the procedure outlined in Section 3.2.2. Recall that an EM model is based on three matrices corresponding to the values of the relative permeability $\mu_r$, relative permittivity $\epsilon_r$, and conductivity $\sigma$ for the breast tissues. The transformations used to derive the values for the relative permittivity and conductivity are described below. These results are based on the steps outlined in Table 3.1 in Chapter 3. For the MRI shown in Fig. 4.1(a), the following values are obtained.

Number $N$ of pixels in the breast region = 126,958.

Sum $S$ of the intensity values of $N$ pixels = 24,400,350.

Average permittivity value $\bar{\epsilon}_r$ of the normal breast tissues = 10.

Average conductivity $\bar{\sigma}$ of the normal breast tissues = 0.4.
Figure 4.1: (a) Example MRI of a normal breast. (b) Equivalent EM model derived from MRI (a). The EM model is used in the FDTD simulations presented in this chapter.
Transformation constant for the permittivity: \( k_{\varepsilon} = \frac{N \cdot \overline{\varepsilon}}{S} = 0.052 \).

Transformation constant for the conductivity: \( k_{\sigma} = \frac{N \cdot \overline{\sigma}}{S} = 0.0021 \).

Transformation expression for the permittivity: \( P(m, n) = 0.052 \times I(m,n) \).

Transformation expression for the permittivity: \( C(m, n) = 0.0021 \times I(m,n) \).

The profile for the conductivity is plotted in Fig. 4.1(b). The profiles for relative permeability and permittivity are similar to the conductivity profile though the variations may not be as obvious and are, therefore, not included to save on space.

We note that the permittivity transformation results in a variability of about 20% in the values of the relative permittivity. This is very much in line with the variability of (16%-24%) observed in tissues of actual patients [37]. Finally, as far as the relative permeability \( \varepsilon_r \) is concerned, it is observed that the values of the relative permeability are fairly similar in both the normal breast and malignant tissues. The relative permeability is set equal to its free space value, i.e., \( \mu_r = 1 \), for all entries within the permeability matrix.

Fig. 4.2 plots the time domain and frequency domain representations for the probing signal - a sinc function with a center frequency of 9GHz and a bandwidth of 1GHz. Within this frequency range, the values of the relative permittivity \( \varepsilon_r \) of the normal breast tissues are widely different from those of the malignant tumour tissues. The difference in the values of the relative permittivity is the source of
Figure 4.2: Waveform for the sinc function used as a probing signal: (a) Time domain representation. (b) Frequency domain representation.
strong backscatters from the tumour. The values for the skin and chest wall including ribs and Pectoralis muscles are based on [49] and are introduced manually in the EM model. The thick line (shown in light green) in Fig. 4.1(b) models the skin, which has a thickness of 2mm, conductivity $\sigma$ of 4S/m, and relative permittivity $\varepsilon_r$ of 30. The breast is assumed to be immersed in a lossless liquid so the region outside the breast has the conductivity $\sigma = 0$S/m and relative permittivity $\varepsilon_r = 10$. Both Arrays A and B contain 12 elements each and are located within the lossless liquid, as shown, respectively, by ‘×’ and ‘*’ in Fig. 4.1(b).

To establish the ground reality against which the performance of the algorithm will be tested, a 2mm tumour is inserted manually within the normal breast MRI after deriving the EM properties of the breast. The location of the tumour, selected at random, is shown as a bright region at spatial coordinates (10.8, 7.9)cm in Fig. 4.1b. Within the tumour, the maximum value for conductivity $\sigma = 50$ and for permeability $\varepsilon_r = 4$S/m.

### 4.3 Estimating The Tumour Backscatter

Two FDTD simulation setups are used to test the performance of the proposed target estimation algorithm: (i) An FDTD simulation is run on an EM breast model without cancerous tissues (Fig. 4.1b), and; (ii) Eleven FDTD simulations are performed on eleven different EM cancerous breast models (Fig. 4.3) with cancerous
tissues inserted at different locations. The recorded backscatters from Setup (i) are referred to as the clutter (background) reflections \( k_c[n] \) and the recorded backscatters from Setup (ii) are referred to as the mixed responses \( k_{c+t}[n] \). The tumour backscatter is estimated using three different methods.

(i) Method 1: Following the background subtraction procedure, the clutter response \( k_c[n] \) recorded from the first FDTD setup is subtracted from the mixed response \( k_{c+t}[n] \) observed at different locations to derive the tumour backscatter \( k_t[n] \) in Method 1. The results of the subtraction for different tumour locations 1, 3, and 6 are shown in Figs. 4.4-4.6 when the 6\(^{th}\) transmitter in Array A probes the channel and the 6\(^{th}\) receiver in Array B records reflections in different FDTD setups. This method produces the best estimate for the target backscatter. Later in Section 4.4, I present results of array imaging algorithms and show that the target backscatter obtained from the background subtraction method also produces the best estimates for the locations of the tumours. Note that this scenario is practically infeasible due to the difficulty in obtaining the clutter and overall responses for the same patient with the same profile (size, shape, and tissue composition) of the breast. I use the results of this method as ground reality against which the performances of other algorithms are compared.
Figure 4.3: A spherical 2mm cancerous tumour is introduced at eleven different locations marked as 1 to 11 in the figure.
Figure 4.4: Results for the Background Subtraction procedure for tumour location 1 when both clutter and overall responses are derived from the EM breast model obtained from a single MRI (Method 1). Relative to the chest wall, both Arrays A and B are diagonal, the 6th transmitter probes the channel, and the 6th receiver records the reflections. (a) Mixed response $k_{c+t}[n]$ for the EM breast model shown in Fig. 4.1b. (b) Background response $k_c[n]$ obtained from the EM FDTD simulation run on the same EM breast model when no tumour is introduced, and; (c) Tumour response $k_t[n] = k_{c+t}[n] - k_c[n]$. 

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Figure 4.5: Same as Fig. 4.4 obtained by the Background Subtraction procedure from a single MRI except for tumour location 3.
Figure 4.6: Same as Fig. 4.4 obtained by the **Background Subtraction** procedure from a single MRI except for tumour location 6.
(ii) Method 2: This procedure is similar to Method 1 except for the clutter responses, which are derived by running FDTD simulations based on an EM breast model (Fig. 4.7) as derived from an MRI of a different patient. As before, the results of the background subtraction are illustrated for tumour locations 1, 3, and 6 in Figs. 4.8-4.10. Compared to the estimates of the target responses obtained from Method 1, note that there are significant differences because the alignment between the clutter and overall responses is lost.

(iii) Method 3: To estimate the tumour response \( k_t[n] \) directly from the mixed response \( k_c[n] + k_t[n] \), three different algorithms (the matched filter, data adaptive filter, and data adaptive filter/envelop detection filter algorithms introduced in Chapter 3) are applied to the mixed response as described below.

(a) The Matched Filter Based Approach: As outlined in Table 3.2, two parameters need to be defined for implementing the matched filter approach. The first is an estimate of the clutter response \( x_0^j[n] \) for the \( j^{th} \) receiver to be used as the clutter signature, while the second is the size and location of the temporal window \( \theta = [a, b] \) to be used in the matched filter. In this thesis, the clutter estimate \( x_0^j[n] \) is obtained by aligning, scaling, and averaging of the overall responses recorded at the receivers with the waveform at the 5\(^{th} \) receiver forming the reference signal. This
Figure 4.7: The EM breast model derived from the MRI of healthy patient 2, which is used to estimate the clutter response.
Figure 4.8: Results of the **Background Subtraction** procedure for tumour location 1 when the clutter response is obtained from the EM model derived from the MRI of a **different patient** (Method 2). Remaining parameters are the same as used in Method 1. (a) Mixed response $k_{c+t}[n]$ for the EM breast model shown in Fig. 4.1b). (b) Background (clutter) response $k_c[n]$ obtained from the EM FDTD simulation run on the EM model derived from Fig. 4.7, and; (c) Tumour response $k_t[n] = k_{c+t}[n] - k_c[n]$. 
Figure 4.9: Same as Fig. 4.8 obtained from the Background Subtraction approach with target and clutter responses derived from different MRIs except for tumour location 3.

\[ (c) \ k_t[n] = k_{c+t}[n] - k_c[n] \]
Figure 4.10: Same as Fig. 4.8 obtained from the **Background Subtraction** approach with target and clutter responses derived from **different MRIs** except for tumour location 6.
procedure is repeated for every single transmitting element probing the channel. The temporal window is defined by picking 100 samples on each side of the peak of the reference signal. The matched filter algorithm listed in Table 3.2 is then used to derive the clutter and target responses for each receiver. For tumour locations 1, 3, and 6, the estimated target and clutter responses are plotted in Figs. 4.11-4.13.

(b) The Data Adaptive Filter: The data adaptive filter requires three input variables - start position $n_0$ of the clutter response, end position $m$ of the clutter response, and the number $s$ of eigenvalues corresponding to the clutter response. Reference [36] does not explain how to initialize these variables, so I tried an experimental approach. As explained in Table 3, the best antenna geometry for this algorithm is parallel to the chest wall as shown in Fig. 3.11a. This antenna geometry has two effects: Separation of the clutter response from the tumour response, and; Weakening of the tumour response as compared to the clutter response specially for deep tumour locations (i.e., locations 6, 7, and 8 in Fig. 3.5). The antenna configuration causes the reflected energy from the clutter and tumour to be separated completely for the majority of the tumour locations, which makes it easy to determine the values of the three variables except for tumour locations 4, 5, and 10. For locations
Figure 4.11: Estimated target response obtained from the matched filter approach for tumour location 1. (a) Mixed response $k_{c+t}[n]$ for the EM breast model shown in Fig. 4.1b with tumour inserted at location 1. (b) Tumour response $k_t[n] = k_{c+t}[n] - k_c[n]$ obtained by direct subtraction, and; (d) Estimated tumour response $k_t[n]$ from the matched filter.
Figure 4.12: Same as Fig. 4.11 obtained using the **matched filter approach** except for tumour location 3.
Figure 4.13: Same as Fig. 4.11 obtained using the **matched filter approach** except for tumour location 6.
Figure 4.14: Illustration of the procedure used to derive the values of the experimentally defined variables $n_0$ and $m$ for the data adaptive filter algorithm for tumour location 1 when the $6^{th}$ transmitter probes the channel and the $6^{th}$ receiver records the backscatters.

where the clutter and tumour reflections are successfully separated in the mixed response, the first peak represents $n_0$ and the last peak with a magnitude close to the magnitude of the first peak represents $m$. For tumour inserted at location 1 with the $6^{th}$ transmitter probing and the $6^{th}$ receiver recording the backscatters, for example, I found $n_0 = 570$ and $m = 1340$ (Fig. 4.14). The number $s$ of significant eigenvalues is set to 4.

We note that the estimated tumour response is not close enough to the estimated tumour response resulting from background subtraction in Method 1. For this specific experiment, the reason is related to value
of the delay $J = 3$ which is suggested by the authors. For removing the clutter effect from sample $n$ in the first receiver, the design of the algorithm is based on calculating the autocorrelation matrix $R$ produced by selecting $(2J + 1)$ concatenated samples window from all receiver except for the first receiver centered at sample $n$. Because the delay between these responses is more than $(2J + 1)$ samples, autocorrelation matrix $R$ does not contain meaningful correlated data corresponding to the clutter. As a result, filter coefficients $q$ calculated based on autocorrelation matrix $R$ does not contain faithful (correlated) data about the clutter response. Increasing the value of delay $J$ is one way to eliminate the problem. Note that increasing the value of delay $J$ produces a bigger autocorrelation matrix $R$ and, as a result, increases the time complexity of the algorithm. In addition the value of delay $J$ is different for each pair of transmitter-receiver and should be determined experimentally which is impractical. The results of estimation of tumour response for tumour locations 1, 3, and 6 are illustrated in Figs. 4.15-4.17.

(c) The DAF/EDF Algorithm: The antenna array geometry used in the DAF/EDF algorithm is diagonal with respect to the chest wall as shown in Fig. 3.11b. Based on the algorithm structure outlined in Fig. 3.9, only two adjacent receivers ($k^{(i-1)}_{c+t} [n]$ and $k^{(i+1)}_{c+t} [n]$ for $2 \leq i \leq N - 1$)
Figure 4.15: Estimated target response obtained from the data adaptive filter approach for tumour location 1. (a) Mixed response $k_{c+t}[n]$ for the EM breast model shown in Fig. 4.1b with tumour inserted at location 1. (b) Tumour response $k_t[n] = k_{c+t}[n] - k_c[n]$ obtained by direct subtraction, and; (d) Estimated tumour response $k_t[n]$ from the data adaptive filter.
Figure 4.16: Same as Fig. 4.15 obtained using the data adaptive filter approach except for tumour location 3.
Figure 4.17: Same as Fig. 4.15 obtained using the data adaptive filter approach except for tumour location 6.
are used. They are aligned and scaled with respect to the peak sample of the receiver \(k_{c+t}^{(i)}[n]\). Using this method makes the algorithm independent of delay parameter \(J\) and produces an autocorrelation matrix \(R\), which has more correlated data on its diagonal. The starting index \(n_0\) is found by using a low pass filter (Hilbert transform as illustrated in Fig. 4.18). The sample at which the energy of the signal starts growing is nominated for the value of \(n_0\). Note that this value is defined automatically and is a function of the input signal. The value of \(m\) is obtained from the expression \(m = n_0 + 50\) for every transmitter-receiver pair. The number of significant eigenvalues \(s\) is determined easily from the autocorrelation matrix \(R\) as the later contains only the clutter reflections. The estimated tumour responses for tumour locations 1, 3, and 6 are plotted in Figs. 4.19 - 4.21. By comparing with the ground reality (results of the background subtraction), it is observed that the estimates of the DAF/EDF algorithm are better than those produced by the matched filter and by the data adaptive filter.

### 4.4 Array Imaging Algorithm Results

In this section, the tumour response estimated from the DAF/EDF algorithm is applied to estimate the location of the tumour using the four array imaging algorithms
Figure 4.18: Illustration of the procedure used in the DAF/EDF algorithm to evaluate the design parameters $n_0$ and $m$. The observed waveform is obtained for tumour location 1 when the 6th transmitter element probes the channel and the 6th receiving element records the backscatter.

(TRAIC/TRBF, TRAIC/MUSIC, DSBF, and DS/MUSIC) presented previously in Chapter 2 through experimental simulations. The section serves two purposes. First it is shown that the tumour response estimated from the DAF/EDF algorithm produces almost identical results as those of the direct subtraction (ground reality) in any of the four array imaging algorithms. The first set of experiments illustrate the superior performance of the DAF/EDF algorithm in estimating the tumour response. The tumour responses obtained from other target response estimation algorithms produce subpar performance. Having justified the use of the practical DAF/EDF algorithm in estimating the tumour response, the second set
Figure 4.19: Estimated target response obtained from the **DAF/EDF approach** for tumour location 1. (a) Mixed response $k_{c+t}[n]$ for the EM breast model shown in Fig. 4.1b with tumour inserted at location 1. (b) Tumour response $k_t[n] = k_{c+t}[n] - k_c[n]$ obtained by direct subtraction, and; (d) Estimated tumour response $k_t[n]$ from the data adaptive filter.
Figure 4.20: Same as Fig. 4.19 obtained using the DAF/EDF approach except for tumour location 3.
Figure 4.21: Same as Fig. 4.19 obtained using the DAF/EDF approach except for tumour location 6.
of experiments compares the performances of the four array imaging algorithms at
different signal-to-noise ratios and tumour locations.

Figs. 4.22-4.25 plot the results of the first set of experiments for tumour loca-
tion 1 with the tumour responses derived from four different schemes. As mentioned
previously, the results of the DAF/EDF algorithm are identical to the results of the
background subtraction and fairly close to the true target locations. The remaining
three tumour response estimation algorithms (Background subtraction with a dif-
ferent MRI used for the training phase, Matched filter, and DAF) do not estimate
the tumour response accurately and localize the tumour at wrong locations.

Having established the superiority of the DAF/EDF algorithm in estimating
the tumour response, Fig. 4.26 repeats the above analysis for tumour location 6
with the tumour response derived from the DAF/EDF algorithm. Among the four
array imaging approaches, we note that the TR approaches (TRAIC/TRBF and
TRAIC/MUSIC) outperforms the conventional approaches (DSBF and DS/MUSIC).
To highlight the differences in the accuracy of estimation of the tumour, Fig. 4.27
plots the absolute value of the differences between the estimated tumour locations
and its true location for three different signal-to-noise ratios (SNR) of 30dB, 15dB,
and 0dB based on a Monte-Carlo run. At higher SNRs of 15 and 30dB, the TR
approaches (TRAIC/TRBF and TRAIC/MUSIC) result in lower absolute values
of estimation errors than the conventional approaches. At the lowest SNR of 0dB,
Figure 4.22: Array imaging pseudospectrum for location 1 and SNR = 30dB obtained from different array imaging algorithms when tumour response obtained by direct subtraction between the overall and clutter responses derived from the EM breast model of the same MRI is used as input to the algorithms. Outputs of the: (a) TRAIC/TRBF; (b) TRAIC/MUSIC; (c) DSBF, and; (d) DS/MUSIC array imaging algorithms. The tumour location is represented by ‘◦’, while the estimated location is given by ‘×’.
Figure 4.23: Same as Fig. 4.22 except the tumour response is estimated by direct subtraction between the overall and clutter responses derived from the EM breast model of different MRIs is used as input to the algorithms.
Figure 4.24: Same as Fig. 4.22 except the tumour response is estimated using the matched filter approach from the overall response.
Figure 4.25: Same as Fig. 4.22 except the tumour response is estimated using the proposed DAF/EDF algorithm from the overall response.
the conventional approaches perform better. This is consistent with the observation made in Moura et al [34], where the susceptibility of TR to high power noise is quantified. In comparison to a single probing step used in the conventional approaches, TR probes the channel twice. At low SNRs, the effect of noise is doubled resulting in poor performance of TR. In practical medical applications, this is not an issue as advanced instrumentation allows for SNRs in the vicinity of 20 to 40 dB.

4.5 Summary

The chapter compares the results of the array imaging algorithms in estimating the location of the tumour obtained by running EM FDTD simulations. To establish ground reality against which the performances of the different algorithms are compared, a 2mm cancerous tumour is inserted at random locations in the reference EM breast model generated from an MRI of a healthy patient.

The array imaging algorithms require an estimate of the target (tumour) response from the overall (tumour and clutter) response. This chapter uses four different strategies (Background subtraction with the reference MRI minus the tumour used for the training phase, Background subtraction with a different MRI used for the training phase, Matched filter, and DAF/EDF) to extract the tumour $k_t[n]$ and clutter $k_c[n]$ responses from the overall response $k_{c+c}[n]$ in the time do-
Figure 4.26: Array imaging pseudospectrums at location 11 using the DAF/EDF algorithm to estimate the tumour reflection without introducing noise. The tumour location is represented by '○' and '×' represents the proposed location by the algorithm. (a) TRAIC/TRBF (b) TRAIC/MUSIC (c) DSBF (d) DS/MUSIC.
Figure 4.27: Range of absolute errors (mean ± standard deviation) in estimating the location of the tumour derived by running a Monte-Carlo simulation for the four array imaging algorithms at: (a) SNR = 30dB; (b) SNR = 15dB, and; (c) SNR = 0dB.
main. The proposed DAF/EDF approach outperforms the remaining approaches and its estimates are closest to the target responses obtained from the direct subtraction approach. Having established the superiority of the proposed DAF/EDF approach, its estimate of the tumour response is applied as input to four array imaging algorithms (DSBF, DS/MUSIC, TRAIC/TRBF, and TRAIC/MUSIC). The TR approaches (TRAIC/TRBF and TRAIC/MUSIC) outperform their conventional counterparts (DSBF and DS/MUSIC) at higher SNR of 15-30dB, commonly available with advanced medical instrumentation.
5 Conclusion and Future Work

In this thesis, I have shown that the TR array imaging algorithms offer superior performance in estimating the locations of breast tumours as compared to the conventional array imaging approaches. Our experimental setup uses an electromagnetic (EM) breast model derived from an MRI. The EM breast model is used in several finite difference, time domain (FDTD) simulations representing EM propagation based on the Maxwell equations.

Estimating the tumour response from the overall response (containing both the clutter and tumour responses) is a fundamental bottleneck in applying array imaging approaches to tumour detection. Approaches based on a training step such as background subtraction are impractical as the training phase (without tumour) is conducted many months in the past and the breast profile changes significantly over such a long duration. As such, the tumour response has to be determined directly from the overall response without a training stage. In this thesis, I examined three different tumour estimation approaches: (i) The matched filter approach; (ii) The
data adaptive filter approach, and; (iii) The proposed data adaptive filter/envelope detection filter (DAF/EDF) approach. Authors of the matched filter approach proposed a crude averaging technique for estimating the background reflection. However, the averaging step generates a high degree of error in the estimated tumour response. As a result, estimated tumour backscatter using the matched filter algorithm are not accurate enough to be used in the array imaging algorithms. Instead of the crude averaging method, I tried a least mean square (LMS) based approach to estimate the background backscatter, which also does not require a training step for the matched filter. Because of considerable disparities between recorded backscatters, the matched filter combined LMS approach also failed to produce an accurate estimate of the tumour backscatter. Although the data adaptive filter is well defined mathematically, its design parameters such as delay $J$ vary from a patient to another and can not be defined generically resulting in a poor estimate of the tumour response. The thesis proposes the DAF/EDF algorithm for tumour response estimation, which uses a diagonal antenna configuration and a low pass filter for detecting the envelope of the mixed response. The resulting envelope is used to compute the values of the design parameters. My simulation results show that the DAF/EDF algorithm successfully estimates the tumour response with high resolution and accuracy as compared to the matched filter and data adaptive filter approaches at high SNRs of 15 to 30dB.
The tumour estimates obtained from the DAF/EDF algorithm is used as input to the TR and conventional array imaging algorithms, namely the TRAIC/TRBF, TRAIC/MUSIC, DS/MUSIC, and DSBF. In most cases, the TR approaches (TRAIC/TRBF and TRAIC/MUSIC) outperform the conventional array imaging approaches.

Future Work

There are several directions in which my research work in the TR based breast cancer detection can be extended. Below we identify two likely directions for extension of this thesis.

(i) *Estimating the Tumour Backscatter:* Although the DAF/EDF algorithm estimates the tumour backscatter for a tumour located in the middle of the breast with reasonable accuracy, the approach requires some fine tuning for locations closer to the skin. Independent component analysis (ICA) [55] has good potential in such cases. The ICA approach decomposes a mixed signal originating from different sources into constituent components corresponding to the transmitting sources. In terms of breast cancer detection, the backscatter sources are the skin, inhomogeneities in the breast tissues, chest wall, and possible cancerous tumours. Although ICA decomposes a mixed response into its fundamental components, it cannot recover the relative magnitudes of the components accurately. A combination of matched filter and ICA can
therefore be designed with the ICA approach used to decompose the overall response into the constituent components and the matched filters used to derive their relative magnitudes.

(ii) *Performing in-vitro Examination:* Although results of the electromagnetic FDTD simulations are widely used in biomedical imaging research, the next step is to test the performance of the proposed algorithms on real data. An experimental verification of the results can be conducted by building a system based on the principle of confocal microwave imaging (CMI). In such a system, simple phantoms, consisting of PVC pipes and objects representing tumors, are used to represent a woman positioned in the prone position with the breasts immersed in a liquid (low loss, dielectric constant similar to that of breast tissue). One or more antennas are mechanically scanned around the breast, forming a synthetic array. A short pulse containing a broad range of frequencies (5 GHz or more) is transmitted from each antenna position and the same antenna receives the backscatters. Such a system would require development of a mechanical model for the female patient as well as a system of a physical electromagnetic antenna array, capable of probing the channel, recording the backscatter, and time reversing the recorded waveform in real time.
Bibliography


