Automated Target Detection in Diagnostic Ultrasound based on the CLEAN Algorithm

by

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A thesis submitted in conformity with the requirements for the degree of Masters of Applied Science
Graduate Department of Electrical and Computer Engineering
University of Toronto

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Abstract

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2011

In this thesis, we present an algorithm for the automated detection of abnormalities (targets) in ultrasound images. The algorithm uses little \textit{a priori} information and does not require training data. The proposed scheme is a combination of the CLEAN algorithm, originally proposed for radio astronomy, and constant false alarm rate (CFAR) processing, developed for use in radar systems. Neither of these algorithms appears to have been previously used for target detection in ultrasound images. The CLEAN algorithm identifies areas in the ultrasound image that stand out above a threshold in relation to the background; CFAR techniques allow for an automated and adaptive selection of the threshold. The algorithm was tested on simulated B-mode images. Using a contrast-detail analysis, probability of detection curves indicate that, depending on the contrast, the method has considerable promise for the automated detection of abnormalities with diameters greater than a few millimetres.
Acknowledgements

I would first like to acknowledge my supervisors Professor Ravi Adve and Richard Cobbold. Professor Adve is responsible for my foray into Biomedical Engineering. I am grateful for his guidance and feedback throughout graduate school. Professor Cobbold has been a monumental source of energy. His unwavering encouragement and enthusiasm are greatly appreciated. Both have been unbelievably supportive of all of my endeavours throughout graduate school, whether related to my thesis or not. I would also like to thank the Natural Sciences and Engineering Research Council of Canada for partially funding my work.

My time at BA7114 and RS407 would not have been as enjoyable without a number of people. Amir Aghaei, William Chou, Yashar Ghiassi, Kianoush Hosseini, Nazmul Islam, Ehsan Karamad, Ali Khanafer, Mohammad Mahanta, Helia Mohammadi, Heesun Park, Maryam Ravan, Sanam Sadr, Diane Silva, Gokul Sridharan, K. V. Srinivas and Adam Tenenbaum from BA7114 and Luis Aguilar, Hisham Assi, AlHassan Aly, Alexia Giannoula, SayedMasoud Hashemi, Amir Manbachi, Renee Warriner and Derek Wright from RS407 provided a much needed outlet from the frustrations of graduate thesis work. I would like to thank them for their friendship and wish them all great success.

I would also like to thank two of my closest friends, Jimmy Chan and Obioma Ohia who I have known from the 6th grade. They have helped me keep things in perspective through the good times and the bad. I am grateful for their friendship and hope that Google Books always has magazines.

Finally, I would like to thank my family without whom I wouldn’t be who I am today. My father has been a testament to what a person can accomplish with hard work. My brother and sister have been extremely supportive of whatever I do. Lastly, I would like to acknowledge my mother to whom I am deeply indebted. From the Peter and Jane books she used to teach me to read, to the standards by which she lives, she has been an integral part of my growth and an unwaivering source of inspiration.
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Chapter 1

Introduction

Ultrasound imaging can be used in the detection of various cancers [1–3], quantitative bone density measurements [4] and for the estimation of blood flow velocity [5]. Because ionizing energy is not involved, ultrasound is a comparatively safer imaging modality for both the patient and operator. This intrinsic safety and the noninvasive nature of ultrasound imaging can be used to increase the rate of cancer detection [6] and be a safe alternative to biopsies. Further, it is a relatively inexpensive imaging modality which has lead to its recommendation as a breast cancer screening tool, especially in limited-resource countries [7].

1.1 Motivation

Early detection of disease is often considered as the key to preventing long-term complications. For example, finding melanoma tumours when they are still localized leads to a 5-year survival rate of 95.8%. If the cancer has spread to other parts of the body, on the other hand, the 5-year survival rate drops to just 16.2% [8]. Similar statements can be made of other forms of cancer. Moreover, screening for disease has provided better long-term outcomes. Prostate-specific antigen (PSA) based screening, for example, has
been shown to reduce the risk of death from prostate cancer by 20% [9]. Thus, early screening of many diseases can lead to drastically better outcomes.

Although ultrasound screening then seems like an important tool for combating disease, it is not without its problems. Biomedical ultrasound images are typically evaluated by health care workers. Although these workers are usually highly trained, oftentimes, the detection and classification of abnormalities is a subjective task [10]. The reading of test results such as diagnostic images often depends on the radiologist’s level of experience [11]. Other factors such as caseload and even the availability of trained staff can also be contributing factors to diagnoses. Moreover, imaging modalities are not perfect. It is estimated that the sensitivity of screening mammography is between 85 and 90% [12]. Of the breast cancer misdiagnoses, 52% can be accounted for by misinterpretation of the results and 43% is due to overlooking signs of the abnormalities. Similar statements can be made of other diseases [13–16].

There are some proposed approaches to reducing the apparent variability of diagnosis by a health care worker. Particularly, double reading has been proposed to help increase the probability of detection and decrease the chance of a misdiagnoses. Double reading is the use of a second health care worker to screen the same image. The second worker can act as an independent party or the two health care workers can jointly interpret screenings. Both of these cases have increased the rate of detection in both breast [17] and lung cancers [18]. However, given a health care system which is already taxed in terms of resources, this may not be the most viable option.

As an alternative to second opinions from other workers, computer-aided detection (CAD) systems have been developed to assist health care workers in detecting abnormalities. Some CAD systems extend detection to classification, i.e., whether the detected abnormalities are benign or malignant and even the likelihood of either case [19]. Still, it is widely accepted that physicians will not be replaced by CAD systems—they are meant to remove operator dependency of ultrasound diagnosis and augment radiologists’
abilities in diagnosing patients. A review of relevant CAD techniques is provided in Section 1.3.1.

Although CAD systems can help health care workers detect abnormalities, they can also be used to provide clearer images through refocusing. Currently, ultrasound scans are performed by ultrasound technicians and the images are interpreted by radiologists. If the radiologists are not satisfied with the quality of the scans, they can request further scans of the same area leading to a delay in diagnosis and a waste of resources. However, if the locations of potential abnormalities are known at the time of performing an ultrasound scan, the ultrasound transducer can be refocused on these locations. The resulting images will provide a clearer representation of potential abnormalities to the radiologists interpreting the scan. Thus, CAD systems can be used to improve the quality of medical images.

1.2 Challenges

Ultrasound imaging is based around the concept of acoustic wave scattering. The ultrasound transducer transmits a focused ultrasound pulse and abrupt changes in the compressibility and density within the medium lead to back-scattering of the transmitted wave. Different scatterer models have been used for studying scattering. One common one is to use spherical scatterers as in Figure 1.1. The incident wave is assumed to be a plane wave and the scatterer has radius $a$. For an infinitely dense spherical scatterer that is sufficiently far from the ultrasound wave source, a simplified expression for the intensity of the scattered wave at an observation point given by $(r, \theta)$ is

$$I(r, \theta) \approx p_o^2 \frac{k^4 a^6}{18 \rho_o c_o r^2} \left(1 - \frac{3}{2} \cos \theta\right)^2,$$

where $p_o$ is the incident wave pressure and $k$ is the wavenumber. These back-scattered waves are then received by the ultrasound transducer.
Figure 1.1: Ultrasound wave propagation. The plane wave is incident on a spherical scatterer of radius $a$. The back-scattered wave is observed at distance $r$ and angle $\theta$ from the direction of incident wave propagation.

Two dimensional ultrasound images (B-mode images) are formed from one dimensional A-lines. These A-lines are created from the pulse-echo response described above; the transducer transmits a focused ultrasound pulse and then immediately begins reception of the back-scattered acoustic signal. Scatterers within the medium then cause a back-scattered response which, if strong enough, can be received by the ultrasound transducer. Assuming a constant speed of sound, the elapsed time between transmission and reception can then be used to compute a distance thus completing the formation of a single A-line. The acoustic beam is then typically shifted laterally so that it may be able to focus on an adjacent region and record another A-line. Successive A-lines are then arranged side-by-side to form a two dimensional B-mode image.

Inherent ultrasound properties pose challenges to developing an ultrasound CAD system. These include physical limitations of the medium such as attenuation and speckle as well as inherent properties of ultrasound image acquisition like focusing.

1.2.1 Attenuation

The loss of ultrasound energy is known as attenuation. Attenuation is a term that encapsulates two phenomena: absorption and scattering. As the acoustic wave propagates, the conversion of wave energy to heat, light or chemical energy is known as absorption. Absorption causes a change in phase velocity with frequency, a process known as dis-
Both absorption and scattering lead to a decrease in the ultrasound wave intensity as given by
\[ I(x) = I(0)e^{-2(\alpha_s+\alpha_a)x}, \] (1.2)
where \( \alpha_s \) and \( \alpha_a \) are the scattering and absorption attenuation coefficients, respectively, and \( I(x) \) is the ultrasound wave intensity at the spatial location given by \( x \) [20]. The scattering and absorption coefficients are typically combined so that the resulting relationship between intensity and attenuation is given by

\[ I(x) = I(0)e^{-2\alpha x}, \] (1.3)

where \( \alpha \) is the amplitude attenuation coefficient.

Absorption and scattering are both frequency dependent so their combined effect, attenuation, is also frequency dependent. Most of the experimental evidence (a compilation of which can be found in [21]) suggests that the relationship between attenuation and frequency can be represented as

\[ \alpha = \alpha_o f^n, \] (1.4)

where \( \alpha_o \) is a propagation medium dependent attenuation coefficient, \( f \) is frequency and \( n \), which is determined by the propagation medium, typically lies between 1 and 2. Thus, the effects of attenuation increase with larger frequencies.

Attenuation has negative consequences for the creation of ultrasound images and, hence, for CAD systems. As described previously, ultrasound image formation is based on the scattering of acoustic waves. Attenuation decreases the magnitude of both the transmit and back-scattered waves as a function of distance. In other words, scatterers of
equal reflectivity (those with equal physical properties) will elicit back-scattered acoustic signals of different magnitudes if their distances to the transducer are also different. This poses problems for CAD systems as many rely on training data or a priori information about the medium. In particular, attenuation may lead to poor classification of potential abnormalities.

A solution to the effects of attenuation is time-gain compensation. Time-gain compensation alleviates the effects of attenuation by increasing the signal power as a function of time (or equivalently, distance). Thus, the backscattered response from regions further from the transducer are magnified. This is done so that regions further from the transducer have the same signal power as regions closer to the transducer. Although this mitigates the effects of attenuation, significant inaccuracies may still be present [22].

1.2.2 Speckle

Speckle is the granular pattern often seen in the background of ultrasound B-mode images. It was originally observed in laser light and was attributed to reflection from sub-wavelength imperfections on the illuminated surface [23]. Incident laser light onto a surface is coherent. When it is reflected, however, imperfections on the reflected surface cause the laser light to lose coherence resulting in a seemingly random interference pattern. However, the pattern is not random. Because it depends on the microscopic structure of the object, under similar measurement conditions, the speckle pattern will be similar.

A similar phenomenon exists in ultrasound imaging. As with laser speckle, it was found that ultrasound speckle was a result of many sub-wavelength scatterers [24]. Indeed, it was found that the speckle could be simulated through the use of many point scatterers [25]. In practise, speckle can be simulated by the presence of many randomly placed scatterers of low reflectivity. Specifically, the density of scatterers required to
simulate speckle ranges from 10 to 100 scatterers/mm$^3$ [26] depending on ultrasound transducer properties.

An example ultrasound scan is given in Figure 1.2. It is a scan of a mother’s womb. The hand of the foetus is clearly visible. The dark areas around the hand represent the amniotic fluid. It does not contain any significant scatterers and so there is no reflected wave, resulting in the dark areas. The areas to the top, bottom right and bottom left of the scan show areas of speckle. These can be related back to the physiology of the mother.

Although speckle is often seen as detrimental to image quality and research has been invested into reducing its effects, some speckle characteristics can be exploited. Speckle is sometimes used in flow rate calculations because the speckle pattern through vessels changes while the speckle pattern in the stationary tissue will be constant. This property can provide quantitative flow rate measurement of fluid. Further, because the speckle pattern of moving objects varies with time, it can be averaged out of the signal thus providing some noise cancellation.
1.2.3 Focusing

Focusing is typically done through the use of many transducer elements. Each transducer is composed of many (sometimes hundreds) of transducer elements. With time-delay focusing, each element produces an identical ultrasound wave that is shifted in time. Focusing increases the incident ultrasound energy on a focus point thereby increasing the scattered power, in turn the image near the focal point. An example of this is given in Figure 1.3. Here, the ultrasound transducer consists of seven equally spaced elements. Each element applies a time delay to focus the ultrasonic energy at a single point (the scatterer).

Focusing can be achieved in various ways. The most common type of focusing is used to focus the transmit ultrasound beam at a particular axial depth. Other transducer arrangements, such as 2D transducer arrays, allow for focusing in the elevation direction as well. As with transmit focusing, receive focusing is often employed to improve the response from a particular region. One advancement to this is dynamic receive focusing [27]. Instead of focusing at a single axial depth, dynamic receive focusing segments the receive data into regions of equal thickness. Time delay focusing is then individually applied to these regions so as to improve the received signal at each receive depth. Other focusing schemes have also been proposed [28, 29].
Chapter 1. Introduction

Focusing poses several challenges for CAD systems. Medical abnormalities such as tumours can appear anywhere within the ultrasound B-mode image. Because transmit focusing is limited to a specific spatial location, it may distort or blur these abnormalities outside of the focusing area. As some CAD systems use a priori information about the abnormalities to effectively detect them, this can lead to issues for areas which are not properly focused. The abnormalities which are not within the focused region may not match a known profile. Properties of the abnormality such as size, shape, contrast or sample statistics can vary based on distance from the focused region. Further, because focusing is done at the stage of image acquisition, the images cannot simply be refocused after being acquired.

1.3 Detection Methods

In this section various methods for detecting abnormalities in ultrasound images will be reviewed. Current CAD systems are briefly discussed in Section 1.3.1. The DORT and FDORT algorithms along with a few simulations showcasing the efficacy of FDORT are given in Section 1.3.2.

1.3.1 CAD Systems

CAD systems take many different approaches in facilitating the detection of abnormalities. Some systems use filtering [30,31] to improve image quality. These can be broken up into linear and nonlinear filters. Linear filters include mean filters where the magnitude of homogeneous regions such as speckle is replaced by the mean. These types of filters typically suffer from blurring at edges so advanced forms have also been proposed [32]. Nonlinear filters include those such as the order statistic filter [33]. These types of filters typically use median values so they are less susceptible to distributions with long tails.
Other filtering techniques such as those using wavelet transforms have also been proposed [34]. The aim of these approaches is removing wavelet coefficients that correspond to noise. Thresholding as well as Bayesian schemes have also been proposed [35, 36]. Whatever the method, the goal of these algorithms is image enhancement which could include speckle reduction, increasing contrast or edge preservation in ultrasound images. After processing, these ultrasound images can either be reviewed by physicians or be used for further image processing.

Segmentation algorithms partition the ultrasound image so that radiologists can better differentiate anatomical and physiological aspects of the image. One approach to this is to compare the statistics of neighbouring regions [37,38]. In these methods, the ultrasound image is typically broken up into small blocks and the statistics of neighbouring blocks is compared. Thus, these algorithms were somewhat adaptive to local statistics of the image.

Another approach is an active contour model (sometimes referred to as a snake model) where regions grow to create an outline that distinguishes an object from the background [39]. In this approach, a seed sample is selected and it begins to grow according to local statistics such as intensity and texture. These regions would grow until they hit the boundaries and thus be able to distinguish areas that are somehow different from each other. However, generating the initial shape and location of the original seed is not a straightforward task and can be prone to errors.

Other solutions such as Markov random fields [40,41] and neural networks [42], among others, have also been proposed [43]. These pattern matching algorithms often require training data or some sort of a priori information about the object being scanned. Thus, the effectiveness of these algorithms depends upon the physical characteristics of the abnormality. Moreover, training data requires significant preprocessing. The profiles for known abnormalities have to be fed into these systems so that a database can be formed. This can be a resource intensive task requiring radiologists to individually identify and
outline known abnormalities. Other pattern matching algorithms are limited in scope so that they cannot process the entire image and thus require some intervention or initial seeding by operators to produce reasonable results.

1.3.2 DORT and FDORT

As an alternative to pattern matching algorithms, time reversal offers a way in which to automatically detect target scatterers without any \textit{a priori} information. The time reversal process relies on a fundamental symmetry that holds in all areas of physics, except in the area of thermodynamics [44]. It states that the reversal of the final conditions of a process will elicit the initial conditions. This was first observed in the field of optics. In the mid 1800s, Stokes showed that reversing the reflected and refracted light beams (due to shining a light upon a boundary) resulted in the same intensity of light directed in the exact opposite direction [45].

A similar observation was made in the field of acoustics. It was found that successive transmissions of the time reversed received acoustic waves began to focus on the brightest scatterer in the insonified medium [46]. In subsequent work by the same group, the DORT (the French acronym for “decomposition of the time reversal operator”) algorithm was introduced [47]. It involved determining eigenmodes of the so-called time reversal operator, a matrix that represents the received signal at each of the receive transducer array elements after a transmission by each individual transmit array element. These eigenmodes were then used to focus on individual abnormalities. Later, the FDORT (Focused DORT) algorithm was introduced. Instead of requiring each transducer element to transmit individually, it allowed the use of focused transmissions by the entire ultrasound transducer.

It is important to note that the goal of the DORT and FDORT algorithms is to provide an automated focusing mechanism on strong scatterers (i.e., abnormalities); it is not a method for determining the spatial locations of those abnormalities. The eigen-
Table 1.1: FDORT Simulation Parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
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</thead>
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<tr>
<td>Ultrasound Speed</td>
<td>1540 m/s</td>
</tr>
<tr>
<td>Center Frequency</td>
<td>3 MHz</td>
</tr>
<tr>
<td>FWHM Bandwidth</td>
<td>2.34 MHz</td>
</tr>
<tr>
<td>Sampling Rate</td>
<td>100 MHz</td>
</tr>
<tr>
<td>Attenuation</td>
<td>1.5 dB/MHz-cm</td>
</tr>
<tr>
<td>Number of Array Elements</td>
<td>64 elements</td>
</tr>
<tr>
<td>Element Lateral Width</td>
<td>0.24 mm</td>
</tr>
<tr>
<td>Element Elevation Height</td>
<td>5 mm</td>
</tr>
<tr>
<td>Inter-Element Spacing</td>
<td>0.01 mm</td>
</tr>
</tbody>
</table>

modes which it returns provide the user with phase shifts that can be applied to each individual transducer element. For example, the eigenvector corresponding to the maximum eigenvalue should provide the delays required to focus on the strongest scatterer. If the eigenvalues are ordered in a nondecreasing fashion, the second eigenvalue will be the second largest eigenvalue. This eigenvector should provide the delays required to focus on the second strongest scatterer, the third should focus on the third strongest scatterer and so on. This then allows for time-delay focusing on specific scatterers.

Some sample results from the FDORT algorithm are now presented. The simulation parameters used are given in Table 1.1. The FDORT algorithm required the specification of several focusing locations. For these simulations, one-hundred focusing locations were placed at an axial depth of 60 mm. They were chosen so that they were equally spaced between a lateral distance of $-15$ to $15$ mm.

The first simulation uses a phantom of two targets, each represented by a single scatterer. The two scatterers are of different magnitudes located at an axial depth of 60 mm. The stronger of the two scatterers has twice the reflectivity and is located at a lateral distance of 5 mm. The weaker of the two is located at a lateral distance of $-10$ mm. A B-mode image of the two scatters is provided in Figure 1.4a. Because the goal of the DORT and FDORT algorithms is automated focusing, one way in which to visualize the results is through a maximum pressure map. The panels in Figure 1.4 show the maximum
pressure induced by the ultrasound transducer at each spatial location. Thus, for the DORT or FDORT algorithms to be successful, they should result in maximum induced pressure at the location of the strongly reflecting scatterers.

The eigenvectors of the time reversal operator provide focusing information for the potential targets. When the first eigenvector is used to focus the transducer, the resulting normalized pressure map is given in Figure 1.4b. Note that the pressure is normalized to the maximum pressure at any spatial location. As is evident, the maximum pressure is elicited at an axial depth of 60 mm and at a lateral distance of 5 mm. Thus, the algorithm is able to focus on the stronger of the two scatterers. Likewise, the second eigenvector is able to focus on the second strongest target (Figure 1.4c). As there are only two targets, the third eigenvector does not provide any meaningful focusing information (Figure 1.4d).

Although a promising approach, the time reversal process has several shortcomings. Both the DORT and FDORT algorithms appear to be unable to handle the case when there are two eigenvalues of similar magnitude. This occurs when the targets are of similar reflectivity and distance from the transducer as is the case in Figure 1.5a. In this example, the two scatterers are at lateral distances of −5 mm and 5 mm and have equal magnitudes. As is evident from the first eigenvector, the algorithm attempts to simultaneously focus on both targets, seemingly unable to disambiguate them (Figure 1.5b). A similar statement can be made for the second eigenvector (Figure 1.5c) and it can be seen that the third eigenvector does not provide any further information (Figure 1.5d).

Another shortcoming of the DORT algorithm is its susceptibility to speckle [48]. Because the DORT algorithm requires transmission by each array element individually, the algorithm appears to be highly dependent upon speckle. Thus it requires high contrast targets to be effective. An attempt was made to address this problem in the newer FDORT (Focused DORT) approach. An example with speckle is given in Figure 1.6. The scatterers that make up the speckle have a density of 10 scatterers/mm$^3$ which, as explained further in Section 2.4, was found to be a good balance between computation
Figure 1.4: FDORT results with two different targets.
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Figure 1.5: FDORT results with two targets of the same magnitude and distance from the transducer.
time and speckle simulation accuracy [26, 49]. As with the first example, there were two highly reflecting scatterers to represent two targets in the phantom. Both of these scatterers were placed at an axial depth of 60 mm. They had magnitudes of 30 and 35 dB (normalized to the magnitude of a single speckle scatterer) and were placed at lateral distances of $-10$ and 5 mm, respectively.

A B-mode scan of this phantom is provided in Figure 1.6a. From this image, it is evident that the highly reflective scatterers are easily visible. They are roughly 20 dB stronger than the background speckle. Note that although they are at least 30 dB stronger than a single speckle scatterer, they are only about 20 dB stronger than the background speckle. This is because the background speckle is composed of many scatterers, each of which contributes to the back-scattered signal. The pressure map for the first eigenvector is given in Figure 1.6b. Although the magnitude of two targets is roughly 20 dB larger than the background speckle, the FDORT algorithm is unable to focus on either. Further, it should be noted that the FDORT algorithm requires specification of the areas within the medium upon which to focus. Therefore, it is not entirely independent of human intervention.
1.4 Objectives

The main purpose of this work is to develop a CAD system to detect abnormalities (targets) in an ultrasound image which uses little to no \textit{a priori} information. The locations of these targets can then be used by radiologists to better determine the location of potential abnormalities or for further processing by other algorithms. Moreover, the target locations can be used to provide areas on which the ultrasound operator can refocus the ultrasound beam thus creating clearer images of potential targets.

As explained in Section 1.3.1, current CAD systems make assumptions about the medium or type of target for which the system is searching. The goal of this work is to find \textit{any} potential target in the B-mode scan. As such, this work is not limited to a single type of target. Some systems limit their scope to achieve better results for specific cases. The aim of this work, on the other hand, is to propose a general scheme for detecting targets. To accomplish this, variations of the CLEAN and CFAR algorithms are proposed. Neither of these appear to have been previously used for target detection in ultrasound images.

The CLEAN algorithm was originally developed for use in radio astronomy [50] to enhance celestial images. It was used to disambiguate true celestial scatters from ones that were falsely created by interference of side lobes between closely spaced scatterers. It was also used to suppress the appearance of background noise, usually a product of atmospheric effects. Without noise or interference, the resulting image is then simply the sum of the signals from the individual stars.

Along with the resulting image free of background noise, the CLEAN algorithm is often used to extract some information about each of the individual targets. This can then be used for further image processing or as a method for feature extraction in its own right. For example, for each located target, the algorithm returns the associated location and backscattered response from the input image. This feature has since allowed the CLEAN algorithm to be used in a number of different applications such as time series
analysis [51] and in wireless communication, where it has been used for channel estimation as well as multi-path propagation analysis for many independent signals [52].

As will be seen, the CLEAN algorithm is highly dependent on the choice of a detection threshold which helps to determine whether a potential target is part of the background or if it is a true target. Choosing the detection threshold requires some intuition and is thus somewhat subjective. In the field of radar, the constant false alarm rate (CFAR) series of algorithms have often been used to circumvent this limitation [53]. Thus, a variation of the CFAR algorithms is proposed. It requires the user to specify a tolerable false alarm rate and calculates a threshold based on regional statistics. In this way, users do not have to choose an arbitrary threshold, rather, the rate of false positives is selected and a threshold is computed based on this. To the best of our knowledge, there has been no work on providing a theoretical basis for the choice of the threshold.

Throughout this manuscript, the term “target” is used to describe an area of medical relevance in an ultrasound B-mode image. It is borrowed from literature on the CFAR algorithm, a technique used in radar where, often, the goal is to discern potential targets from background noise. Likewise, it is the goal of this work to differentiate between areas of medial interest (targets) and speckle. More specifically, it is used to describe a region of high contrast relative to background speckle. For the purposes of this work, contrast is thus defined as

\[ C = \frac{S_{out} - S_{in}}{S_{out}} \]

where \( S_{out} \) is the mean of the back-scattered signal outside of the target area and \( S_{in} \) is the mean of the signal inside of the target area [54].

1.5 Thesis Structure

The remainder of this work is organized as follows. Chapter 2 presents the CLEAN algorithm and how it can be used for target detection. As will be seen, the CLEAN
algorithm relies heavily on a user specified threshold. To place the choice of the threshold on a sound theoretical footing, the CFAR algorithm is adapted from radar systems. The combined CLEAN/CFAR algorithm, along with some simulation results, is presented in Chapter 3. Finally, some concluding remarks and potential areas for future work is given in Chapter 4.
This chapter presents the CLEAN algorithm and its modification for use with ultrasound B-mode images. It is used to determine the location of potential targets. The algorithm itself is developed in Section 2.1. To show how the CLEAN algorithm works, a simple example is provided in Section 2.2. The CLEAN algorithm has several parameters. Their effect on the algorithm output is given in Section 2.3. Then, the algorithm is tested on phantoms using Field II, a software package for simulating ultrasound B-mode images [55]. The simulation setup is provided in Section 2.4 and the results are presented in 2.5. Finally, a summary is given in Section 2.6.

2.1 Proposed Algorithm

In the following section a modified version of the CLEAN algorithm is introduced and an example of its use is presented. The goal of the algorithm is to locate potential targets and to remove, from the input signal, any noise or interference from background speckle. Thus, the output of the algorithm is simply the locations of the targets. With these locations, a new ultrasound B-mode scan can be created that contains only the response
from the potential targets so that the resulting image will be free of speckle and noise\(^1\).

As will be seen, the CLEAN algorithm can extract features from each of the targets, including their locations and the temporal responses to the transmitted signal. These responses can then be used to recreate a B-mode scan free of speckle and its associated noise.

The CLEAN algorithm begins with the input data samples \(D_1[n], n = 0, \ldots, N - 1\), equivalently a vector \(D_1\). For simplicity, assume that \(D_1\) is one dimensional (this assumption will be relaxed later). In the case of ultrasound, this vector corresponds to samples of the returned signal arranged as a vector. In the first step of the algorithm, the maximum value of the absolute value of \(D_1\) is found. If the maximum value is below the detection threshold, \(T_{\text{det}}\), the algorithm terminates and declares no targets to be present. Otherwise, in the next step, the maximum's location is noted as \(v_1\) and its amplitude is noted as \(a_1\), i.e.,

\[
v_1 = \arg \max_n |D_1[n]|,
\]

and

\[
a_1 = D_1[v_1].
\]

Next, a portion of \(D_1\) around the location \(v_1\) is decreased according to a decimation function \(G[n], n = -w, \ldots, w\), equivalently a vector \(G\), and the result is stored in \(D_2\), i.e.,

\[
D_2[n] = D_1[n]G[n - v_1].
\]

The algorithm, which is presented in Figure 2.1, iterates with each new target location identified in every iteration. The algorithm terminates when it determines that there are no more targets within the image.

\(^1\)Another option, not expanded upon here, is to retransmit the incident signal, but now focused on the locations specified by the CLEAN algorithm.
Chapter 2. The CLEAN Algorithm

Inputs
- \( D_i \) The input data vector.
- \( G[n] \) Decimation function.
- \( T_{det} \) Detection threshold.

Outputs
- \( a \) Magnitudes of detected targets.
- \( v \) Locations of detected targets.

Algorithm
1. \( \text{while } \max(D_i) > T_{det} \text{ do} \)
2. \( v_i = \arg \max_n |D_i[n]| \)
3. \( a_i = D_i[v_i] \)
4. \( D_{i+1}[n] = D_i[n]G[n - v_i] \text{ for } n = 0, \ldots, N - 1 \)
5. \( i = i + 1 \)
6. \( \text{end while} \)
7. \( \text{return } v = [v_1, \ldots, v_M], a = [a_1, \ldots, a_M] \)

**Figure 2.1:** The CLEAN algorithm as proposed for ultrasound.

The decimation function \( G \) is a windowing function which decreases the magnitude of \( D_i \) near the location of a potential target. Its width is \( 2w + 1 \) where \( w \) (called the decimation window half-width) defines the bounds of the target response. It decreases the signal by the decimation factor, \( \beta \), such that \( 0 \leq \beta < 1 \). The decimation function leaves the remainder of \( D_i \) unchanged. It is defined as

\[
G[n] = \begin{cases} 
\beta & \text{if } -w \leq n \leq w \\
1 & \text{otherwise}
\end{cases}
\]  

Among other things, the decimation function \( G \) defines the range of indices of the signal to be attributed to the target detected in each iteration. In the example above, for instance, it is assumed that the maximum response from the target has a width of \( 2w + 1 \) samples and that its maximum is centred in this window. The decimation function
decreases the value of $D_i$ in this window and leaves the remainder of the signal unchanged. A more thorough discussion of the decimation function is given in Section 2.3.1.

Upon its completion, the outputs of the CLEAN algorithm are the spatial locations $(v_i, i = 1, \ldots, M)$ and amplitudes $(a_i, i = 1, \ldots, M)$ of the $M$ detected targets. These locations can then be used to form an “ideal” receive signal, which is typically an application specific task. For example, template target responses can be inserted in a new data vector at the locations specified by $v$ with amplitudes specified by $a$. In the case of ultrasound, these target responses could be the point spread functions (PSF) of the scatterers. Further, the user can choose to extract the target response to the transmitted signal in $D_i[v_i - w, \ldots, v_i + w]$. Some applications have used this feature to repopulate an output image [52]. An example of this is provided in Section 2.2.2. For the purposes of this thesis, we are only interested in the locations since they correspond to the location of the detected targets.

\section{2.2 A CLEAN Example}

In this section, an example of the CLEAN algorithm is presented. It is applied to a data vector with two targets of differing magnitudes. After the CLEAN algorithm returns the locations and amplitudes of the targets, an output vector is created. This corresponds to the “ideal” response, free of any speckle and its associated noise. Two methods are presented for this.

\subsection{2.2.1 Step 1: CLEAN}

Consider a scenario in which the transmitted signal is a Hanning modulated sine wave with a duration of 85 samples (as shown in Figure 2.2a). Suppose that there are two targets located 62 and 122 samples from the transducer as measured on the receive time scale. In this example the detection threshold ($T_{det}$) is set to 0.5, the decimation factor
$(\beta)$ is 0.1 and the decimation window half-width $(w)$ is 42 samples. If each target has a Dirac impulse response and there is no attenuation, the received signal would be as shown in Figure 2.2b. This received signal is $D_1$, and is also the input to the CLEAN algorithm. Note that the signal from the scatterer at sample 122 is slightly weaker than that of the scatterer at sample 62. The detection threshold, $T_{det}$ is visible as a dotted line across the plot. Because the algorithm uses the magnitude of the input vector, $-T_{det}$ is also visible on the plot for reference.

In the first iteration of the algorithm, the maximum magnitude of $D_1$ is found to be 1.0. Because the maximum is above the detection threshold, it is recorded as $a_1$ and its location, sample 62, is recorded as $v_1$. In the next step, the range of samples up to $w$ samples from $v_1$ is decimated by $\beta$. The result is recorded in $D_2$ as

$$D_2[n] = \begin{cases} 
0.1D_1[n] & \text{if } 20 \leq n \leq 104 \\
D_1[n] & \text{otherwise}
\end{cases}, \quad (2.2)$$

and is illustrated in Figure 2.2c.

In the second iteration, the maximum magnitude is found to be at sample 122 (stored in $v_2$) and the amplitude at this location (0.8) is recorded as $a_2$. The range of samples around sample 122 is then decimated such that

$$D_3[n] = \begin{cases} 
0.1D_2[n] & \text{if } 80 \leq n \leq 164 \\
D_2[n] & \text{otherwise}
\end{cases}, \quad (2.3)$$

which is shown in Figure 2.2d.

At this point, the maximum magnitude of the data vector ($D_3$) is 0.1, well below the detection threshold $T_{det}$. Therefore, the algorithm determines that there are no more targets in the signal and it terminates. Since the goal of applying CLEAN to ultrasound is to detect targets, the algorithm returns the vectors $v = [v_1, v_2] = [62, 122]$.
and \( \mathbf{a} = [a_1 \ a_2] = [1.0 \ 0.8] \) signifying the locations and amplitudes, respectively, of the potential targets.

### 2.2.2 Step 2: Re-population

After the CLEAN algorithm is run, an output image of the “ideal” response can be formed. The “ideal” response is typically the response from the medium being scanned without noise, speckle or interference. Essentially, it is the response from just the targets. Thus, only the targets should be visible in this output image.

Because this is an application specific task, there are many ways in which to do this. Two of these methods are presented here. The first method requires knowledge of the impulse response of the targets. The second method uses the responses from the input data vector and places these responses at the target locations found by the CLEAN algorithm. Because this resembles individually placing the responses at the determined target locations, in this work this is called “repopulating” the data vector.

**With the Impulse Response**

The impulse response of the targets, if known, can be used to create the output image. In this example, it is assumed that each point scatterer has an impulse response of the Dirac delta function. However, it is possible to use more accurate approximations of the spatial impulse response such as the point spread function.

First, a new data vector \( C[n], n = 0, ..., N - 1 \), equivalently \( \mathbf{C} \), is created such that for every \( v_i \) found by the CLEAN algorithm,

\[
C[v_i] = a_i,
\]

(2.4)

and \( C[n] = 0 \) otherwise. In other words, the amplitude of each target is placed where it was found. For this example, \( \mathbf{C} \) is represented in Figure 2.3a, where a pulse is present.
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Figure 2.2: An example of the CLEAN algorithm. Two targets exist at samples 62 and 122. When the transmit signal (a) is used, the resulting signal is shown in (b). This is also the input to the CLEAN algorithm. The algorithm finds the first target at sample 62 and decimates the surrounding region resulting in (c). In the next iteration, the target at sample 122 is found and decimated resulting in (d). At this point, the maximum signal magnitude is below the detection threshold so the algorithm terminates.
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Figure 2.3: Reconstructing the receive signal with the targets’ impulse response. The output of the CLEAN algorithm is arranged into a vector (a). It is then convolved with the impulse response of the targets (b).

at sample 62 with an amplitude of 1.0 and another is at sample 122 with amplitude 0.8.

Next, $C$ is convolved with the “ideal” or template signal. In the case of this example, it is convolved with the transmit pulse, a Hanning modulated sine wave (Figure 2.2a). The resulting signal should then resemble the response from the scatterers. It is illustrated in Figure 2.3b and closely resembles the input signal, Figure 2.2b.

Without the Impulse Response

In the presented version of the CLEAN algorithm, the decimated portions of the data vectors $D_i$ are disregarded. Some variations, however, use these to repopulate the output image [52]. Such an approach is particularly useful in dispersive media where the insonating signal changes shape as it propagates. A new step could be added to the algorithm presented in Figure 2.1 that records the decimated portion of the data vector. For example, the following equation

$$R_i = D_i[v_i - w, ..., v_i + w], \quad (2.5)$$
where $R_i$ is the response of the target identified in iteration $i$, can be added just before line 4 of the algorithm. For this example

$$R_1 = D_1[20, ..., 104], \quad (2.6)$$

and

$$R_2 = D_2[80, ..., 164]. \quad (2.7)$$

These are illustrated in Figures 2.4a and 2.4b, respectively.

As in the previous case, an output vector is next created. In this case, however, it is created from the these extracted responses using the locations of the maximums, $v_i$. The responses would first be placed at their respective locations as

$$C_i[n] = \begin{cases} 
R_i[n - v_i] & \text{if } v_i - w < n < v_i + w \\
0 & \text{otherwise}
\end{cases}, \quad (2.8)$$

where $C_i$ is a temporary vector that represents the target found in iteration $i$. For the example of this section, $C_1$ and $C_2$ are given in Figures 2.4c and 2.4d, respectively.

Once each of the extracted responses is placed at the corresponding target location, these are then added to form the output vector as

$$C[n] = \sum_{i=0}^{N-1} C_i[n], \quad (2.9)$$

where $C$ is the final output vector. The result is shown in Figure 2.4e. Again, this is comparable to the input signal Figure 2.2b.

The purpose of this example was to present the CLEAN algorithm and demonstrate how it functions. Because of this, it was a relatively trivial example—there was no speckle, there was no noise and there were only two scatterers. More complex simulations will be given in Section 2.2.
Figure 2.4: Reconstructing the receive signal without the targets’ impulse response.
2.3 CLEAN Parameters

The CLEAN algorithm has several parameters whose influence on the algorithm’s output is not immediately obvious. In this section, the choice of these parameters will be discussed.

2.3.1 Decimation Function

The decimation function $G$, defined by window length $w$, and decimation factor $\beta$, serve three functions. They help extract the target response from the signal, help prevent (but do not guarantee) a target from being detected in future iterations of the algorithm and ensure that the algorithm terminates.

Of the CLEAN algorithm’s parameters, $\beta$ has a unique role in extracting the target response and controlling the speed at which the algorithm terminates. The decimation factor ensures that in each iteration, the maximum value in the data vector, $D_i$, decreases over the course of the algorithm. In any single iteration, $i$, of the algorithm, the maximum value of the data vector is not guaranteed to decrease. For example, suppose that there are two equally large maxima separated by more than $w$ samples. In other words, suppose that

$$|D_i[j]| = |D_i[k]| = \max_n |D_i[n]|,$$  

(2.10)

where $j$ and $k$ are the locations of the two maxima and that $|k - j| > w$ so that the two maxima are more than a decimation window away from each other. Then, when the CLEAN algorithm is run, one of the two maxima will first be operated upon. If this is location $j$, the area around this location will be decimated. However, because $|k - j| > w$, the maximum at location $k$ will not be reduced. Then, $\max_n |D_i[n]| = \max_n |D_{i+1}[n]|$ so that the maximum did not decrease between these two successive iterations. However, the number of maxima does decrease. Eventually, then, the maximum value of $D_i$ will be smaller than the detection threshold.
For smaller values of $\beta$, a reduced portion of $D_i$ is kept for the next iteration since the smaller the $\beta$ the larger the reduction within $w$ samples of $v_i$. This can help reduce the runtime of the algorithm by increasing the speed at which the maximum values fall below the detection threshold. On the other hand, if $\beta$ were close to one, a very small fraction of $D_i$ would be removed on each iteration. In some cases, this may result in the same target being detected in several iterations of the algorithm. It will then slowly be decreased to below the detection threshold. Each target may be detected multiple times thus increasing the number of iterations and resulting in an increase in the runtime of the CLEAN algorithm.

Although small values for $\beta$ can increase the algorithm runtime, they may introduce large discontinuities in the target responses that are extracted from the data vector. For example, if two targets were detected more than a window width but less than two window widths of each other such that

$$w < |v_j - v_k| \leq 2w,$$  \hspace{1cm} (2.11)

for any two iterations $j$ and $k$ where $j < k$, their decimation windows will overlap. If a small $\beta$ was used, the signal decimated in iteration $j$ will include some of the response from the target at location $v_k$ (which is later found in iteration $k$). Then, in iteration $k$, a portion of the signal, having been removed earlier in iteration $j$, will be missing. Thus, a discontinuity will be formed at $v_j + w$ in the extracted waveform from iteration $k$. This is visible in the example from Section 2.2. The extracted vectors for the first and second iterations are shown in Figures 2.4a and 2.4b, respectively. Because the responses from the two targets overlap, a discontinuity can be seen at sample $-18$ of the response from $v_2$ (Figure 2.4b).

To prevent this from happening, a large $\beta$ can be used. Then, on each iteration of the algorithm, a smaller fraction of the data vector will be removed from the signal. In this
way, the algorithm will have the opportunity to decrease a different maximum. Consider the example in Section 2.2. There are two large maxima at samples 62 and 122 and they are of similar magnitudes. If $\beta$ is now 0.9 (it was 0.1 in the previous discussion), the algorithm would have to decimate both of these maximum seven times before they are below the detection threshold. In other words, for the maximum at sample 62 to be decimated to below the detection threshold,

$$T_{det} > D_1[62](0.9^m)$$

would have to hold, where $m$ is the number of times the sample is found and decimated by the CLEAN algorithm. This relationship holds when $m \geq 7$ so the sample is decimated 7 times.

The resulting responses, $R_i$, can then be summed for each of the two maxima. For the target at sample 62, this is shown in Figure 2.5a and for the target at sample 122, this is shown in Figure 2.5b. Although there still exists a discontinuity, it is much smaller when compared to Figures 2.4a and 2.4b.
2.3.2 Decimation Half-Width

The number of samples attributed to a target that is then decimated is controlled by the detection window half-width, $w$. The detection window sets the boundaries for what is considered to be a signal caused by a target. Intuitively, the best choice of $w$ depends upon the bandwidth of the transmitted signal, the acoustic properties of the transducer and the insonified medium through which the ultrasound waves travel. Systems with larger bandwidths, for example, require a smaller $w$ because the width of the corresponding point spread function is shorter. Thus, it may seem reasonable to set the detection window according to the width of the transmitted pulse. However, effects within tissue may reduce the validity of this assumption.

The dependence of ultrasound attenuation on frequency as stated in Chapter 1 is given by

$$\alpha = \alpha_0 f^n$$

(2.13)

where $\alpha$ is the attenuation coefficient, $f$ is the frequency and $n$ is a medium dependent parameter that lies in the range between 1 and 2. As a consequence of increased attenuation on larger frequencies, the effective bandwidth of the transmitted pulse decreases. This then causes a broadening of the transmitted pulse with depth in the time domain. Therefore, to adequately decimate the response from the transmitted pulse, the detection window could change as a function of depth.

As mentioned earlier, so far, only one dimensional signals have been discussed. This is appropriate when dealing with ultrasound A-lines but not B-mode images. The CLEAN algorithm can be applied to individual A-lines of the B-mode image but doing so ignores the lateral information between successive A-lines. The data vector, $D$, can be extended to two dimensions so that consecutive A-lines could be columns of the two dimensional matrix and each row would represent a different depth. Then, the decimation half-width $w$ can be extended to the lateral and axial directions. It will then represent both
the lateral and axial half-widths. By doing so, the information stored in subsequent A-lines can be used to better locate the targets and extract a more accurate response, similar to the point spread function.

Throughout this discussion, it has been assumed that the window is chosen so that the location of the maximum value, \( v_i \), is at the centre of the window. This does not preclude the choice of other windows. The window can be chosen according to the properties of the excitation wave. In the case of the example in Figure 2.2, the excitation wave has a maximum in the centre so the window was chosen such that its maximum was also in the centre. If the maximum is not in the centre, an asymmetric decimation function can be used.

### 2.3.3 Detection Threshold

The efficiency of the CLEAN algorithm relies heavily on an appropriate choice for the detection threshold. For a target to be detected, its maximum response must be greater than the detection threshold. As such, the detection threshold differentiates between objects of interest and the background of the image. Setting the threshold too low leads to many false positives. Conversely, if the threshold is set too high, legitimate targets could be missed, thereby increasing the rate of false negatives.

Because the detection threshold sets the minimum power of a target, it can be interpreted as setting the noise floor. However, it can also separate scatterers of different magnitude. For example, it can be used to differentiate between tissue and background speckle, as long as the tissue has a higher contrast than the speckle. On the other hand, it can also be used to differentiate between high contrast targets, such as calcifications, and tissue. The detection threshold, then, is more than just the noise floor.

The detection threshold also effects the runtime of the CLEAN algorithm. Larger detection thresholds will require fewer iterations thus speeding up the algorithm. Smaller detection thresholds will generally result in more targets being detected and may also
result in the same target being detected in multiple iterations of the algorithm. Specifically, if $T_{\text{det}}$ is lowered, one decimation of a target response may not be enough to bring it below $T_{\text{det}}$. Thus, it will again be detected in future iterations and will therefore increase the runtime of the algorithm.

### 2.4 Simulation Methods

To test the CLEAN algorithm, several simulations of the algorithm were performed using Field II, a widely used method for simulating images generated by transducer arrays [55, 56]. The software allows for the change of many parameters having to do with the physical properties of the system. Similarly, the user also designates the shape and arrangement of the ultrasound transducer. As well, the user specifies the spatial locations and magnitudes of all scatters and the simulation software then calculates the pulse-echo response between the transmit transducer, point scatter and receiver.

Field II treats all scatterers as point scatterers. A key property of the simulated medium is the density of point scatterers. The density should be chosen so as to represent the interference effects of the medium and transducer with sufficient accuracy. If the density of the scatterers is too low, the speckle characteristics are not effectively simulated. Conversely, if the speckle density is too high, the medium begins to appear homogeneous. Furthermore, the computation time increases linearly with the number of scatterers. Therefore, there is a trade-off between the accuracy of the simulated speckle and computation time.

After several simulations, it was found that the lateral speckle size remained relatively constant for speckle densities of greater than 10 scatterers/mm$^3$. For the assumed centre frequency of 3 MHz and the chosen transducer parameters, this is consistent with the values reported in the literature [26,49]. Thus, in this thesis, a density of 10 scatterers/mm$^3$ was selected as being a reasonable compromise between the accuracy with which the
speckle was represented in the ultrasound images and the computation time required to perform an ultrasound scan.

Like the background speckle, targets are also composed of many point scatterers. The density of scatterers within the targets was the same as the density of speckle (10 scatterers/mm$^3$). However, the reflectivity of the scatterers within the target areas was set according to the target’s desired contrast. For example, for the targets to appear brighter than the background speckle, the reflectivity of scatterers within the targets needs to be greater than that of the scatterers of the surrounding speckle. The higher reflectivity of target scatterers will result in an increase in the backscattered signal power. Thus, the target areas will appear brighter than the background.

It should be noted that although the term speckle is reserved for the background of ultrasound images (the areas of the ultrasound image that are not attributed to targets), the targets themselves possess a speckle pattern. As discussed in Chapter 1, speckle is an inherent property of the insonified medium. It arises from scatterers that cannot be resolved and thus targets themselves have a speckle pattern. For example, a tumour encompassed by a background of speckle itself is composed of small scatterers. These scatterers also elicit a speckle pattern. For the simulations, as described above, targets comprise of point scatterers of the same density as the background speckle. It is thus expected that targets themselves have a speckle pattern. However, because the scatterers that make up targets have a larger reflectivity than the surrounding speckle, the statistics of the samples within the target area is different from that of the samples of the background.

Throughout the simulations, a number of parameters were kept constant. They have been summarized in Table 2.1. Field II allows for each transducer element to be broken up into smaller sections to more accurately represent the transduction of ultrasound waves. For these simulations, the transducer was subdivided into 10 rectangular pieces so that each portion had a lateral width of 0.24 mm and an elevation height of 0.5 mm.
Table 2.1: CLEAN Simulation Parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ultrasound Speed</td>
<td>1540 m/s</td>
</tr>
<tr>
<td>Centre Frequency</td>
<td>3 MHz</td>
</tr>
<tr>
<td>FWHM Bandwidth</td>
<td>2.34 MHz</td>
</tr>
<tr>
<td>Sampling Rate</td>
<td>100 MHz</td>
</tr>
<tr>
<td>Attenuation</td>
<td>1.5 dB/MHz·cm</td>
</tr>
<tr>
<td>Number of Array Elements</td>
<td>256 elements</td>
</tr>
<tr>
<td>Number of Active Elements</td>
<td>64 elements</td>
</tr>
<tr>
<td>Element Lateral Width</td>
<td>0.24 mm</td>
</tr>
<tr>
<td>Element Elevation Height</td>
<td>5 mm</td>
</tr>
<tr>
<td>Inter-Element Spacing</td>
<td>0.01 mm</td>
</tr>
</tbody>
</table>

The transmit wave chosen was that of a sine wave modulated by a Hanning window. Its time-domain and frequency-domain representations are given in Figures 2.6a and 2.6b, respectively.

Focusing properties were kept consistent throughout the simulations. Transmit focusing was set at an axial depth of 60 mm. Note that because each transducer element was subdivided into 10 units, elevation focusing to this depth was also possible. Of the 256 transducer elements, 64 consecutive elements were active at any given time. These 64 elements were chosen such that their centre was located on the array at the closest point to the area being scanned. In other words, a line perpendicular to the transducer array that passes through the area to be scanned would pass through the centre of the 64 elements used to transmit the ultrasound wave. Dynamic receive focusing was used with the receive focal zones spaced by 10 mm.

Creation of the ultrasound B-mode images was also kept consistent between simulations. Each of the images is a composition of 50 equidistant A-lines. The scans covered the lateral area from \(-20\) mm to 20 mm. Thus, the spacing between consecutive A-lines was 0.82 mm. Interpolation between consecutive A-lines was used for display purposes. To increase the range of data visible in the B-mode images, logarithmic compression was employed to compress the data into a range of 30 dB.
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Figure 2.6: The excitation wave used in the simulations. The time (a) and frequency (b) domain representations are given above.

After creation of the simulated phantom, the output ultrasound B-mode images were tested. The parameters for the CLEAN algorithm were kept consistent throughout the testing. The window half-width ($w$) in the axial direction was set to half of the width of the excitation wave (42 samples or 0.65 mm) and, based on the experimental point spread function, it was set to 1.63 mm (two ultrasound A-lines) in the lateral direction. This means that the CLEAN algorithm used a rectangular window to decimate the data vector. The decimation factor, $\beta$, was set to 0.5.

The output of the CLEAN algorithm is the location and amplitude of potential targets. As described in Chapter 1, these locations can be used directly to assist health care workers in the detection of abnormalities or they can be used for further processing. For the simulations presented here, the target locations are used to generate a new ultrasound image—one that is a composition of all of the target locations found by the CLEAN algorithm and is thus free of speckle. Note that because targets can be of any size, it is possible and even desirable that the CLEAN algorithm returns the location of many points within a large target.
2.5 Results

In this section, some results obtained using the CLEAN algorithm will be presented and discussed. Although the algorithm reduces the appearance of speckle, it would be prudent to first test the algorithm’s ability without the effects of speckle. Therefore, the first example will illustrate the algorithm on a simulated phantom of four targets without any speckle. The second simulation uses the same phantom as the first but introduces speckle.

2.5.1 Simulation without Speckle

To test how the algorithm responds to a phantom without speckle, it was tested on a phantom of four spheres. The four spheres have centres located at a lateral distance of $-10 \text{ mm}$, axial depths of 45, 53, 63 and 75 mm, and have diameters of 2, 4, 6 and 8 mm, respectively. The density of scatterers within the spheres was 10 scatterers/mm$^3$. The phantom is given in Figure 2.7a. Note that time-gain compensation was used to counteract the effects of attenuation.

A range of detection thresholds were tested. These thresholds are presented in decibels and are relative to the maximum magnitude of the B-mode image. A lower detection threshold should allow for more targets to be detected at the risk of increasing the false positive rate. The results for a detection threshold of $-10 \text{ dB}$ are presented in Figure 2.7b. The four spherical targets are visible and, for the most part, their circular shape is conserved. However, the targets no longer appear as dense as they appeared in the initial scan (Figure 2.7a). Because the target spheres are not homogeneous, the areas below the detection threshold are removed, leaving a more sparse representation of the target.

As the detection threshold is increased to $-7 \text{ dB}$, this trend continues (Figure 2.7c). The 4 mm and 6 mm diameter targets are no longer as well defined in terms of their
Figure 2.7: CLEAN results on the lateral phantom without speckle.
shape and the 2 mm target is now altogether missing. When the detection threshold is increased even further to $-6$ dB (Figure 2.7d), the 2 mm target is again not visible. The 4 and 6 mm targets are still visible but each is now being represented by fewer points. The 6 mm target is still visible.

These results illustrate the role of the detection threshold in the algorithm. It can be seen, as expected, that likelihood of a target being detected decreases as the detection threshold increases. Moreover, it is evident that larger targets are more likely to be detected. The results in this section are limited to phantoms without speckle. In the next example, the CLEAN algorithm will be tested against the same phantom with speckle.

### 2.5.2 Simulation with Speckle

In this section, the same phantom as in Section 2.5.1 will be tested but it will now include speckle. The locations and magnitudes of all the scatterers which make up the four target spheres are the same as in the previous section. The only difference is the addition of speckle. Speckle was added such that the four targets have a contrast, as defined by (1.5), of 12 dB relative to the speckle. The parameters to the CLEAN algorithm and the acoustic properties of the simulation are all otherwise the same as those in the previous section.

The results for this test are illustrated in Figure 2.8. When a threshold of $-10$ dB (relative to the maximum signal magnitude) is used, the CLEAN algorithm returns the locations of targets in the B-mode scan given in Figure 2.8b. Each of the four spherical targets are visible in the scan. The smallest target, however, (diameter of 2 mm) consists of just two scatterers. The other three maintain their shape for the most part. However, at this detection threshold there are quite a few false positives, especially at axial depths smaller than the focal point of the transducer array, 60 mm. The large number of false positives makes it difficult to disambiguate the smallest of the four targets.
When the detection threshold is increased to $-7 \text{ dB}$, the number of false positives falls sharply (Figure 2.8c). At this threshold there is only a single false positive. However, the smallest target is now represented by just a single scatterer and the other three targets are beginning to lose their shape. This trend continues as the detection threshold is raised to $-6 \text{ dB}$ (Figure 2.8d). At this threshold, the smallest target is no longer detected by the CLEAN algorithm.

### 2.6 Summary

This chapter introduced the CLEAN algorithm and its application to B-mode ultrasound images. The algorithm was presented, an example was given and some of the algorithm’s parameters were discussed in more detail. Finally, a few simulations were given showcasing the efficacy of the algorithm in the detection of high contrast targets both with and without speckle.

The results appear promising but, as evident from the simulations, the results of the CLEAN algorithm heavily depend upon the detection threshold. As presented here, it is a user specified value and, unfortunately, there is a sense of arbitrariness in its selection. In practice, the operator of the ultrasound device or even the image processor (as the algorithm can be run post image capture) requires a sense of understanding of what a good detection threshold should be. Although an application specific measure, in general there is a trade off between the rate of false positives and false negatives. Therefore, this could potentially be an arbitrary choice contingent upon the user’s preferences and past experiences.

Moreover, the algorithm as described assumes that the threshold is constant throughout the image. In many cases, this is an idealization. Variation in tissue properties can induce a dependence on spatial location for the point spread function. Moreover, this can lead to localized changes in speckle. Further, although time-gain compensation helps
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Figure 2.8: CLEAN results on the lateral phantom with speckle.
alleviate the effects of attenuation in tissue, it may be inaccurate [22]. Thus, it would be ideal for the detection threshold to adapt to the local information within the B-mode image. As a result, there is a need for an automated choice of the detection threshold. This is discussed further in the following chapter.
Chapter 3

Adaptive Thresholding

The form of the CLEAN algorithm presented in Chapter 2 demonstrated the ability to detect targets with little input from the user. It did not require training data nor was it restricted by the size or shape of the target. However, the detection threshold parameter required the user to have some experience or intuition as to its proper choice. Moreover, because it is kept constant for the entire image, the algorithm does not have the ability to adapt to the local statistics of the speckle. To address these concerns, an algorithm for adaptive thresholding is now proposed.

The remainder of this chapter is organized as follows. Some background information on CFAR, how it works, its advantages and disadvantages is first provided in Section 3.1. Then, a specific CFAR algorithm for use with CLEAN is proposed in Section 3.2. Several simulations are then run to test the algorithm. The choice of simulation parameters is presented in Section 3.3 and the results are provided in Section 3.4. Finally, some concluding remarks are given in Section 3.5.

3.1 Constant False Alarm Rate

The CFAR algorithm was originally developed for radar systems to detect targets among background noise with unknown statistics. As in the CLEAN algorithm, a radar detects
a target by comparing the return signal to a threshold. It was designed such that the user inputs their tolerable false alarm rate and the algorithm determines a threshold based on this preference \[53\]. If the user is willing to accept a large false alarm rate, their probability of detection will increase. If, however, they are willing to sacrifice the probability of detection, they will have fewer false positives. Thus, the user does not have to be concerned with the magnitude or statistics of the background—they must simply decide on an appropriate tolerance for false positives. This removes the ambiguity of choosing a detection threshold. Moreover, it helps to standardize the algorithm’s results within different sections of the same image. This can help to mitigate the effects of imperfect time-gain compensation. Further, it also helps to standardize the algorithm’s results over different ultrasound images which can help reduce the dependency of diagnosis on the attending health care worker. For these reasons, the CFAR method is adapted here for use in conjunction with the CLEAN algorithm.

A general CFAR algorithm is illustrated in Figure 3.1. The input to the algorithm is a discrete signal \( x[n], n = 0, \ldots, N - 1 \), or equivalently \( x \), and the user specified false alarm rate \( P_{FA} \). The output is a binary decision: whether or not the target sample is different from its surroundings. In the figure, the sample being tested is sample \( n_o \). The samples surrounding sample \( n_o \) (those that are in the reference window) are passed on to the selection logic. Specifically, as illustrated in the figure, \( K \) samples preceding and \( J \) samples succeeding \( x[n_o] \) are placed through the selection logic. The selection logic typically uses a maximum likelihood estimator to estimate the background noise statistics and then select a threshold \( (L) \) based on the user’s specification for false positives. This threshold is then compared to \( x[n_o] \) to test if it does, indeed, correspond to a potential target.

The selection logic is chosen based on the application. Because of this, there are many types of selection logics. Three popular variations (and the three discussed here) include cell-averaging, greatest-of and smallest-of \[57\]. In cell-averaging CFAR, the mean of the
neighbouring cells is used to estimate the noise floor. In other words,

$$p_{CA} = \frac{1}{J+K} \left( \sum_{i=1}^{J} x[n_o - i] + \sum_{i=1}^{K} x[n_o + i] \right), \quad (3.1)$$

where $p_{CA}$ is the mean of the samples in the reference window. This mean is then used to compute the threshold $L$ which is compared against $x[n_o]$. It has been shown that cell-averaging is the selection logic that maximizes the detection probability in a homogeneous background that contains independent and identically distributed samples which have an exponential distribution [58]. However, there are two common scenarios in which the cell-averaging CFAR produces poor results. Specifically, cell-averaging does not work well near edges and in the case of multiple targets within the reference window [57, 59].

Edges can be defined as areas in the image where, within a single reference window, there are at least two regions of significantly different power levels. Assume that the regions are called $A$ and $B$ where region $A$ has a lower power level than that of region $B$. In this case, the threshold determined by the CFAR algorithm will be a compromise between these two regions. It will be higher than it would have been if the reference cells were only from region $A$. Conversely, it will be lower than it would have been if all the reference cells were taken from region $B$. This has two consequences for the CFAR
algorithm. If the target is close to an edge and is located within region $A$, the threshold will be unnecessarily high. This will cause the target to be missed leading to a false negative and thus decreasing the probability of detection [60, 61]. On the other hand, if the target were in region $B$ close to an edge, the threshold computed by CFAR will be unnecessarily low. Although this will increase the probability of detection, it can also lead to noise samples from region $B$ being detected as potential targets. Thus, this may lead to an increase in the false positive rate [60, 62].

A potential solution to the problem around edges was posed through the greatest-of selection logic [62]. In this selection logic, the samples before and after the target are not averaged together. Rather, a mean is computed for each of the two groups (the $K$ samples leading and the $J$ samples lagging $x[n_0]$) of samples. The larger of the two means is then used to compute the detection threshold while the smaller is disregarded. Thus, only one of the two groups (leading or lagging) of samples is used to estimate the background noise. In other words,

$$p_{GO} = \max \left( \frac{1}{J} \sum_{i=1}^{J} x[n_0 - i], \frac{1}{K} \sum_{i=1}^{K} x[n_0 + i] \right).$$

(3.2)

where $p_{GO}$ is the largest of the two means. In this way, the group of samples with the largest power is used to calculate the detection threshold. This method was shown to reduce the probability of false positives [62, 63]. However, as the estimation of the background noise depends on the samples in the window with a larger mean, the probability of detection for targets in the group with the lower power is clearly worsened. Further, as one of the two windows is disregarded, fewer samples are being used to estimate the background noise as compared to cell-averaging CFAR. This may lead to decreased estimation of background speckle, especially in homogeneous regions.

A similar problem is present when there are multiple targets within the reference window. By definition, targets have a greater power level than their background. Conse-
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Quently, if there are targets present within the reference window, there will be an increase in the computed average and, consequently, the detection threshold. As discussed previously, an unnecessarily large detection threshold will lead to a decrease in the probability of detection. A potential solution to this is called the smallest-of CFAR processor [64]. Instead of using the largest of the two reference windows, the smallest of the two was used such that

\[
p_{SO} = \min \left( \frac{1}{J} \sum_{i=1}^{J} x[n_0 - i], \frac{1}{K} \sum_{i=1}^{K} x[n_0 + i] \right). \tag{3.3}
\]

where \( p_{SO} \) is the smallest of the two means from the reference windows. With this selection logic, the smallest of the two reference windows is used to compute the detection threshold. This then helps to nullify interference from other targets in the reference window thus increasing the probability of detection. Likewise, in the case of a target appearing in group A (the group with a lower power level) close to an edge, this method can help increase the probability of detection. However, it has been noted that this method does not work well when there are targets in both the leading and lagging reference windows [57]. Further, the smallest-of selection logic exacerbates the problem of an increased rate of false positives around edges [57]. Finally, like the greatest-of selection logic, it may not provide the best background noise estimate as it ignores the samples in either the leading or lagging window.

Other processing schemes have also been proposed. Median filters have shown promise for reducing influence from impulsive noise as well as preserving edges. From this idea arose the ordered-statistics CFAR scheme [65]. In this method, the reference window samples are ordered and the \( m \)th largest sample is used to determine the detection threshold. However it has been shown that this method does not prevent excessive false alarm rates around edges unless a sample close to the maximum of the order is also used [57]. Thus, a more generalized version called the trimmed-mean CFAR processor
was created [57]. In this selection logic, the largest and smallest samples are removed from the reference window before a threshold is computed. Other selection logics based on second order statistics have also been proposed [66,67].

Whatever the selection logic, its output $v$ is then compared to the target sample ($x[n]$). Generally, if $x[n]$ is greater than $v$, the sample is marked as a target. Otherwise, $x[n]$ is not considered to be a target and the algorithm then shifts the window over to the next sample.

### 3.2 Proposed Method

In this section, the CFAR thresholding scheme to be used in conjunction with the CLEAN algorithm is proposed. There are two aspects to this: the reference window and the selection logic. In Section 3.2.1, the choice of selection window for the CFAR algorithm is discussed. It uses the lateral information of an ultrasound B-mode image along with the axial information to select a detection threshold. In Section 3.2.2, a potential selection logic is discussed.

#### 3.2.1 Reference Window

In the CFAR algorithm, the reference window defines the area of the input signal (and thus the samples of the input signal) to be considered as part of the background for noise power estimation. In the previous section, the reference window consisted of $K$ samples leading the target sample and $J$ samples lagging it. These $K + J$ samples were passed on to the selection logic. Depending on the selection logic, an estimate of the background noise power was then computed based on the statistics of the samples within the reference window. From this and the user-specified false alarm rate, a threshold $L$ was then computed. When adapting the CFAR approach for use with CLEAN, two issues arise from this generalized version of the CFAR algorithm.
The first issue with the general CFAR algorithm is that it assumes the input vector \( x \) is a one dimensional signal. Although this may work with ultrasound A-lines, it would ignore the lateral information provided in ultrasound B-mode images. Further, samples along a single A-line correspond to a different depths. In ultrasonic imaging, attenuation plays a large role in the power of the backscattered signals. Samples closer to the transducer are subject to less attenuation than samples further from the transducer. This may artificially raise or lower the detection threshold (depending on the location of the target sample) and lead to the problems found around edges as described in Section 3.1. Thus, it would be prudent to use the lateral information provided in ultrasound B-mode images.

The second issue which the general CFAR algorithm is the quantity of samples to use in the reference window. It has been shown that for a homogeneous background, as \( J + K \) increases the probability of detection also increases [57, 60]. As just noted, however, ultrasound images are heavily dependent upon attenuation. Thus, using an arbitrarily large number of samples in the axial direction may not be the best option. Further, focusing also plays a role in the backscattered signal and so may affect the statistics of the background speckle. Note, however, that B-mode samples of a similar axial depth have roughly the same attenuation applied to them; attenuation is a function of depth and frequency, not lateral distance (see Section 1.2.1). Thus, lateral samples can be used to estimate the speckle statistics. Likewise, if the focusing depth is kept constant as the ultrasound beam is steered through the medium, the effects of focusing can also be minimized.

Samples with a similar axial depth across the entire B-mode image can be used to estimate the detection threshold. This will allow for a large number of independent samples and decrease the effects of attenuation a large effect in the axial direction). However, the number of samples to use in the axial direction still needs to be considered. The size of the reference window should be large enough so that it can adequately represent the
statistics of the speckle. Conversely, it should be small enough to provide local information for the target sample thus offsetting the effects of attenuation and inhomogeneities within the medium.

In radar, it is not uncommon to use reference windows as small as a dozen samples. However, note that for the processing schemes discussed in Section 3.1, the samples in the reference window are assumed to be independent and identically distributed. For speckle, this is not the case.

Speckle arises as a result of sub-resolution scatterers (see Section 1.2.2). In simulations, these scatterers are represented as many point scatterers. To gain a better understanding of speckle, consider the spatial impulse response of a single scatterer. The spatial impulse response of a scatterer depends upon a number of system parameters. These include the focusing properties of the system, its attenuation, the bandwidth of the transmit pulse and the physical properties of the transducer array. For the simulation methods used in this work (described in Section 2.4), the point spread function of a single scatterer is shown in Figure 3.2 (note that unlike most of the ultrasound images displayed in this work, this image has a linear magnitude scale). The full-width at half-maximum (FWHM) for this spatial impulse response is 0.51 mm in the axial direction and 1.72 mm in the lateral direction.

To adequately estimate the statistics of speckle, the CFAR reference window width in the axial direction should take into account the size of the point spread function of at least a single scatterer. For the system used in the simulations, the axial FWHM was found to be 0.51 mm. Thus, the CFAR reference window should be larger than this so that at least an entire scatter can be encompassed within the window. Otherwise, the statistics of the speckle within the reference window may not be representative of the background speckle.

To better understand this, consider the ultrasound B-mode image shown in Figure 3.3. It is a phantom of speckle only; there are no targets within this phantom. It is composed
of 50 A-lines across the lateral width and the focusing is fixed at a depth of 60 mm. An axial slice of this phantom can be used to estimate the speckle statistics. The white bounded rectangle shows an example reference window for the CFAR algorithm. It is centred at a depth of 60 mm, has a width of 10 mm and spans the lateral axis of the phantom.

To see the effect of various axial widths on the speckle estimation, consider the histograms given in Figure 3.4. These four histograms show the speckle distribution acquired from reference windows with different axial widths. The magnitudes were normalized to the sample with the largest magnitude. The histograms are normalized to the number of samples. Superimposed on the histograms in the dotted line is the corresponding Rayleigh distribution probability density function. It was computed from the samples within the reference window using a maximum likelihood estimator.

In each of the four cases, the slice was taken across all 50 A-lines so that it spans the lateral width of the phantom and is centred at an axial depth of 60 mm (the focusing depth). For the histogram given in Figure 3.4a, the reference window has an axial width of 0.5 mm. Within this window were a total of 3300 samples (note that the
Figure 3.3: A phantom of speckle with an example CFAR reference window.

sampling frequency was 100 MHz). When the reference window width is increased to 1 mm (Figure 3.4b), the data fits better with a Rayleigh distribution. However, 1 mm is slightly less than twice the axial FWHM for a single scatterer. As the axial reference window width is increased to 2 and 4 mm (Figs. 3.4b and 3.4b, respectively), the data fits better with the expected Rayleigh distribution. There does not appear to be any significant change in the goodness of fit between 2 and 4 mm so an axial width of 2 mm was chosen for the CFAR algorithm.

Thus, for the CFAR algorithm to be used in conjunction with the CLEAN algorithm, the reference window was set to have an axial width of 2 mm and spans laterally across the entire B-mode image. This appears to be the best compromise between using local information for each target and having enough samples to accurately estimate the speckle statistics.

There are, however, a few disadvantages for this choice. Some CFAR selection logics use guard bands so that samples adjoining the target sample \( (x[n_o]) \) are ignored and
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Figure 3.4: Normalized speckle data and its fit to the Rayleigh distribution.
thus do not contribute to the noise estimation [59,66,68]. This is typically done when a potential target may interfere with its neighbours (i.e., $x[n_o]$ is not independent from its immediate surrounding samples, for example, $x[n_o + 1]$ or $x[n_o - 1]$). In the case of ultrasound, a target could be large and thus may span the adjoining samples. Further, as shown in Figure 3.2, the point spread function of a single scatterer itself may span more than a single sample. In these cases, the threshold will be artificially raised as there will be more samples with a larger magnitude. This also follows if multiple targets exist at the same depth. As all targets are presumed to have a higher contrast than the background, the detection threshold may be artificially raised. This will thus lead to a decrease in the probability of detection.

In the case of multiple targets within the reference window, several things can be done to prevent the detection threshold from being artificially increased. First, as mentioned in the previous section, the smallest-of selection logic mitigates the effects of targets being present in the reference window. Although this helps increase the probability of detection, as mentioned before it is not effective when there are targets within both the leading and lagging reference windows. Another solution is increasing the axial width of the reference window. By doing this, the increase in the number of speckle points can counteract the presence of multiple scatterers. This, of course, can lead to a poorer estimation of the background speckle as the information is no longer taken from local regions of the ultrasound B-mode scan.

Another approach for preventing the effects of multiple scatterers within the reference window can be to exploit the output of the CLEAN algorithm while it is being run. The problem with multiple targets within the reference window is that by definition, targets have a higher signal power than background speckle. This then, skews the reference window distribution to the larger magnitudes and leads to a larger estimation of the detection threshold. However, on every iteration of the CLEAN algorithm, a potential target is detected and the region surrounding it is decimated to prevent that target from
being detected in future iterations. Thus, the signal power from a single potential target is decreased on every iteration of the algorithm. If the detection threshold is recomputed on every iteration of the algorithm, it follows that a more accurate estimation of the speckle is found. The speckle within the reference window will no longer be skewed to the larger magnitudes and so the detection threshold will not be artificially increased.

In essence, there exists a symbiosis between the CLEAN and CFAR algorithms. For the CLEAN algorithm to accurately detect targets, it requires a good estimation of the detection threshold. The CFAR algorithm aims to provide this but suffers from the well-known problem of targets within the detection window. To solve this, the CLEAN algorithm detects and nullifies targets within the CFAR reference window. Thus, both algorithms use the other to attain a more accurate output.

Recomputing the detection threshold on every iteration of the CLEAN algorithm may have its own disadvantages. Depending on the decimation factor $\beta$, the data still may not reflect the true statistics of the speckle. If $\beta$ is too small, the speckle statistics may be skewed the other way, to the lower magnitudes, and lead to a smaller detection threshold. Moreover, if the CLEAN decimation window is too large, speckle itself might be decimated further exacerbating the problem. This will, inevitably, lead to an increase in the rate of false positives. Further, too large a window may increase the computation time depending upon the implementation.

### 3.2.2 Selection Logic

For the purposes of the CLEAN algorithm, the selection logic was chosen so that it is based on the estimated statistics of the speckle. It is known that the statistics of speckle magnitude follow the Rayleigh distribution [69]. The probability density function, $f(x)$, of a Rayleigh distributed random variable $X$ is given by

$$f(x) = \frac{x}{\sigma^2} \exp\left(-\frac{x^2}{2\sigma^2}\right),$$

(3.4)
and the Rayleigh distribution’s corresponding cumulative distribution function, \( F(x) \), is given by

\[
F(x) = 1 - \exp^{-x^2/2\sigma^2},
\]

(3.5)

where \( \sigma \) is the parameter of the Rayleigh distribution. Thus, to determine the statistics of the background speckle, \( \sigma \) must be found.

In the presented algorithm, data neighbouring of the test sample \( (x[n_0]) \) is used to estimate \( \sigma \). One way in which to do this is through a maximum likelihood estimator. Given \( K + J \) Rayleigh distributed random variables, the maximum likelihood estimate of \( \sigma \) is given by

\[
\hat{\sigma} = \sqrt{\frac{1}{2(K + J)} \sum_{i=1}^{K+J} x_i^2},
\]

(3.6)

where \( x_i \) is one of the \( K + J \) Rayleigh distributed random samples surrounding the test sample. Once \( \hat{\sigma} \) has been calculated, Equation (3.4) can be used to determine the local detection threshold, \( T_{\text{det}} \), for the test sample according to the specified false alarm rate \( (P_{\text{FA}}) \).

False alarms occur when the test sample is marked as a potential target even though it is part of the speckle. These errors happen when the randomness of the background speckle causes it to have a large enough magnitude to be considered a target. In other words, the Rayleigh distributed random variable \( X \) has to be greater than the detection threshold \( T_{\text{det}} \). The probability of this happening is given by

\[
P_{\text{FA}} = \int_{T_{\text{det}}}^{\infty} f(x)dx,
\]

(3.7)

where \( f(x) \) is the probability density function of the Rayleigh distributed random variable \( X \) as given in Equation (3.4). Solving this for \( T_{\text{det}} \) results in

\[
T_{\text{det}} = \sqrt{-2\hat{\sigma}^2 \ln(P_{\text{FA}})},
\]

(3.8)
where $\hat{\sigma}$ is found using the maximum likelihood estimator for Rayleigh distributed random variables as in Equation (3.6). Thus, computation of the detection threshold is automated using the user specified false alarm rate and the neighbouring samples.

### 3.3 Simulation Methods

The simulations in this chapter are setup much in the same way as in Chapter 2. As with those simulations, Field II was used to test the efficacy of the algorithms. Transducer, medium and focusing parameters were kept similar to those in the aforementioned chapter. For more information on the specific parameter values, see Section 2.4. Introduction of the CFAR algorithm warrants some mention of a few of the CLEAN parameters, notably those that may influence the CFAR algorithm. These include the CLEAN window axial half-width which was set to half of the width of the excitation wave (42 samples or 0.65 mm) and, based on the experimental point spread function, it was set to 1.63 mm (two ultrasound A-lines) in the lateral direction. Thus, for these simulations, the CLEAN algorithm used a rectangular window to decimate the data vector. The decimation factor, $\beta$, was set to 0.5.

Different from the previous simulations, however, is the introduction of the CFAR algorithm. The chosen selection logic was presented in Section 3.2 and is summarized here. The reference window was chosen to be a 2 mm thick lateral slice of the B-mode image. As explained previously, this proved to be small enough to provide local information for each potential target but was large enough to adequately represent the speckle statistics. A maximum likelihood estimator was then used to estimate the Rayleigh parameter from the samples within this slice. Using the specified false alarm rate, an appropriate detection threshold was then computed and used in the CLEAN algorithm for the detection of targets. Thus, the detection threshold adapted to the local information of the ultrasound B-mode image.
3.4 Results

In this section, some simulation results for the CLEAN algorithm with CFAR thresholding are presented. The first simulation is that of the phantom from Section 2.5.2 (the four targets with a background of speckle). Next, to illustrate a potential downfall of the proposed CFAR selection logic, a phantom with multiple targets within a reference window is introduced. Then, a solution to this case (re-computation of the the detection threshold on each CLEAN iteration) is tested. Finally, a probability of detection plot for a fixed false alarm rate is given.

3.4.1 Four Axial Targets

To test the efficacy of the CFAR algorithm in conjunction with the CLEAN algorithm, a simulation from the previous section (Section 2.5.2) was revisited. In that simulation, the phantom used consisted of four targets of various sizes over a background of speckle. The four target spheres have centres located at axial depths of 45, 53, 63 and 75 mm, and have diameters of 2, 4, 6 and 8 mm, respectively. They shared a lateral distance of −10 mm and so are lined up axially. Because of this, this phantom is henceforth referred to as “four axial targets”. The simulated phantom is given in Figure 3.5a. As in the previous simulations, the density of scatterers within the phantom (including the targets) was 10 scatterers/mm³.

To gauge how the false positive rate affects the detection of targets, several scenarios were tested. The result of the simulation when the false positive rate was set to $2 \times 10^{-3}$, is provided in Figure 3.5b. From this image it can be seen that the four target spheres are visible as are nine false positives. The shapes of the target spheres are somewhat preserved. However, the smallest target is represented by a single scatterer. As the false positive rate is decreased to $0.5 \times 10^{-3}$, the number of false positives decreases to just one. The four targets are still visible in the image (Figure 3.5c) but the largest target
of 8 mm diameter is now beginning to lose its shape. Finally, the false positive rate was lowered even further to \(0.125 \times 10^{-3}\). The resulting ultrasound B-mode image is given in Figure 3.5d. As this false positive rate, the smallest target of 2 mm is no longer detected and the target of diameter 8 mm now appears to be rectangular in shape. However, there are now no false positives in the image.

### 3.4.2 Four Lateral Targets

To illustrate a potential disadvantage to the proposed selection logic (that of multiple targets within the reference window), a new simulation is now presented. Like the previous example in Section 3.4.1, the phantom consists of four targets. However, unlike the previous example, the targets are no longer along the axial axis. Rather, the targets are lined up so that they are next to next to each other laterally (hence the term: “four lateral targets”). Specifically, the centres of the four targets spheres are located at an axial depth of 60 mm. Their lateral distances are \(-15, -5, 5\) and \(10\) mm, and they have diameters of 2, 4, 6 and 8 mm, respectively. An ultrasound B-mode image of this phantom is given in Figure 3.6a. To clarify the locations of the targets, they are outlined in Figure 3.6b.

First, the results of the CLEAN/CFAR algorithm are presented when the CFAR algorithm is implemented as described in Section 3.4.2. In other words, the detection threshold for each 2 mm slice is computed prior to running the CLEAN algorithm. These detection thresholds are then static throughout the duration of the algorithm (hence the term: “Static Detection Thresholding”). As previously described, an alternative to this approach is to recompute the detection thresholds on each iteration of the CLEAN algorithm. Thus, because the CLEAN algorithm removes targets from the data vector, the problem of multiple targets within the reference window is mollified. Because the detection thresholds change with every iteration of the algorithm, this is termed “Dynamic Detection Thresholding”.
Figure 3.5: CLEAN/CFAR results on the axial phantom. The CLEAN algorithm was run with CFAR thresholding. The same phantom (a) was used as in Figure 2.8. The results for various false alarm rates are shown in (b), (c), and (d).
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Static Detection Thresholding

The CLEAN algorithm with the CFAR extension was run on the four lateral targets phantom with various false positive rates. The false positive rate was started comparatively high at 0.1. The resulting B-mode scan is given in Figure 3.7a. At this high rate of false positives, there are many false positives throughout the image. However, the four targets are clearly still visible. Also note that the speckle within the region between an axial depth of roughly 55 mm and 65 mm is mostly free of speckle. Because 2 mm slices of this region invariably contain many targets, the CFAR algorithm has returned an artificially raised detection threshold. This helps to remove the effects of speckle in this region. However, in regions of the B-mode image without targets, this high false alarm rate leads to many false positives.

As the rate of false positives is decreased from 0.1 to 0.01, the smallest target is no longer detected (Figure 3.7b) and the remaining targets are losing their shape. Moreover, there are still many false positives in the image. When the rate is further decreased to 0.002, there are far fewer false positives. However, even the target of diameter 4 mm is now barely detected, being represented by only a single scatterer (Figure 3.7c).
Moreover, when the false alarm rate is reduced to $0.125 \times 10^{-3}$, this target is no longer detectable (Figure 3.7d).

The results of this simulation provide a stark contrast to the simulations in the previous section (Section 3.4.1) of the four axial targets. Whereas in the previous simulation a false positive rate of $0.5 \times 10^{-3}$ was still able to adequately retain all four targets, in this example even a false positive rate of 0.01 masks the smallest target of 2 mm. Further, at this high false positive rate there are far too many false positives for the results to be meaningful.

The reason for the large discrepancy in results can be attributed to the proposed selection logic. The reference window proposed in Section 3.2.1 makes uses of the lateral neighbours to the sample target. These reference samples are used to estimate the background speckle and thus compute an appropriate threshold. Therefore, if the samples lateral to the test sample were of the speckle background, it follows that they should provide an accurate estimate of the speckle. In the previous simulations this was not a problem because most of the lateral samples were indeed from speckle. However, the new phantom includes targets which are placed laterally. Thus many of the samples within some reference windows can be attributed to targets. In fact, as the reference window has a width of 2 mm in the axial direction, almost half of the samples between the depths of 60 and 62 mm can be credited to targets.

As explained at the end of Section 3.2.1, targets within the reference window artificially raise the detection threshold. The reason for this is that they shift the weight of the density function to the larger magnitudes. Then, when the Rayleigh parameter is estimated, it is larger than it should be. This, in turn, raises the detection threshold. This is clearly evident in Figure 3.7a. Between the depths of roughly 59 to 66 mm, the detection threshold is visibly raised. Compared to neighbouring areas, very little speckle is visible within this range. It has all been removed as a consequence of the large local detection threshold.
Figure 3.7: CLEAN/CFAR results on the lateral phantom. Results for various false positive rates are shown.
To prevent this from happening, the selection logic can be modified. Instead of using an entire lateral slice of data, an ordered scheme can be used that removes some of the largest samples. Another option is to entirely change the scheme so that it smaller, more local areas are used in the estimation of speckle rather than an entire slice. Still, the reference window can, potentially, contain target samples. However, it should be noted that the phantom presented in this example is more of an extreme case—for example, almost half of the samples from the reference window between depths 60 and 62 mm were from targets.

**Dynamic Detection Thresholding**

As explained in Section 3.2.1, another solution to the presence of multiple targets within the reference window is to recompute the detection threshold on every iteration of the CLEAN algorithm. Because the CLEAN algorithm iteratively removes the targets from the input data vector, this should potentially lead to better estimates of the detection threshold as the algorithm progresses.

To solve the problem of targets within the reference window, the CLEAN algorithm was modified so that the CFAR algorithm was run on every iteration to get an up-to-date estimate for the detection threshold. In this way, the CLEAN algorithm knows which samples can be attributed to targets and can treat these samples accordingly. Because the CLEAN algorithm decimates the power of potential target samples, it brings down the target’s power to the noise floor. Thus, the target is effectively removed from the scan. However, as previously mentioned in Section 3.2.1, there can be consequences to this. When the decimation factor is very low, the samples from the phantom will be decreased by a large amount. Thus, the data distribution will be skewed to the lower magnitudes for this region. This, in turn, will decrease the detection threshold leading to more false positives within this region. This is further exacerbated when the CLEAN detection window does not accurately encompass the target, specifically if the target window is
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Figure 3.8: CLEAN/CFAR results with threshold re-computation. The detection threshold was recomputed using the target samples found by CLEAN on every iteration of the CLEAN algorithm.

(a) False positive rate of $0.25 \times 10^{-3}$. (b) False positive rate of $0.125 \times 10^{-3}$.

larger than the target point spread function. In this case, the detection window may contain areas of speckle, thus decreasing the magnitude of the speckle.

To test this, the algorithm was run on the four lateral targets phantom. The results are presented in Figure 3.8. The result when the false positive rate is set to $0.125 \times 10^{-3}$ is presented in Figure 3.8b. From the figure it is evident that all four target spheres are visible, detectable and that there are no false positives. However, when the detection threshold is set to $0.25 \times 10^{-3}$, there appear to be more false positives, especially at the same axial depth as the four targets (Figure 3.8a).

The results of Figure 3.8 can be explained as a consequence for recomputing the detection threshold on every iteration. As the targets between the axial depths of 60 and 62 mm are detected, they are decimated by the CLEAN algorithm. They are decimated to below the noise floor and so the distribution of the samples within this range is left-shifted. As well, any speckle that may be within the decimation window is also decimated, further exacerbating the problem. Then, when the CFAR algorithm uses the distribution of the speckle points to compute the detection threshold, it will be artificially lower, even to
below the actual speckle power, as the samples are left shifted. If the detection threshold is below the speckle power, the CLEAN algorithm will begin to mark the speckle points as potential targets. This also explains why the problem is worse with larger false positive rates. In these cases, more targets are initially found and so more targets are decimated. This means that more samples are left shifted and the detection threshold is thus lowered even further.

An alternative to using the decimated target samples in the computation of the detection threshold is to simply disregard these samples. Any samples that were within the detection window of a potential target can be marked. Then, the CFAR algorithm can ignore these samples in the speckle estimation. Thus, these target samples will not skew to the data to the larger magnitudes (as in the case of using a precomputed detection threshold from Section 3.4.2) nor will they skew the data to the lower magnitudes as in the previous example (Figure 3.8).

To test if the results improve when the CFAR algorithm omits potential targets, the lateral target phantom was again used. As described, targets within a decimation window were ignored for the computation of the detection threshold. These results are presented in Figure 3.9. Results from false positive rates of $1 \times 10^{-3}$ and $0.5 \times 10^{-3}$ are given in Figures 3.9a and 3.9b, respectively. In both of these cases, all four targets are visible along with several false positives. Next, the false positive rate was decreased to $0.25 \times 10^{-3}$ (Figure 3.9c). In this case, all four targets are detected and there is only one false positive. Note that compared to Figure 3.8a, there are far fewer false positives when the found targets are ignored for the CFAR algorithm. This is especially true when there are many targets within the reference window, as in the region between axial depths of 60 and 62 mm. At a false positive rate of $0.125 \times 10^{-3}$, the smallest target of diameter 2 mm is no longer visible.

The results of this test show that dynamic re-computation of the detection threshold can be very effective in reducing the effects of multiple targets within the CFAR reference
Figure 3.9: CLEAN/CFAR results with threshold re-computation and target omission. The detection threshold was recomputed on each CLEAN iteration without the target samples found by CLEAN.
window. Simply removing potential targets found by the CLEAN algorithm from the CFAR computation proves to have a drastic effect in reducing the rate of false positives. However, it should be noted that removing samples from the CFAR computation can result in a less accurate estimation of the speckle statistics (as previously described in Section 3.2.1).

3.4.3 Probability of Detection

In the final simulation, a contrast-detail analysis is presented. It plots the probability of detection against the contrast and target diameter. As with the four spheres, spherical scatterers were used to simulate a target. Their diameter ranged from 1 mm to 6 mm (in increments of 0.25 mm) and their contrast was varied from 0 to 12 dB (in increments of 0.5 dB) relative to the background speckle as given by Equation (1.5). This means that a total of 525 contrast/detail pairs were tested.

For each contrast/diameter pair, 400 sample targets were tested to estimate the probability of detection. A target was marked as detected if the CLEAN algorithm returned at least one point within the perimeter of the target. Otherwise, the CLEAN algorithm marked the target as not found. The probability of detection was then simply the ratio of the number of targets found to the total number of targets that were tested for that contrast/diameter pair (400).

The targets were placed in a background of speckle. They were placed between 40 mm and 80 mm in the axial direction and anywhere between −20 mm and 20 mm in the lateral direction. As with the previous simulations, focusing was employed at a depth of 60 mm both in the axial and the elevation direction. This means that the targets could be as far as 20 mm from the focusing point. For this simulation, the rate of false positives was kept constant at $1 \times 10^{-3}$ and static detection thresholding (as described in Section 3.4.2) was employed.
The results for this simulation are presented in Figure 3.10. The figure is shaded so that the gradient from blue to red represents an increasing probability of detection. Thus, red depicts a high probability of detection and blue represents a low probability of detection. As expected, the probability of detection increases as a function of both target diameter and contrast. Essentially, small weak targets are not detectable consistently, as expected. The range at which a target is detectable is also depicted in the image. For example, if a target has a diameter of 6 mm and contrast of 6 dB, it is consistently detected. For a target contrast of 8 dB, a target of only 4 mm diameter is required.
3.5 Summary

This chapter introduced the CFAR algorithm for use in conjunction with the CLEAN algorithm. Although it was possible to achieve good results with the CLEAN algorithm, its performance heavily depended upon the user specified detection threshold. As it turned out, choosing a good detection threshold, was a somewhat ambiguous task that required some intuition on the part of the user. To remove this user dependency, the CFAR algorithm was introduced.

The CFAR algorithm used the statistics of neighbouring data to make a decision about the target sample. As was shown in Section 3.2.1, the amount of neighbouring data used for estimating the background statistics heavily depends upon the application. Using large windows counteracts the advantages of using local data for accurate estimation of background statistics while using small windows adds the risk of not using enough independent samples to form a good estimate. The way in which a user uses the neighbouring data is also application specific. The data is passed on to the selection logic which uses the specified false alarm rate to form a detection threshold. One such scheme was presented in Section 3.2.2.

Finally, several results were presented. The four axial targets example from Section 2.5.2 was revisited. The example showed the efficacy of the CFAR selection of the detection threshold. However, a consequence of the chosen selection logic was presented in Section 3.4.2. The presence of multiple targets within a reference window artificially increased the detection threshold and thus caused a decrease in the probability of detection. One way in which to counteract this is by recomputing the detection threshold on every iteration of the CLEAN algorithm using the data vector \( \mathbf{D}_i \). Because the CLEAN algorithm removes targets from the data vector, it provides a better estimate of the background speckle. Clearly, however, this benefit is at the cost of an increased computation load. Lastly, the probability of detection was plotted against contrast and target size (Section 3.4.3).
Chapter 4

Conclusions and Future Work

4.1 Conclusions

The goal of this work was to develop a method for the detection of targets in ultrasound B-mode scans using as little a priori information as possible. The CLEAN algorithm with CFAR thresholding does not make any assumptions about the medium nor the target. Furthermore, unlike previously proposed schemes, it does not rely on training data. The algorithm finds potential targets in the input data vector. As explained previously, this could be in single A-lines or even the B-mode image. It uses a detection threshold to set the lower limit on what it considers to be target. The CFAR algorithm automates the process of determining this detection threshold based on the local statistics of the ultrasound B-mode image.

This study was performed using simulated ultrasound images of spherical targets in a background of point scatterers whose density was sufficient to enable speckle to be properly represented. By increasing the scatterer magnitude within the targets, the effects of various contrast levels were studied over an axial depth range from 40 mm to 80 mm and ±20 mm in the lateral direction. All targets were placed on the elevation axis. Focusing in the axial and elevation directions was at a depth of 60 mm. Nonetheless, based
on the encouraging results, an experimental investigation using a physical phantom in conjunction with an ultrasound imaging system and trained observers, could be justified. Such an investigation could make use of an array of test spheres in a tissue mimicking phantom similar to the one described in [70]. This arrangement was subsequently used in their experimental study that compared the ability of automated and human observers to detect lesions [71].

Figure 3.10 illustrates the boundary between targets that are detectable with respect to size and contrast. It is also called a contrast-detail curve and closely matches the results for detectability for similarly shaped targets by trained physicians [72]. It should be noted, however, that the work presented in [72] is based on real phantoms whereas the work presented here is based on simulations in Field II. Still, the results prove to be promising.

It is, nonetheless, difficult to discuss the implications of this work because the CLEAN algorithm was not designed for a particular application, e.g., the detection of cancers. However, the detection of cancerous tumours with a diameter of 5 mm is, in many cases, in line with current standards for early detection. In breast cancer, for example, the gold standard of mammography is able to detect cancers roughly as small as 5 mm in diameter [73]. Prostate cancers, on the other hand, have a minimum detectable size of roughly 10 mm in diameter through the use of CT scans [74,75]. Meanwhile, lung cancers are typically operated on when they grow to at least 10 mm in diameter [76]. Based on this information, the CLEAN algorithm appears to perform well. For a target of 5 mm diameter, a contrast of roughly 5 dB is enough to allow the target to be consistently detected. When the size is increased, the required contrast decreases.

Lastly, it should be noted that the algorithm runs relatively quickly on general purpose hardware. This can potentially give ultrasound sonographers the ability to adjust focusing or positioning of the transducer during the ultrasound scan to achieve the best image quality.
4.2 Future Work

Some limitations of this work should also be noted. As mentioned earlier, simulated phantoms contained within a homogeneous background of speckle were used; the normal physiology of the human body was missing. The introduction of different tissue mimicking phantoms, especially those that contain inhomogeneities, will potentially make it more difficult for the CFAR algorithm to determine an adequate threshold and thus the CLEAN algorithm for determining targets. Problems surrounding multiple targets within a reference window may become a bigger issue as more representative phantoms are used. However, there are many variations of the selection logic which have not been explored. The selection logic chosen for the simulations used all of the neighbouring samples in the lateral direction. An ordered statistics approach, on the other hand, may help to disregard the largest or the smallest samples to attain a better estimate of the background speckle.

Along with the selection logic, different reference windows for the CFAR algorithm can be explored. This thesis used 2 mm lateral slices of data to estimate the background statistics. Although this was sufficient for the simulations in this work, ultrasound scans of normal physiology can be far more inhomogeneous. To deal with this possibility, the ultrasound image can be partitioned so that regions close to the sample can be used for the CFAR reference window. Thus, a new approach for the CFAR reference window may be warranted when the algorithm is adapted for specific applications.

The CLEAN algorithm is not without its own potential optimizations. A rectangular window was used for the decimation window but variations are also possible. With more accurate representations of the point spread function, it should be possible to better estimate the boundaries of potential targets. Further, different decimation factors can also be explored.

Another improvement for the CLEAN/CFAR algorithm could be to use multiple ultrasound scans of the target area. Spatial compounding and frequency compounding
have both proven useful in the suppression of ultrasound speckle [77, 78]. Both of these methods rely on using images where the speckle pattern has changed. In the case of spatial compounding, the transducer is shifted in the elevation direction or a different viewing angle is used. With frequency compounding, the frequency spectrum of the transmit wave is changed. Both methods result in an uncorrelated speckle pattern. In either case, the CLEAN/CFAR algorithm can be run on these B-mode images. Because the speckle pattern is different between scans of the same target area, the probability that a false positive occurs in the same location in successive scans is decreased. Thus, if targets are detected in the same location in successive scans, they are more likely to signify the location of a true target.

It should be noted that noise was not present in the simulations. It was assumed that the effects of speckle far outweighed that of noise so that the major hurdle facing the detection of target was speckle. However, as with all electronic devices, noise is present in ultrasound systems. The piezoelectric material used for the transducer elements, amplifier, connecting wires and matching layers (among other components) all contribute to the system’s noise. For a more accurate simulation of an ultrasound system, all of these properties should be taken into account.

Finally, although hypo-echoic lesions are of clinical interest, at present it is not known whether a modified version of CLEAN could be developed to detect such regions. Targets were defined in this work as areas of high contrast relative to the background speckle. As such, the CLEAN algorithm determines the location of targets based on local maxima in the input signal. Hypo-echoic lesions like fluid filled cysts, on the other hand, are areas of low contrast relative to the background speckle. Thus, as presented, the CLEAN algorithm would not be able to detect these regions. However, it may be possible to alter the input data vector so that the CLEAN algorithm is able to detect these regions.

Given these limitations and potential improvements, the simulation results presented here demonstrate that small spheres with relatively low contrast are consistently de-
tectable within speckle. While it is only possible to make definitive statements based on experiments with, e.g., phantoms, the results are very promising.
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