

Enhanced Physics Modelling and Multistatic Data Integration for Breast Tissue Reconstruction in Microwave Radar Imaging

by
Illia Prykhodko

A Thesis submitted to the Faculty of Graduate Studies of The University of Manitoba
in partial fulfillment of the requirements of the degree of

MASTER OF SCIENCE

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ABSTRACT

Microwave breast imaging offers a low-cost, portable, and non-ionizing alternative for breast cancer detection by exploiting the contrast in dielectric properties between malignant and healthy tissues. Its simplicity and safety make it particularly attractive for screening in under-served or remote communities where conventional imaging modalities may be unavailable.

However, three core challenges have limited its diagnostic performance: (1) standard Delay-and-Sum (DAS) beamformers assume a homogeneous medium and ignore tissue heterogeneity; (2) they neglect the frequency dependence of dielectric properties; and (3) true propagation speeds in complex breast tissues are unknown and must be estimated. Moreover, existing image-quality assessments rely on single-pixel contrast and localization metrics, offering little guidance for algorithmic refinement.

This thesis addresses these gaps through three methodologies. Firstly, an enhanced-physics beamforming algorithm was developed as a combination of an analytical binary-partitioning model with a full frequency-dependent propagation-speed formulation, yielding piecewise time delays. The enhanced physics modelling was observed to improve image quality. Secondly, a robust, sinogram-based boundary detection algorithm was proposed to extract realistic breast outlines from raw data from the Vector Network Analyzer (VNA), replacing idealized circular models and allowing for a boundary-aware beamforming and skin suppression for the differential imaging. Thirdly, a phase-based technique of experimental propagation speed extraction was developed using the multistatic microwave data.

Thesis supervisor: Stephen Pistorius

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Chapter 1

Introduction

1.1 Background Motivation for Breast Cancer Imaging Research

Breast cancer has been a leading type of cancer in terms of incidence for many years. It caused 670 000 deaths worldwide in 2022, and it remains the most common cancer in women in 157 countries. According to the International Agency for Research on Cancer (IARC), breast cancer has the highest incidence - 46.8 and the second-highest mortality - 12.7, after lung cancer, per 100 000 people. In 2040, it is predicted that the incidence will increase to over 3 million cases and 1 million deaths every year. Global data shows an egregious inequity in the breast cancer burden with respect to human development. In countries with a very high HDI (Human Development Index), 1 in every 12 women will be diagnosed with breast cancer within their lifetime, and 1 in every 71 women will die of breast cancer. In comparison, in the countries with low HDI, 1 in every 27 women is diagnosed and 1 in 48 women will die from breast cancer [1], [2], [3].

The rise in incidence in transitioned countries not only reflects the persistent prevalence of hormonal, reproductive, and behavioural risk factors, but also, and arguably more importantly, the increased detection of small tumours due to regular screenings.

Breast cancer originates in mammary epithelial cells that can grow abnormally while remaining confined within ducts or lobules (non-invasive cancer), a stage associated with a high 5-year survival rate of ~98%. However, prognosis worsens significantly once cells breach this ducto-lobular boundary and invade surrounding tissue (invasive cancer), with survival dropping to 83% when spread to regional lymph nodes. If distant metastases are present at diagnosis, 5-year survival falls sharply to just 23% [4]. Meaning that effective early-stage screening significantly reduces the risk of mortality as breast cancer metastasises in late stages and targets vital organs [5].

1.2 Breast Cancer Imaging

There are many clinically available tools for screening, such as X-ray mammography, ultrasound imaging and magnetic resonance imaging (MRI). However, all of them are associated with several fundamental limitations [6].

Mammography is a very efficient imaging modality with sensitivity for different types of

mammography ranging from 55% to 91% and specificity ranging from 84% to 97%. Digital breast tomosynthesis combined with other modalities such as digital mammography, shows high cancer detection rates with few false positives [7].

Regular screening starting at the age of 40 can drastically improve the mortality rates of breast cancer, according to [8], up to 20% reduction over 20 years. However, the usage of ionizing radiation poses a risk of exposing the patient to a dose, which can, repeated over the number of years, outweigh the benefit of reliable screening by increasing the chance of cancer in the future. Mammography also requires breast compression to account for the magnification and to space out the overlapping tissues, which may be uncomfortable for the patient undergoing the procedure. On average, a woman beginning annual screening at age 40 will encounter one false-positive recall every 10 years, while one starting at age 50 will experience one false-positive recall every 11.5 years. False-positive recalls require additional imaging exposing the patient to a redundant dose of X-ray radiation [9]. Even though not exclusive to mammography, overdiagnosis, i.e., cases of cancer that were detected on screening that never would have shown clinical symptoms, poses a risk of additional screening, anxiety, and potential surgical intervention [10].

The American College of Radiology classifies breast density into four BI-RADS (Breast Imaging Reporting and Data System) categories: A (almost entirely fatty), B (scattered fibroglandular densities), C (heterogeneously dense), and D (extremely dense). Higher density (C and D) reduces mammographic sensitivity and is a key motivation for supplemental modalities [11], [12].

Magnetic resonance imaging (MRI) is a non-ionising modality that uses strong magnetic fields and radiofrequency pulses to generate detailed cross-sectional images of soft tissues. It is particularly useful due to its superior contrast resolution for detecting and characterizing lesions that may not be visible on mammography or ultrasound, especially in dense breasts. By acquiring both morphological and functional information, such as contrast enhancement kinetics, MRI can distinguish benign from malignant tissue with high accuracy.

Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is one of the best imaging modalities for breast cancer detection in terms of sensitivity (93%), also exhibiting an acceptable level of 71% specificity [13]. There is also evidence of MRI outperforming mammography in image quality and sensitivity, for women with extremely dense breasts, while retaining a comparable level of specificity [14], [15], [16].

However, the high cost associated with building and maintaining an MRI system does not make it affordable and accessible for people living in transitioning countries and rural or isolated areas. Moreover, because MRI uses powerful magnetic fields, patients with metal implants, such as pacemakers, cochlear implants, or vascular clips, or any ferromagnetic foreign bodies, are ineligible for MRI scans.

Ultrasound is relatively affordable compared to MRI and mammography, but it is highly operator-dependent, requiring skilled personnel to both perform the scan and interpret the images, and suffers from acoustic shadowing behind bone or air interfaces. As an adjunct in women with dense breasts, supplemental hand-held or automated whole-breast ultrasound detects roughly 3.8 additional cancers per 1 000 women beyond mammography alone [17].

For the past 50 years, a new promising imaging modality has been emerging – *Microwave Breast Imaging* (MBI) [18], [19]. MBI operates in the microwave range of the electromagnetic

spectrum and employs low-power signal. The images are acquired using microwave antennas that can serve as both the transmitter and the receiver of the signals.

Microwave imaging offers inherently high tumour-to-tissue contrast due to dielectric differences between tissues, potentially surpassing X-ray mammography. Early investigations [20], however, compared fatty versus malignant tissues, neglecting that most tumours develop within fibroglandular regions [21]. More recent work [22], [23], [24], [25] shows that malignant-to-fibroglandular dielectric contrast may be as low as 1:1.1 (~10%), a dramatic reduction from the 1:10 adipose-to-malignant values previously celebrated.

Generally, MBI is divided into one of the two major categories: microwave tomography (MWT) and radar imaging. Microwave radar imaging will be described in detail in the following section.

Microwave tomography is concerned with imaging the dielectric properties directly [18]: the permittivity ϵ and the conductivity σ of the object under test. MWT usually operates in the frequency range from approximately 0.3 GHz to 30 GHz [26]. This method requires the medical physicists to solve the ill-posed 2-dimensional non-linear inverse scattering problem, which usually means the utilization of computational methods. MWT is a prominent field in microwave imaging that is rapidly improving and growing [27], [28], [29], [30], [31], [32], [33] with potential to be coupled with other imaging modalities such as ultrasound [34], [35].

Since the dielectric properties of various tissues, such as skin, adipose tissue, and fibroglandular tissue, differ significantly from those of air, as microwaves propagate, they experience noticeable power reduction. The skin is the first layer that ‘shields’ the inside of the breast from the microwave penetration, and the signal that gets through suffers from power loss due to reflection and conversion into heat. To mitigate this, both radar and tomographic approaches may employ coupling liquids, and many research groups continue to use them [32], [36], [37]. Their ability to match the dielectric properties of the skin has improved drastically as initially regular water was used [18]. This approach makes it easier to build the system, allows for more predictable loss and is able to accommodate a wide variety of organs, however, the sanitary concern, the spillover, the attenuation due to loss, and difficulties associated with maintaining such a system prevented us from using the coupling liquids, thus they are not going to be mentioned further. Moreover, the initial skin reflection can serve as an important tool in enhanced physics modelling (see Chapter 3).

1.3 Radar Microwave Imaging

This thesis is primarily concerned with Radar Microwave Imaging, a modality that, unlike Microwave Tomography, focuses on image reconstruction based on the microwave signal, rather than solving the field equations.

Image acquisition is based on the scattering phenomenon of electromagnetic radiation. The irradiated object represents a specific distribution of tissues with varying dielectric properties. When the microwave radiation encounters the contrast in these properties, the signal undergoes scattering, and it is recorded using a MW sensor (in most cases, the antennas can serve as the sensor). The data is conventionally represented as a set of scattering parameters, or S -parameters. In general, there are two types of S -parameters of interest: the ones that correspond to the reflection ($S_{11}, S_{22}, \dots$) and transmission ($S_{21}, S_{12}, \dots$)¹. Vector Network Analyzers (VNA) are ubiquitous tools used in microwave imaging. VNAs are capable of accurately measuring the S -parameters for an

N-port system (systems with N antennas acting as either the transmitter or the receiver). The most common type of VNA, and the one that is used in the experimental part of this thesis, is the 2-port VNA - it measures S_{11} , S_{22} , S_{21} , and S_{12} parameters.

The S-parameters are complex-valued. The magnitude of S_{ji} denotes the fraction of the incident root-power wave at port i that exits the device at port j , and the phase of S_{ji} indicates the phase shift experienced by the wave between ports i and j . Using the accurately recorded S-parameters, radar approaches are able to reconstruct the contrast between the dielectric properties of the media.

Although a growing number of clinical investigations have demonstrated the feasibility of in-vivo microwave imaging [31], [38] (a more comprehensive overview of microwave clinical efforts is conducted by O’Loughlin et al. [39]), most experimental work still relies on tissue-mimicking phantoms. Physical phantoms provide an ability to control the dielectric properties, an unambiguous ground-truth, and high repeatability, making them the most prevalent means of validating MBI systems and reconstruction algorithms [23], [27], [40], [41], [42], [43], [44], [45], [46], [47], [48], [49], [50], [51], [52], [53].

Complementary numerical phantoms, constructed from anatomically realistic dielectric maps or simplified geometric models, are also widely used, particularly in microwave tomography, to explore parameter spaces and carry out large-scale algorithmic assessments [28], [29], [36], [45], [53], [54], [55], [56], [57], [58]. Such studies may even combine both the numerical phantom simulations and physical phantom experiments [45], [53].

1.3.1 Imaging System

The experimental system used at the Medical Physics Laboratory at the University of Manitoba is fully described in [52]. In this thesis, we refer to it as the ‘bed system’. The system and its main functional module are illustrated in the Figure 1.1.

It is equipped with a 2-port VNA, model C1209 (Copper Mountain Technologies, IN, USA), and two Horn antennas. The system operates over the 2 to 9 GHz frequency range with an output power of 15 dBm. The rotating antenna module revolves around the breast, which is placed in the circular aperture centred with respect to the imaging domain.

1.3.2 Image Reconstruction

Raw microwave radar data cannot be easily interpreted by a radiologist or even a physicist. The response in the frequency domain provides almost no visual information about the location, size or shape of the possible malignant growth. A typical frequency-domain dataset collected at the University of Manitoba is shown in Figure 1.2. To mitigate this, MW radar imaging offers a way to ‘translate’ the signal into a more visual form through image reconstruction. Many reconstruction algorithms have been developed both in the time and frequency domains. The most prevalent algorithm in the literature is called DAS (*Delay-and-Sum*), which is a frequency-domain approach that employs principles of the Discrete Fourier Transform to reconstruct the relative intensity of pixels in a selected image domain [56], [59], [60].

¹The indexing of microwave S-parameters follows this convention: S_{RT} , where R corresponds to the index of the receiving antenna and T is the index of the transmitting one.

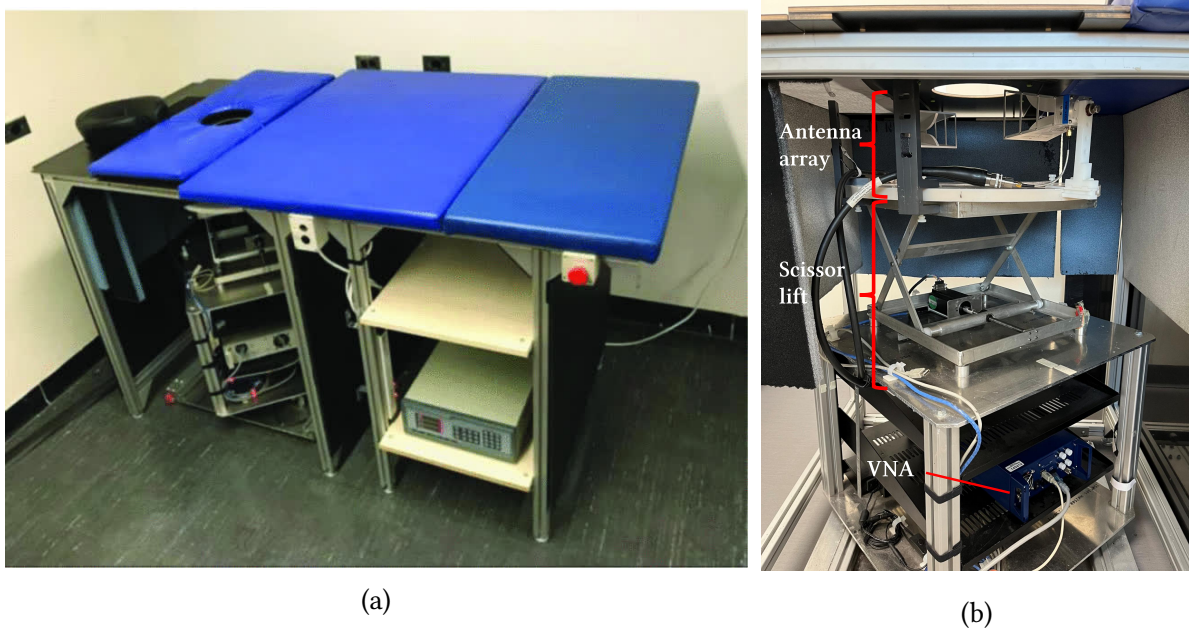


Figure 1.1: (a) - the Breast Imaging Rotating-Radar system (bed system). (b) - rotating radar module.

The value of intensity on the resulting image corresponds to a relative reflectivity, attempting to quantify how well a certain region of the image reflects the microwave radiation compared to other regions. The algorithm is formulated as follows:

$$I(\mathbf{r}) = \sum_{\mathbf{r}_a} \sum_f S_{11}(\mathbf{r}_a, f) e^{-2\pi j 2ft(\mathbf{r}, \mathbf{r}_a)}, \quad (1.1)$$

where S_{11} is the measured reflected signal at the antenna position $\mathbf{r}_a$ and frequency f [hertz], $I(\mathbf{r})$ is the relative image intensity at the position $\mathbf{r}$ in the imaging domain, and $t(\mathbf{r}, \mathbf{r}_a)$ [seconds] is the one-way time-delay of the microwave radiation from the position of the antenna $\mathbf{r}_a$ to the point $\mathbf{r}$. Because S_{11} is monostatic, the true time-delay corresponds to a round-trip, thus a factor of 2 is required in the exponent.

It is important to note that this thesis refers to *frequency domain* DAS. There are research groups that explicitly refer to time domain DAS when talking about image reconstruction in microwave imaging [44], [49], [56], [57], [58].

Figure 1.3 presents a typical image acquired using the DAS algorithm. Compared to a mammogram, these images are noticeably less sharp and might exhibit various artifacts that increase what is called ‘clutter’ - the non-negligible response or noise on the image that does not correspond to breast tissues or malignant growths.

The time-delay factor represents the time it takes for the signal of a specific frequency to propagate from the phase centre of the antenna to the corresponding point in the image domain. It is defined by:

$$t(\mathbf{r}, \mathbf{r}_a) = \frac{|\mathbf{r} - \mathbf{r}_a|}{v}, \quad (1.2)$$

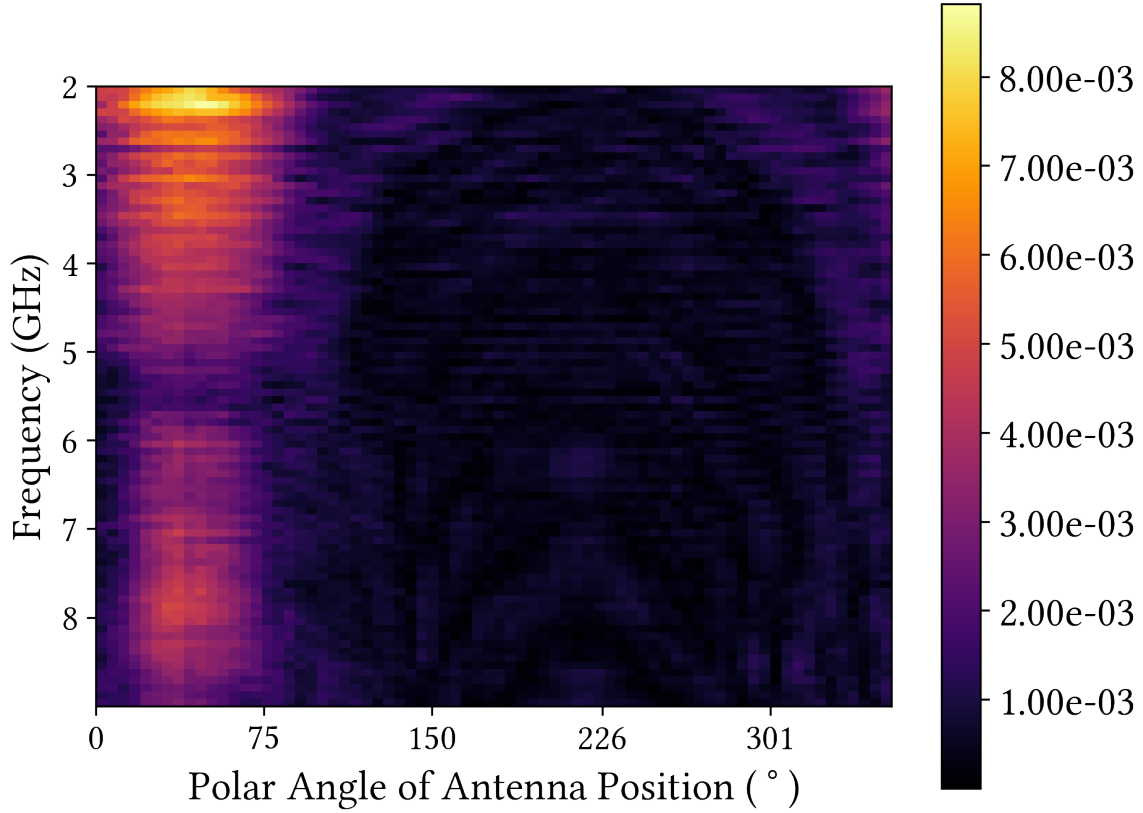


Figure 1.2: Raw signal data collected on the microwave imaging system.

where v is the average propagation speed [meters/second] in the domain. Radar MBI attempts to estimate the propagation speed or the relative permittivity based on a priori information [49], [61], [62], [63], [64] as opposed to the tomographic studies that focus on the direct reconstruction of the dielectric properties [65], [66]. There are also enhanced versions of the DAS algorithm in the literature, such as Improved DAS [47] and Iterative DAS [43].

Another successful reconstruction algorithm is called DMAS (*Delay-Multiply-and-Sum*) [51], [67]. It manages to improve the contrast of the tumour response by incorporating a signal-pair multiplication from each antenna with every other antenna. Mathematically, it is equivalent to:

$$I(\mathbf{r}) = \sum_{\mathbf{r}_a} \sum_{\mathbf{r}'_a} \sum_f S_{11}(\mathbf{r}_a, f) e^{-2\pi j 2ft(\mathbf{r}, \mathbf{r}_a)} S_{11}(\mathbf{r}'_a, f) e^{-2\pi j 2ft(\mathbf{r}, \mathbf{r}'_a)}, \quad (1.3)$$

where the additional $\mathbf{r}'_a$ are the antenna positions that correspond to the ‘cross’ multiplication terms. There is evidence that DMAS outperforms DAS and most other reconstruction algorithms e.g. Improved Delay-and-Sum (IDAS) [47], Coherence Factor Based DAS (CF-DAS) [48], Channel Ranked DAS (CR-DAS) [68], and Robust Capon Beamformer (RCB) [69], [70] in terms of localization accuracy of the tumour and the reduction of the clutter [71], [72]. There exist several other methods of image reconstruction, e.g., Wideband Adaptive [54] or Time-Difference-of-Arrival (TDOA) Imaging [73], but the main algorithm of interest for this thesis is Delay-and-Sum, thus while

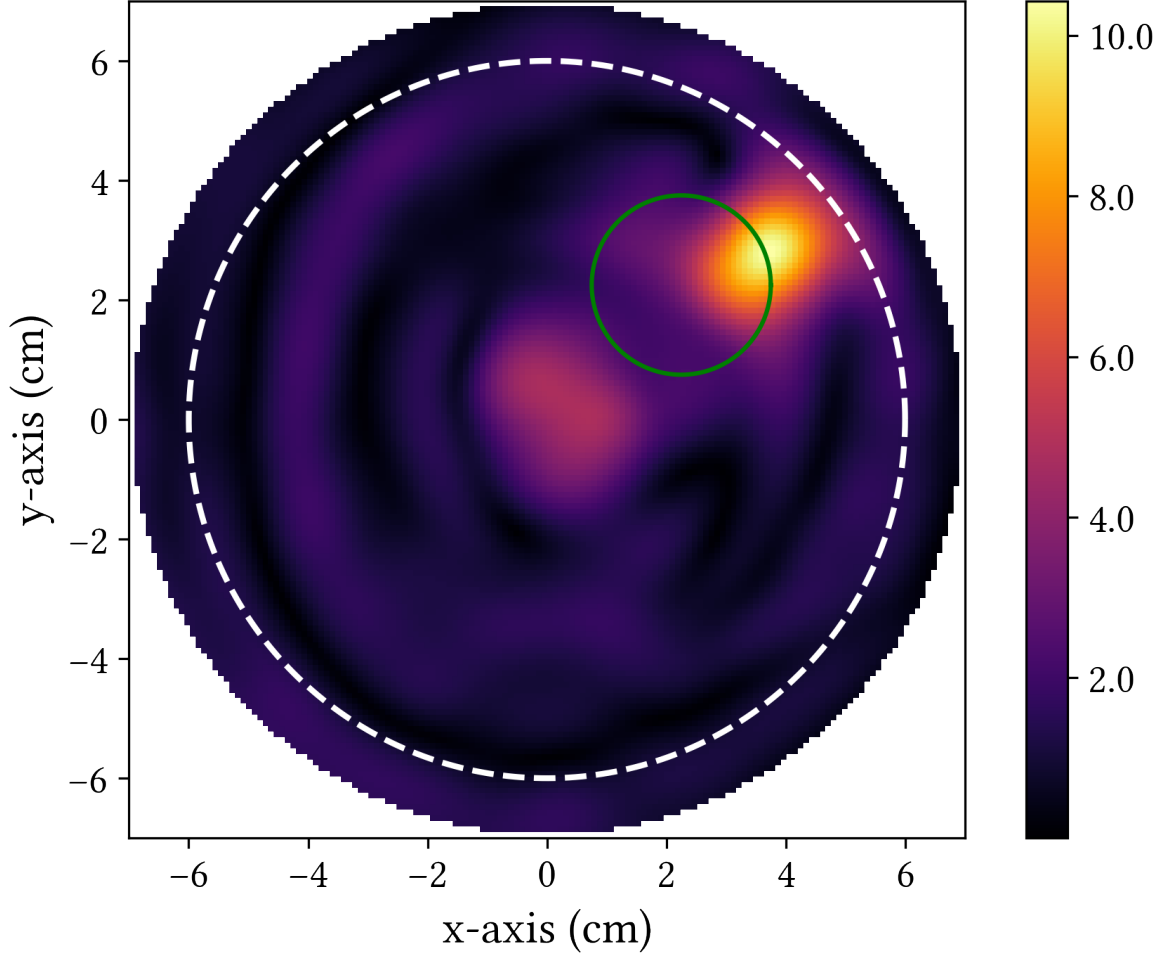


Figure 1.3: Typical Delay-and-Sum reconstructed image of the MW radar data. The scan is taken in the Medical Physics Laboratory at the University of Manitoba. The green line denotes the observed position of the malignancy.

others are worth mentioning, the DAS beamformer will serve as the basis for all the enhancements presented later.

1.3.3 Limitations of Microwave Imaging

The two major reconstruction algorithms - DAS and DMAS rely on the time-delay term $t(\mathbf{r}, \mathbf{r}_a)$, which is associated with several crude assumptions for estimating the time-delay.

- *The heterogeneity of the imaging domain is not taken into account.*

The heterogeneity of the breast tissues is known to degrade the quality of reconstructed images [60]; however, most literature standard algorithms are formulated reflecting no known dielectric contrast. The propagation speed v in equations (1.1) & (1.3) is a scalar value, independent of the location or the type of tissue the MW radiation is propagating through. The effective relative

permittivity of adipose tissue at 1 GHz is roughly 10, compared to about 35 for fibroglandular tissue [74]. Since

$$v_{\text{in}} = \frac{c}{\sqrt{\epsilon_r}}, \quad (1.4)$$

waves travel in adipose tissue at $\frac{c}{\sqrt{10}} \approx 0.32 c$, and approximately half that speed in fibroglandular tissue ($\frac{c}{\sqrt{35}} \approx 0.17 c$).

Moreover, unless the image is taken with the antennas and the breast submerged in the coupling liquid, the wave must travel through air before reaching the skin. Meaning that, according to DAS, the propagation speed of the MW radiation in air ($\epsilon_r \approx 1$) is not c , but is defined according to the average propagation speed model.

Chapter 2, specifically sections 2.1-2.5, investigates this assumption and presents novel ways of modelling the imaging domain as a heterogeneous medium. These sections include the analytical solutions to the geometrical problems of the simplified domain model, as well as various applications of such modelling, presented alongside images and quality metrics.

Chapter 3 proposes a new algorithm that allows the use of the high-intensity skin peak to reconstruct the approximate outline of the breast, reducing reliance on a priori information and improving the accuracy of the aforementioned geometric modelling. Sections 3.2 and 3.3 explore the extraction of the skin boundary using the DAS reconstruction and the sinogram, respectively. The ray-tracing approach based on Siddon's algorithm [75] is presented in Section 3.4. The chapter includes a quantitative comparison of the extracted outlines from the phantom experiments with the known STL data.

Section 3.5 of Chapter 3 is devoted to differential imaging, a strategy that reduces reliance on explicit skin-suppression techniques and brings microwave imaging closer to clinical viability [41] by employing synthetically created pairs of 'left' and 'right' breasts. Moreover, these sections demonstrate how to incorporate the boundary detection algorithm to achieve accurate skin alignment, ensuring that subtraction is performed on well-registered data and improving the robustness of the reconstructed images.

- ***The propagation speed is assumed to be frequency-independent.***

As noted previously, the propagation speed v is a scalar value, which implies frequency independence. In reality, the difference in permittivity between tissues at different frequencies results in significant differences in propagation speed. For example, the relative permittivity of the fibroglandular tissue at 1 GHz is approximately 35, and it is roughly 25 at 10 GHz. From (1.4), we note a relative difference of almost 17% in the propagation speed. Moreover, according to [74], all the tissues that the wave encounters in the breast exhibit strong frequency dependence.

Sections 2.3-2.5 of Chapter 2 present a physically rigorous way of modelling the propagation speed inside various dielectrics based on the known dielectric properties. This chapter also discusses the influence of the frequency-dependent modelling on the reconstructed images and attempts to quantify it based on quality metrics.

- ***Propagation speed is assumed to be known in advance.***

Chapter 4 focuses on extracting the propagation speed of microwave radiation inside breast tissue using the phase shift of the wave. This approach eliminates the need to model propagation

speed based on guesses or prior information. The chapter presents comparisons between the extracted propagation speed spectra and the theoretically predicted spectra for multiple tissue-mimicking liquids. It also introduces a method to reconstruct a spatial map of propagation speed for use in a ray-tracing algorithm, thereby eliminating the need for analytical modelling of the imaging domain.

- *The algorithm does not account for the effects of multiple scattering.*

Multiple scattering occurs when an incident microwave interacts with an object and is scattered more than once before reaching the receiver, leading to higher-order wave interactions that significantly complicate both forward modelling and inversion. In microwave tomography, several advanced algorithms explicitly account for these effects [76], [77], [78], [79], [80], all of which demand intensive computations and careful regularization. By contrast, radar imaging typically relies on single-scattering and therefore largely neglects multiple scattering effects. A rigorous consideration of multiple scattering, while important for quantitative tomographic reconstructions, is beyond the scope of this thesis.

Chapter 2

Enhanced Physics

2.1 Binary Domain Partitioning

In the most general case, the time-delay can be represented as a line integral over the propagation trajectory L defined as follows:

$$t = \oint_L \frac{dl}{v(\mathbf{r})}, \quad (2.1)$$

where $v(\mathbf{r})$ is the real frequency-independent value of propagation speed through the dielectric medium at the point $\mathbf{r}$. There are several levels of complexity associated with this model: the propagation speed is related to the distribution of the dielectric properties, which makes it a two-dimensional function instead of the scalar value like in (1.1). Moreover, this distribution is bound by the skin of the breast, which is not a uniform surface.

In order to reduce the initial complexity of the realistic case, we propose a simplified model of the breast's two-dimensional boundary corresponding to an axial slice at the height of the microwave antenna. This method can be easily enhanced to account for the imperfections in the real tissue morphology.

2.2 Model Geometry

We begin by simplifying the boundary of the breast to a perfect circle. Two geometric objects of interest in this configuration are the line connecting the phase center of the emitting antenna and the circular boundary of the breast. The analytical representation of the geometry follows this system of equations:

$$\begin{cases} \frac{x - p_x}{a_x - p_x} = \frac{y - p_y}{a_y - p_y} \end{cases}, \quad (2.2a)$$

$$(x - o_x)^2 + (y - o_y)^2 = R^2 \quad (2.2b)$$

where (p_x, p_y) corresponds to a position of the pixel¹ $\mathbf{r}$, (a_x, a_y) - to the antenna position, (o_x, o_y)

¹The imaging domain is discrete, so the word 'pixel' will be used interchangeably with the word 'point' in context of the spatial coordinates.

- to the center of the circle, R - to its radius, and the solution to this system corresponds to the pair of intersection points between the line and the circular boundary of the breast.

This system of equations can be transformed the following way:

$$\begin{cases} y = \frac{a_y - p_y}{a_x - p_x}(x - p_x) + p_y, & (2.3a) \\ y = \pm \sqrt{R^2 - (x - o_x)^2} + o_y & (2.3b) \end{cases}$$

and can be further expanded into the quadratic equation (2.4) with respect to y . Finding the roots of this equation and plugging them into (2.2a) will output the intersection points.

$$\begin{cases} ay^2 + by + c = 0 \\ a = k^2 + 1 \\ b = 2kp_y - 2k^2 p_x - 2o_x + 2ko_y \\ c = o_x^2 + p_x^2 k^2 - 2kp_x p_y + 2kp_x o_y + (p_y - o_y)^2 - R^2 \\ k = \frac{a_y - p_y}{a_x - p_x} \end{cases} \quad (2.4)$$

If the equation (2.4) does not have real roots - the solution is trivial, the ray does not encounter the dielectric and time-delay is determined by the distance between the pixel and the antenna phase center. If, however, the equation has two real roots, we must determine whether the pixel is: (a) in front of the breast - i.e., the ray does not penetrate the breast, (b) inside the breast, (c) behind the breast - the ray propagates through air then through the breast and then through air again. Figure 2.1 presents these three cases.

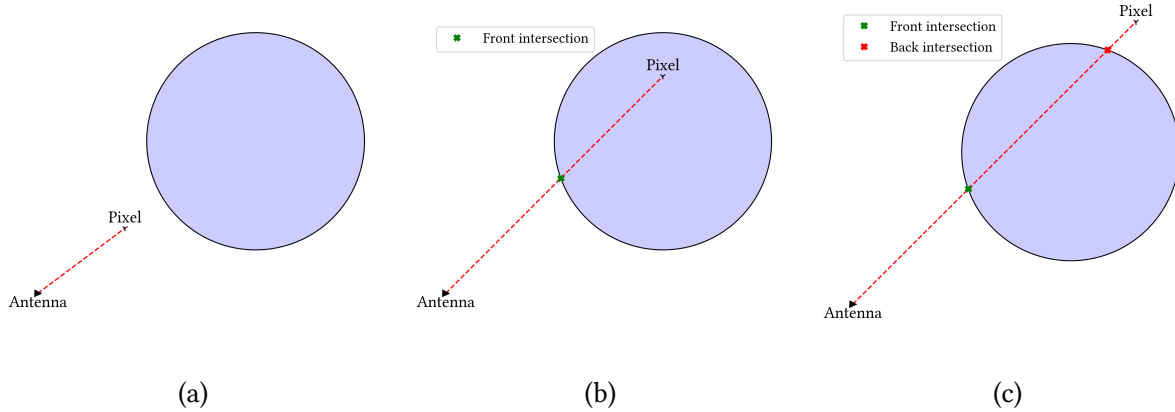


Figure 2.1: Schematic representation of the propagation if the point is (a) in front of the breast - equation (2.5a), (b) inside the breast - equation (2.5b), (c) behind the breast - equation (2.5c).

In general terms, with the simplified model the line integral (2.1) can be expanded into a piecewise function with only one unknown:

$$t(\mathbf{r}, \mathbf{r}_a) = \begin{cases} \frac{|\mathbf{r} - \mathbf{r}_a|}{c}, & \text{in air only} \end{cases} \quad (2.5a)$$

$$t(\mathbf{r}, \mathbf{r}_a) = \begin{cases} \frac{|\mathbf{r} - \mathbf{r}_{\text{front}}|}{v_{\text{in}}} + \frac{|\mathbf{r}_{\text{front}} - \mathbf{r}_a|}{c}, & \text{air - breast} \end{cases}, \quad (2.5b)$$

$$t(\mathbf{r}, \mathbf{r}_a) = \begin{cases} \frac{|\mathbf{r} - \mathbf{r}_{\text{back}}|}{c} + \frac{|\mathbf{r}_{\text{back}} - \mathbf{r}_{\text{front}}|}{v_{\text{in}}} + \frac{|\mathbf{r}_{\text{front}} - \mathbf{r}_a|}{c}, & \text{air - breast - air} \end{cases} \quad (2.5c)$$

where $\mathbf{r}_{\text{front}}$ and $\mathbf{r}_{\text{back}}$ are the front and back intersection points found from (2.4) defined as $(x_{\text{front}}, y_{\text{front}})$ and $(x_{\text{back}}, y_{\text{back}})$ respectively, $\mathbf{r}_a$ is the coordinate of the antenna. The only unknown in this equation is the propagation speed inside the breast v_{in} that needs to be modelled.

In order to distinguish between the cases (a-c) we can employ two simple geometric observations: if the pixel is inside the breast its coordinate position will satisfy the inequality (2.6), if the pixel is outside the breast and the inequality (2.7) is satisfied - the pixel is in front of the breast, if not - behind.

$$(p_x - o_x)^2 + (p_y - o_y)^2 \leq R^2, \text{ (pixel inside the breast)}, \quad (2.6)$$

$$\sqrt{(a_y - p_y)^2 + (a_x - p_x)^2} \leq \sqrt{(a_y - o_y)^2 + (a_x - o_x)^2} - R^2, \text{ (pixel is in front of the breast if outside)}. \quad (2.7)$$

The last stage of the algorithm is point assignment. Instead of re-evaluating the inequalities (2.6) & (2.7) for every antenna-pixel pair at run time, we pre-assign to each pixel the two intersection points $(\mathbf{r}_{\text{front}}, \mathbf{r}_{\text{back}})$ according to the following assignment rules:

$$(\mathbf{r}_{\text{front}}, \mathbf{r}_{\text{back}}) = \begin{cases} (\mathbf{r}, \mathbf{r}), & \text{(pixel is outside the breast or no intersection)} \end{cases} \quad (2.8a)$$

$$(\mathbf{r}_{\text{front}}, \mathbf{r}_{\text{back}}) = \begin{cases} (\mathbf{r}_{\text{sol}}^{(1)}, \mathbf{r}), & \text{(pixel is inside the breast)} \end{cases}, \quad (2.8b)$$

$$(\mathbf{r}_{\text{front}}, \mathbf{r}_{\text{back}}) = \begin{cases} (\mathbf{r}_{\text{sol}}^{(1)}, \mathbf{r}_{\text{sol}}^{(2)}), & \text{(pixel is behind the breast)} \end{cases} \quad (2.8c)$$

where $\{\mathbf{r}_{\text{sol}}^{(1)}, \mathbf{r}_{\text{sol}}^{(2)}\}$ are the solutions to the system of equations (2.2) sorted in ascending order with respect to the distance from the antenna. With these points fixed, the two-medium travel time reduces to a single closed-form expression.

$$t(\mathbf{r}, \mathbf{r}_a) = \frac{|\mathbf{r} - \mathbf{r}_{\text{back}}|}{c} + \frac{|\mathbf{r}_{\text{back}} - \mathbf{r}_{\text{front}}|}{v_{\text{in}}} + \frac{|\mathbf{r}_{\text{front}} - \mathbf{r}_a|}{c}. \quad (2.9)$$

If the pixel is associated with intersection points (2.8b), the first two terms in equation (2.9) go to zero yielding equation (2.5a). Similarly, if the pixel is associated with intersection points (2.8b), the first term in equation (2.9) goes to zero resulting in (2.5b). Thus, for every pixel-antenna pair in the imaging domain we define an array of pairs of intersection points

$$\mathbf{R}(\mathbf{r}_a, \mathbf{r}) = (\mathbf{r}_{\text{front}}(\mathbf{r}_a, \mathbf{r}), \mathbf{r}_{\text{back}}(\mathbf{r}_a, \mathbf{r})). \quad (2.10)$$

A very similar solution can be derived for a more complex shape - e.g., an ellipse. A system of equations of the form (2.2) for a configuration line-ellipse looks like this:

$$\begin{cases} \frac{x - p_x}{a_x - p_x} = \frac{y - p_y}{a_y - p_y} \\ \frac{x^2}{a^2} + \frac{y^2}{b^2} = 1 \end{cases}, \quad (2.11a)$$

$$\frac{x^2}{a^2} + \frac{y^2}{b^2} = 1 \quad (2.11b)$$

where a and b correspond to the radii of the breast along the x - and y -axes respectively. It can be shown through the transformations similar to (2.3) and (2.4) that the solution to the system of equations (2.11) is acquired using the following quadratic polynomial:

$$\begin{cases} Ax^2 + Bx + C = 0 \\ A = a^2k^2 + b^2 \\ B = a^2(2kp_y - 2k^2p_x) \\ C = a^2(k^2p_x^2 - 2kp_xp_y + p_y^2 - b^2) \\ k = \frac{a_y - p_y}{a_x - p_x} \end{cases}. \quad (2.12)$$

Analytical determination of the exceptions is more involved than the similar process in the case of a circle, since it requires more advanced geometry.

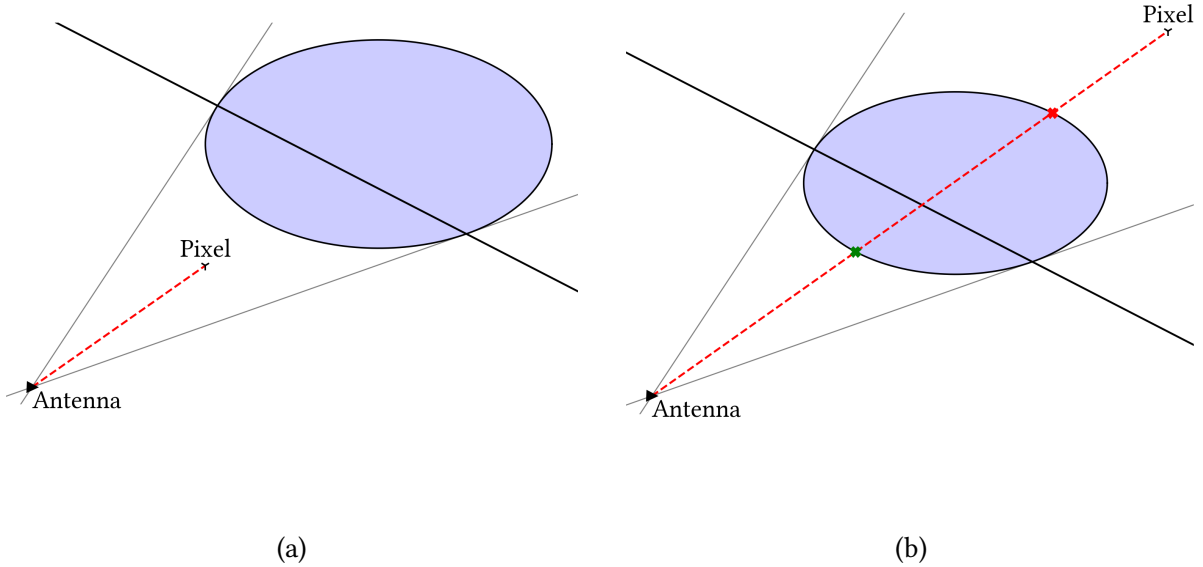


Figure 2.2: Two possible configurations of the ray-ellipse system if the pixel is outside the phantom and has two real roots of the system (2.11). The intersection points are marked analogously to Figure 2.1. Two grey lines are the tangents and the black line corresponds to the chord of contact.

As can be seen from Figure 2.2, the pixels that are outside the ellipse and are associated with two real roots of the system (2.11) can be classified as being ‘in front’ or ‘behind’ the phantom by determining its position with respect of the *chord of contact* shown as a black line on the figure.

The equation for the chord of contact of an ellipse

$$\frac{a_x x}{a^2} + \frac{a_y y}{b^2} = 1 \quad (2.13)$$

disambiguates whether the pixel is located behind or in front of the ellipse. Following the analogous logic to the circle, we can derive a system of inequalities similar to (2.6) & (2.7):

$$\left\{ \begin{array}{l} \frac{x^2}{a^2} + \frac{y^2}{b^2} \leq 1, \text{ (pixel is inside the breast)} \\ \frac{a_x x}{a^2} + \frac{a_y y}{b^2} \geq 1, \text{ (pixel is in front of the breast if outside)} \end{array} \right\}, \quad (2.14a)$$

$$(2.14b)$$

which exhaustively distinguishes between the three cases in equation (2.5). We pre-assign the intersection points according to (2.8) and are left with the array $\mathbf{R}(\mathbf{r}_a, \mathbf{r})$ analogous to the one acquired with circular geometry (2.10).

2.3 Frequency-Dependence

As was outlined in Section 1.3.3, the literature standard way of propagation speed estimation does not take into account any frequency dependent effects, such as tissue attenuation or conductivity. Even the modelling presented in Section 2.1 provides an attempt to model the propagation speed as a scalar value based on the dielectric properties of the material. Expressing the real behavior of the wave is much more complicated and requires knowledge of both the permittivity and conductivity of the material.

2.3.1 Derivation

To derive a full expression for the frequency-dependent propagation speed in a lossy non-magnetic medium, we start with Maxwell's equations:

$$\nabla \cdot \mathbf{D} = \rho \quad (2.15)$$

$$\nabla \cdot \mathbf{B} = 0 \quad (2.16)$$

$$\nabla \times \mathbf{E} = -\frac{\partial \mathbf{B}}{\partial t} \quad (2.17)$$

$$\nabla \times \mathbf{H} = \mathbf{J} + \frac{\partial \mathbf{D}}{\partial t}. \quad (2.18)$$

Where the units are defined as usual: $\mathbf{E}$ - electric field [volts/m], $\mathbf{H}$ - magnetic field [amperes/m], $\mathbf{B}$ - magnetic flux density [tesla], $\mathbf{D}$ - electric displacement [coulombs/m²], $\mathbf{J}$ - electric current density [amperes/m²], ρ - electric charge density [coulombs/m³].

Constitutive relations, assuming non-magnetic media (such that $\mu_r = 1$) are as follows:

$$\mathbf{D} = \varepsilon_r \varepsilon_0 \mathbf{E} \quad (2.19)$$

$$\mathbf{B} = \mu_0 \mathbf{H} \quad (2.20)$$

$$\mathbf{J} = \sigma \mathbf{E}, \quad (2.21)$$

where ϵ_0 is the vacuum permittivity [farads/m], ϵ_r relative permittivity of the material, μ_0 vacuum permeability [newtons/ampere²], and σ is the conductivity of the material [siemens/m]. Converting equations (2.15)-(2.18) to the differential phasor form

$$\nabla \cdot \mathbf{E} = \frac{\rho}{\epsilon_r \epsilon_0} = 0 \quad (2.22)$$

$$\nabla \cdot \mathbf{H} = 0 \quad (2.23)$$

$$\nabla \times \mathbf{E} = -j\omega\mu_0\mathbf{H} \quad (2.24)$$

$$\nabla \times \mathbf{H} = \mathbf{J} + j\omega\epsilon_r\epsilon_0\mathbf{E} \quad (2.25)$$

we use equation (2.21) to get:

$$\nabla \times \mathbf{H} = \sigma\mathbf{E} + j\omega\epsilon_r\epsilon_0\mathbf{E} = (\sigma + j\omega\epsilon_r\epsilon_0)\mathbf{E} = j\omega \underbrace{\left(\epsilon_0\epsilon_r - j\frac{\sigma}{\omega}\right)}_{\epsilon} \mathbf{E}. \quad (2.26)$$

Here, we define *complex permittivity* as

$$\epsilon = \epsilon_0\epsilon_r - j\frac{\sigma}{\omega}, \quad (2.27)$$

thus simplifying equation (2.26) to

$$\nabla \times \mathbf{H} = j\omega\epsilon\mathbf{E}. \quad (2.28)$$

Now we can take the curl of both sides of the equation (2.25)

$$\nabla \times \nabla \times \mathbf{E} = -j\omega\mu_0 \nabla \times \mathbf{H}, \quad (2.29)$$

$$\nabla \times \nabla \times \mathbf{E} = \nabla(\nabla \cdot \mathbf{E}) - \nabla^2\mathbf{E}, \quad (2.30)$$

$$-\nabla^2\mathbf{E} = -j\omega\mu_0(j\omega\epsilon\mathbf{E}), \quad (2.31)$$

$$\nabla^2\mathbf{E} + \omega^2\mu_0\epsilon\mathbf{E} = 0. \quad (2.32)$$

Here we have used $\nabla \cdot \mathbf{E} = 0$ from (2.22), and arrived to the Helmholtz wave equation

$$\nabla^2\mathbf{E} + \gamma^2\mathbf{E} = 0, \quad (2.33)$$

where γ is the *propagation constant* defined as

$$\gamma = \sqrt{\omega^2\mu_0\epsilon}, \quad (2.34)$$

by expanding ϵ we can show that the propagation constant is a complex quantity

$$\gamma^2 = \omega^2\mu_0 \left(\epsilon_0\epsilon_r - j\frac{\sigma}{\omega}\right) = \omega^2\mu_0(\epsilon' - j\epsilon''), \quad (2.35)$$

here we used the substitution $\epsilon' = \epsilon_0\epsilon_r$ and $\epsilon'' = \sigma/\omega$. Since the propagation constant is a complex number, we can write:

$$\gamma = \alpha + j\beta \quad (2.36)$$

where α is the *attenuation constant* [nepers/m], and β is the phase constant [radians/m]. To solve for both constants we use equation (2.35):

$$(\alpha + j\beta)^2 = \omega^2 \mu_0 \epsilon' - j\omega^2 \mu_0 \epsilon'' , \quad (2.37)$$

and separate real and imaginary parts of the both sides of equation (2.37) acquiring:

$$\begin{cases} \alpha^2 - \beta^2 = \omega^2 \mu_0 \epsilon' \\ 2\alpha\beta = -\omega^2 \mu_0 \epsilon'' \end{cases} . \quad (2.38)$$

Solving the system (2.38) we get the final expressions for α and β :

$$\alpha = \omega \left\{ \frac{\mu_0 \epsilon'}{2} \left[\sqrt{1 + \left(\frac{\epsilon''}{\epsilon'} \right)^2} - 1 \right] \right\}^{1/2} , \quad (2.39)$$

$$\beta = \omega \left\{ \frac{\mu_0 \epsilon'}{2} \left[\sqrt{1 + \left(\frac{\epsilon''}{\epsilon'} \right)^2} + 1 \right] \right\}^{1/2} . \quad (2.40)$$

The uniform plane wave travelling in a linear media along x direction can be represented by [81, eq. (1.32)]:

$$U(x) = Ae^{-\gamma x} + Be^{+\gamma x} . \quad (2.41)$$

We assign the direction of transmission to be positive, meaning that the first term of the equation (2.41) corresponds to the transmitted wave, or in MBI terms, to the S_{21} signal in a bistatic system:

$$S_{21} = Ae^{-\gamma x} = Ae^{-(\alpha + j\beta)x} . \quad (2.42)$$

Since β represents the rate of change of the phase with distance, we can connect it to the wavelength and hence to the propagation speed:

$$\beta = \frac{2\pi}{\lambda} = \frac{2\pi f}{v} = \frac{\omega}{v} , \quad (2.43)$$

from where

$$v = \frac{\omega}{\beta} , \quad (2.44)$$

and substituting β using (2.40), we arrive to the full expression of the frequency-dependent propagation speed in a lossy dielectric:

$$v = \left\{ \frac{\mu_0 \epsilon'}{2} \left[\sqrt{1 + \left(\frac{\epsilon''}{\epsilon'} \right)^2} + 1 \right] \right\}^{-1/2} . \quad (2.45)$$

And we can verify that in case $\sigma = 0$ we indeed get (1.4):

$$\varepsilon'' = \frac{\sigma}{\omega} = 0 \Rightarrow v = \left\{ \frac{\mu_0 \varepsilon'}{2} \left[\sqrt{1 + \left(\frac{\varepsilon''}{\varepsilon'} \right)^2} + 1 \right] \right\}^{-1/2} = \sqrt{\frac{1}{\mu_0 \varepsilon_0 \varepsilon_r}} = \frac{c}{\sqrt{\varepsilon_r}}. \quad (2.46)$$

Here we used the fact that $c = 1/\sqrt{\mu_0 \varepsilon_0}$.

2.4 Experiments

In this thesis we refer to several experimental datasets for image quality analysis. The primary dataset is the third-generation University of Manitoba Breast Microwave Imaging Dataset (UMBID) [42], [82], an open-access collection developed by our group. It was acquired using 3D printed breast phantoms derived from real patient MRI data first described in [83]. Each phantom comprises two shells filled with tissue mimicking liquids representing the dielectric properties of adipose and fibroglandular tissues. Figure 2.3 illustrates the full set of the phantoms available for scanning. The top image shows the collection of the adipose shells and the bottom image shows the set of the fibroglandular shells. Adipose shells are printed with two diametrically opposite dowel pins that fit into the locating holes in the 'F'-type shells to accommodate for a various angular configuration of the two shells, allowing for a more extensive dataset construction without the need to print additional phantoms. Measurements were performed at 1001 frequencies over the 1-9 GHz bandwidth, with the antenna rotated to 72 equally spaced positions along a circular trajectory spanning 355 degrees. tumour mimicking targets consisted of water filled glass spheres ranging from 10 mm to 30 mm in diameter.

We also employed two simpler cylindrical phantom datasets collected as a part of this project. Cylindrical phantom (Figure 2.4) allows verification of the model geometry suggested in Section 2.2 without the approximations of the breast shape and to use a single tissue mimicking liquid creating the homogeneous region inside the phantom.

The first dataset uses glycerin as the adipose mimicking liquid with a metal rod as a target to enhance reflections compared with a dielectric target. Due to the viscosity of glycerin, it is important to perform the 'adipose reference' immediately after the target scan to account for the liquid agitation, which effectively doubles the required amount of scans. This dataset contains 16 unique rod positions and will be further referred as 'rod' set. The benefit of using the rod is in its vertical extent that aligns with the E-field of the antenna. However, it also causes the antenna to receive responses from the rod later in time due to reflections from above or below the plane of the antenna.

The second set uses a 90% Diethylene Glycol Butyl Ether (DGBE) solution mixed with water, and a metal sphere attached to a glass rod to reduce the target's vertical extent. Glass was used as a nearly transparent material to the microwave radiation. This dataset contains 68 unique target positions and will be further referred to as 'ball' or 'big' set.

Equation (2.45) gives the propagation speed at any spatial point once the local dielectric properties are known. Because our phantoms are filled with tissue-mimicking liquids, we can measure the dielectric properties of the filling directly and treat this information as a priori knowledge, allowing us to assign precise propagation speed values throughout the shell region.

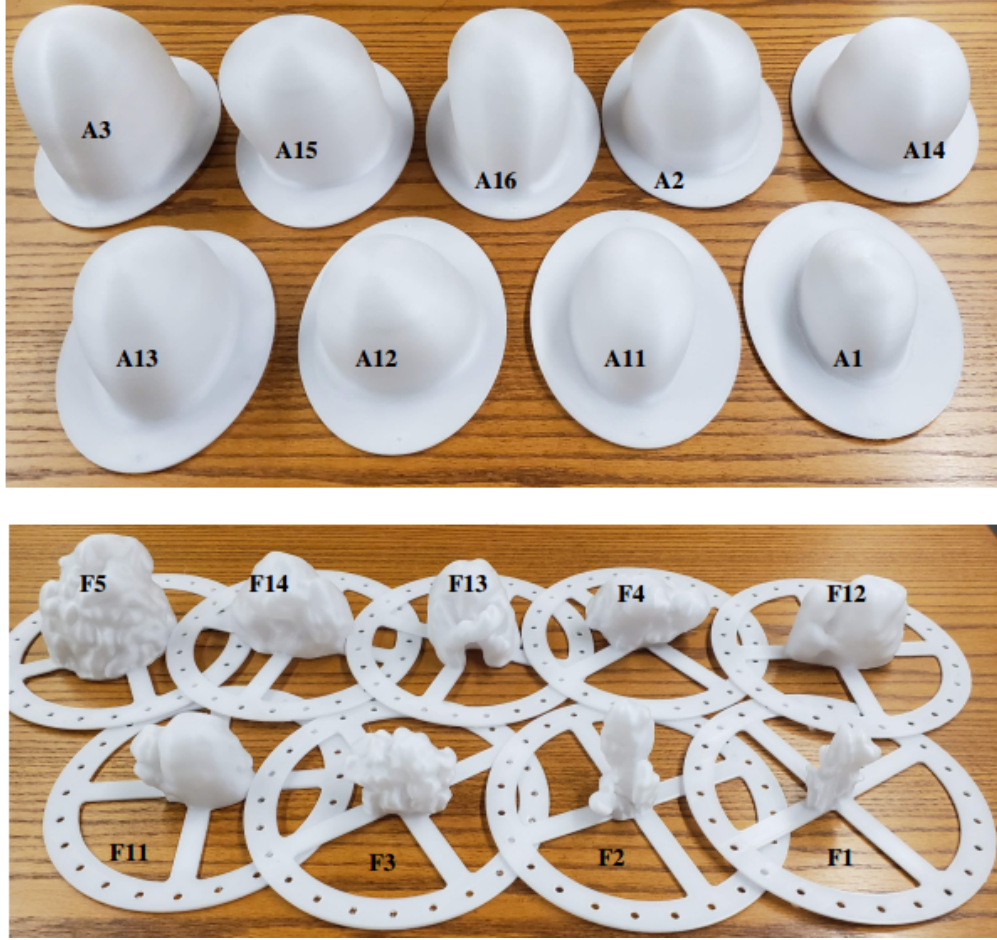


Figure 2.3: The set of 3D printed MRI-derived realistic breast phantoms manufactured at the University of Manitoba.

The dielectric properties were measured with a DAK 3.5 open-ended coaxial probe (*Speag*, Zurich, Switzerland). The probe operates from 200 MHz to 20 GHz and its readings are repeatable within $\pm 1\%$. The probe's 0.93 mm inner conductor, centered in the flange, must make firm contact with the sample; trapped air or incomplete submersion of the sensing tip will compromise accuracy. During acquisition the probe is positioned to minimize cable motion, as the measured S_{11} phase is vulnerable to movement-induced shifts.

A more comprehensive study of the dielectric properties of the tissue-mimicking liquids used at the University of Manitoba can be found in Krenkevich et al. [84]. Henceforth, the dielectric properties of the test liquid are measured with the probe and treated as known inputs for modelling. These values are used whenever we estimate the propagation speed, except in Chapter 4, which explores whether the speed can be recovered without prior knowledge of the dielectric properties.

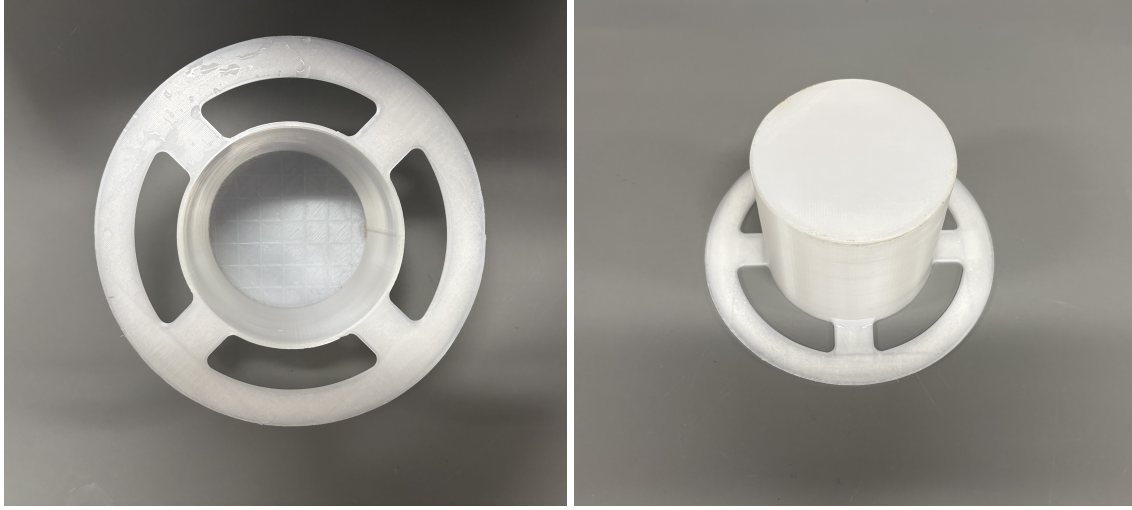


Figure 2.4: 3D printed cylindrical phantom used to produce the datasets.

2.5 Image Quality Performance

In order to quantify the feasibility and quality of the enhancements on the images, we adopt three evaluation criteria: localization error, size of response, and contrast.

- **Localization error**

The localization error quantifies the ability of the image reconstruction algorithm to accurately spatially localize the malignant response to allow the physician examining the image to understand where the tumour is located. One way of the location estimation is finding the pixel of highest intensity, however this method does not take into the account the shape of response, which can be distorted due to imperfect beamforming, or the fact that the noise on the image can constructively interfere and add up to create a region of high intensity that does not correspond to the malignancy. We employ a more robust method of determining the location of the signal - the centre of mass method.

First we find the location of the pixel of the highest intensity, assuming that it corresponds to the target response:

$$\mathbf{r}_{\max} = \arg \max_{\mathbf{r}} I(\mathbf{r}), \quad (2.47)$$

where the $I(\mathbf{r})$ is the reflectivity profile acquired using the DAS beamformer. We then define the region of interest (ROI) as the circular domain centered on the $\mathbf{r}_{\max}$, with radius R equal to the greatest distance between that peak and any pixel whose intensity is half the maximum:

$$R = \max_{\mathbf{r} : I(\mathbf{r}) = \frac{1}{2} I_{\max}} \|\mathbf{r} - \mathbf{r}_{\max}\|. \quad (2.48)$$

We require the intensity distribution to be continuous so that the ROI boundary does not take up a large portion of the image. That ROI allows us to select all the pixels' positions $\mathcal{r} = \{\mathbf{r}_i \mid i = 0, \dots, K\}$ and intensities $\mathcal{I} = \{I_i \mid i = 0, \dots, K\}$ that correspond to the tumour region, where K is the size of those discrete sets. The centre of the mass is defines as follows:

$$\mathbf{r}_c = \frac{\sum_i \mathbf{r}_i I_i}{\sum_i I_i}, \quad (2.49)$$

and the localization error corresponds to the difference between the extracted position $\mathbf{r}_c$ and the known corrected position:

$$\Delta r = \|\mathbf{r}_c - \mathbf{r}_{\text{cor}}\|, \quad (2.50)$$

where $\mathbf{r}_{\text{cor}}$ is the recorded position in the positioning mechanism frame of reference with the systematic corrections applied to convert it to the frame of reference of the antenna:

$$\mathbf{r}_{\text{cor}} = \begin{bmatrix} \cos \delta\varphi & -\sin \delta\varphi \\ \sin \delta\varphi & \cos \delta\varphi \end{bmatrix} \mathbf{r}_{\text{rec}} + \begin{bmatrix} \delta x \\ \delta y \end{bmatrix}, \quad (2.51)$$

where $\mathbf{r}_{\text{rec}}$ is the target position recorded using the positioning mechanism on the bed system. Values of system-specific parameters $(\delta x, \delta y, \delta\varphi)$ from the equation (2.51) can be found in the Table 2.1. These values are calculated using air-based ‘rod’ datasets and their acquisition is outside of the scope of this thesis.

Table 2.1: Bed-system positioning errors.

Parameter	Value
δx	$(2.7 \pm 0.1) \text{ mm}$
δy	$(2.8 \pm 0.1) \text{ mm}$
$\delta\varphi$	$(-3.0 \pm 0.2)^\circ$

- ***Size of the response***

To quantify the size of the response, we employ two metrics, $\hat{\rho}$ and $\hat{\varphi}$, defined as the full-width at half-maximum (FWHM) along the positive directions of the polar radius and the polar angle, respectively. By using these two orthogonal measurements, we can also assess the symmetry of the response, which is especially meaningful given that the targets used in this thesis are themselves symmetric. It is important to notice that $\hat{\varphi}$ metric does not correspond exactly to the extent of the target along the polar angle, due to us measuring it strictly orthogonally to the $\hat{\rho}$. A schematic shown on the Figure 2.5 illustrates the measuring procedure.

- ***Contrast***

To quantify image contrast, we employ two metrics: the signal-to-clutter ratio, as presented in [85], and the signal-to-mean ratio. Here, ‘clutter’ is defined as the region of the image that does not correspond to the tumour response, so the signal-to-clutter ratio measures how well the tumour stands out against background artifacts, while the signal-to-mean ratio compares the tumour response to the average image intensity of the clutter region. Mathematically, we denote these two metrics as follows:

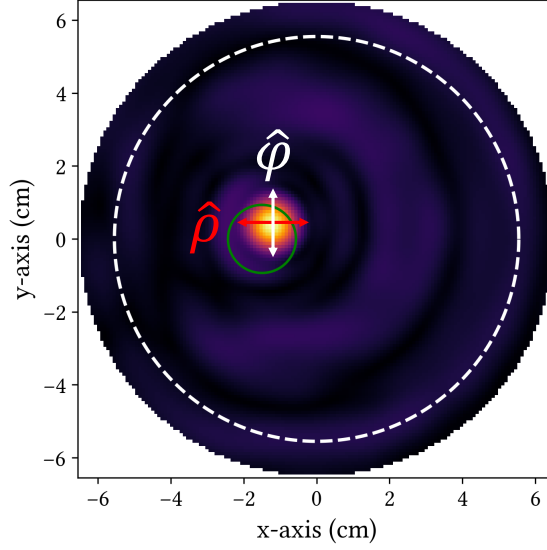


Figure 2.5: The measuring convention of the target size.

$$\text{SCR} = 20 \log_{10} \frac{T_{\max}}{C_{\max}}, \quad (2.52)$$

$$\text{SMR} = 20 \log_{10} \frac{T_{\max}}{C_{\text{mean}}}, \quad (2.53)$$

where $T_{\max}$ is the maximal intensity in the tumour region, $C_{\max}$ is the maximal intensity of the clutter and C_{mean} is the mean intensity of the clutter. The resulting values are in the units of [dB].

In the following two subsections we present the analysis performed on the two cylindrical-phantom-based datasets based on the three aforementioned criteria.

2.5.1 Cylindrical Phantom Dataset with Metal Rod as Target

Figure 2.6 provides an example of the four image-reconstruction algorithms considered in this analysis: homogeneous DAS (the literature standard DAS under the assumptions outlined in Chapter 1), binary DAS (in which the domain is partitioned into two uniform regions and only one value of v_{in} was used), and frequency-dependent DAS (where the propagation speed inside the breast region varies with frequency). The frequency-dependent approach is further split into two variants: frequency-dependent ($\sigma = 0$), which treats the breast medium as non-conductive, and frequency-dependent (full model), which incorporates conductivity, allowing us to assess the influence of conductivity on image reconstruction. The white outline on the image corresponds to the approximate position of the boundary of the cylindrical phantom and the green circle corresponds to the known position of the steel rod.

Upon visual inspection of the reconstructed images, the apparent size of the rod response shrinks as we move from homogeneous DAS to more sophisticated methods. In the binary-DAS case, the boundary exhibits the largest $\hat{\phi}$ stretch, which reduces when frequency dependence is

introduced. All enhanced algorithms share a similar clutter profile, concentric rings surrounding the rod response, that is absent in the homogeneous reconstruction, likely arising from later-time reflections due to the rod's z-extent. Finally, image intensity drops sharply from roughly 100 in the homogeneous DAS to about 60 in the binary case, then increases slightly to about 65 once frequency-dependent propagation speed is accounted for.

Table 2.2 provides the values of the localization error in mm for the four reconstruction techniques. The enhanced methods improve the localization error, most notably, binary DAS, reducing it to 1.91 mm. Since the size of the pixel on the images is approximately 0.9 mm, the sub-millimeter differences in the localization error between the two frequency-dependent approaches can be attributed to the random uncertainty.

Figure 2.8 provides the localization error distributions with the smoother kernel density estimate. The mean is denoted with a vertical purple line. Due to the lack of data in this set, we can not conclude whether the errors are normally distributed. The methods however yield minimal statistical outliers and lower the mean of the distribution compared to the homogeneous DAS.

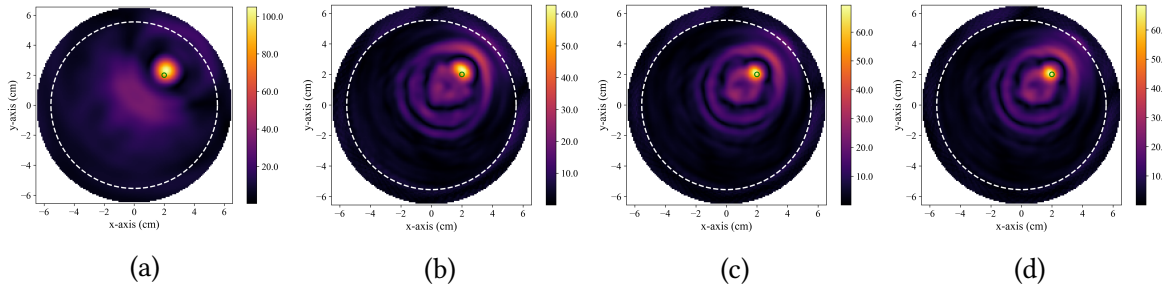


Figure 2.6: DAS reconstructions of the same ‘rod’ image with the target present in the phantom sorted by increased complexity of physics enhancements. (a) - homogeneous DAS, (b) - binary DAS, (c) - frequency-dependent DAS ($\sigma = 0$), (d) - frequency-dependent DAS (full model).

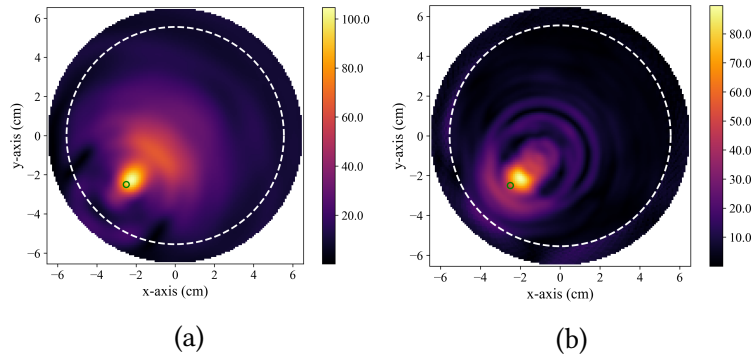


Figure 2.7: The reduction of the $\hat{\rho}$ -stretch at the positions farther from the center of the imaging domain. (a) - homogeneous DAS, (b) - frequency-dependent DAS (full model).

Table 2.3 confirms the fact that the proposed physics enhancements reduce the spread of the response and produce a symmetrical tumour on the image. The binary case experiences slight asymmetry in the $\hat{\phi}$ direction, which was evident from the reconstructions. The inclusion of the frequency-dependence manages to eliminate the asymmetry: both frequency-dependended

Table 2.2: The mean localization error in mm in the ‘rod’ dataset for various reconstruction algorithms sorted by the increased complexity.

Homogeneous	Binary	Frequency-dependent ($\sigma = 0$)	Frequency-dependent (full)
2.96	1.91	2.34	2.53

reconstruction techniques have almost identical values of $\hat{\rho}$ and $\hat{\phi}$ - approximately 40% smaller than the homogeneous case. Such a reduction is an indicator of better temporal alignment of the response due to the enhanced physics modelling of the time delay.

It is of interest that the homogeneous DAS algorithm was associated with an artifact that occurred when the target was close to the boundary of the phantom. On Figure 2.7 we can see the exaggerated stretch in the $\hat{\rho}$ -direction that is mitigated with the inclusion of physics enhancements. This artifact may be attributed to the imaging equations neglecting the frequency-dependence of the phase center of the antenna. It may also explain the reduction in the $\hat{\phi}$ -stretch with the inclusion of frequency-dependence of the propagation speed.

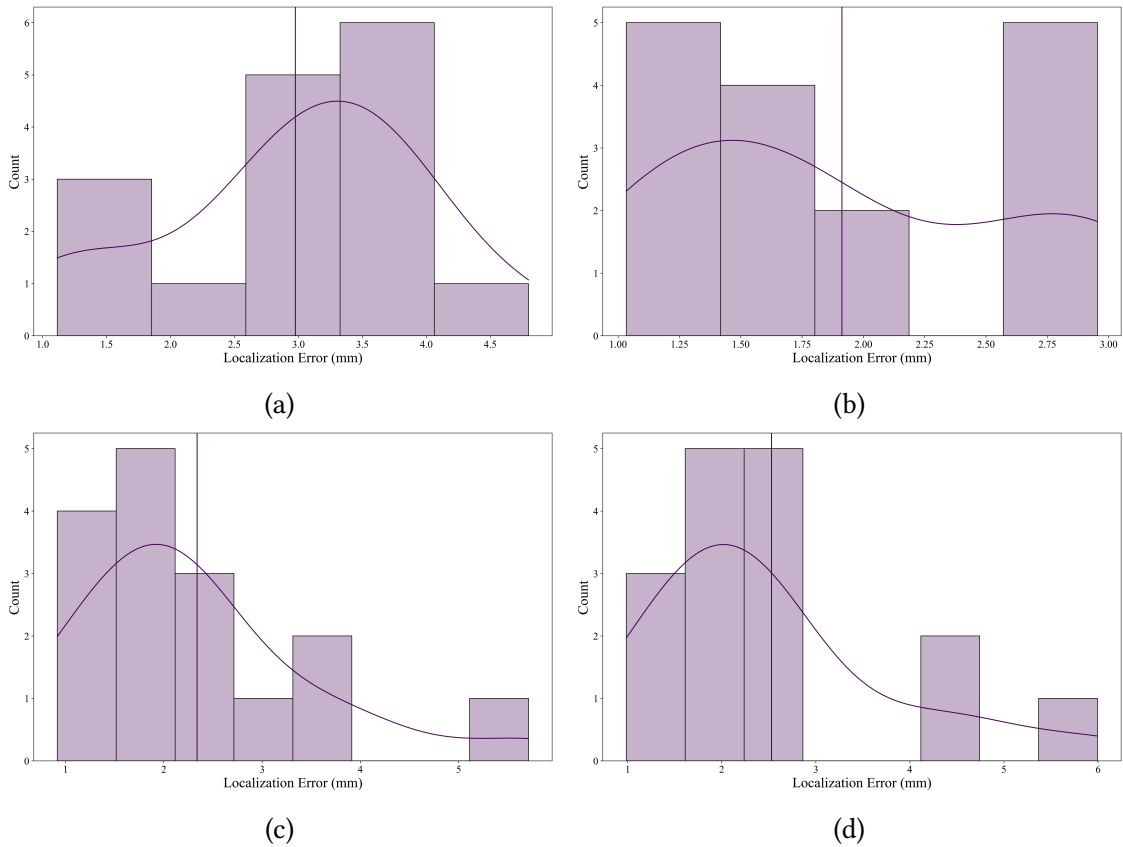


Figure 2.8: The localization error distributions in the ‘rod’ dataset for various reconstruction algorithms. (a) - homogeneous DAS, (b) - binary DAS, (c) - frequency-dependent ($\sigma = 0$), (d) - frequency-dependent (full model).

Table 2.3: The mean $\hat{\rho}$ - and $\hat{\phi}$ -extents in mm in the ‘rod’ dataset for various reconstruction algorithms sorted by the increased complexity.

	Homogeneous	Binary	Frequency-dependent ($\sigma = 0$)	Frequency-dependent (full)
$\hat{\rho}$	95.0	68.6	62.0	61.5
$\hat{\phi}$	96.7	87.9	61.5	62.0

Table 2.4: The mean Signal-to-Clutter (SCR) and Signal-to-Mean (SMR) ratios in dB in the ‘rod’ dataset for various reconstruction algorithms sorted by the increased complexity.

	Homogeneous	Binary	Frequency-dependent ($\sigma = 0$)	Frequency-dependent (full)
SCR	8.49	6.42	7.94	7.92
SMR	35.83	29.66	32.69	32.67

Table 2.4 presents the contrast metrics across the various reconstruction algorithms. The binary DAS algorithm experiences a 25% drop in SCR and a 17% drop in SMR compared to the homogeneous case. The higher drop in SCR can be explained by the high-intensity hot-spot present in the clutter of the binary DAS reconstructions (Figure 2.6b). This is further supported by the 19% increase in SCR between the binary and both frequency-dependent algorithms. The frequency-dependent algorithms also experience a 9% increase in SMR. These results indicate that the inclusion of the frequency dependence is able to redistribute the intensity of the hot-spot and improve the focusing abilities of the reconstruction algorithm. The conductivity did not seem to contribute to the contrast. The overall drop in contrast compared to the homogeneous reconstruction is attributed to the clutter around the response which is likely caused by the late-time contributions from the vertical extent of the rod.

2.5.2 Cylindrical Phantom Dataset with Metal Ball as Target

Figure 2.9 illustrates a typical set of reconstructed images in the ‘ball’ dataset. The homogeneous image looks very similar to the one extracted from the ‘rod’ dataset, however, the enhanced images experience arching of the target response. The drop in the intensity compared to the homogenous reconstruction is consistent with the results presented in Section 2.5.1.

Notably, this dataset is associated with overall noisier images (Figure 2.10), which can be attributed to the fact that due to the small ball having negligible vertical extent, the antenna is receiving lower relative reflected power. This particular fact can also explain an inhibited ability of the reconstruction algorithms to localize the target with reasonable contrast.

Table 2.5 provides the means of the distributions illustrated on the Figure 2.11. The localization error is significantly higher compared to the ‘rod’ dataset for all the reconstruction algorithms. The results indicate that for a small ball enhanced physics modelling does not improve the localization error, but slightly increases it with higher modelling complexity. This is attributed to the outliers present in the localization error distributions. Even though the majority of the points

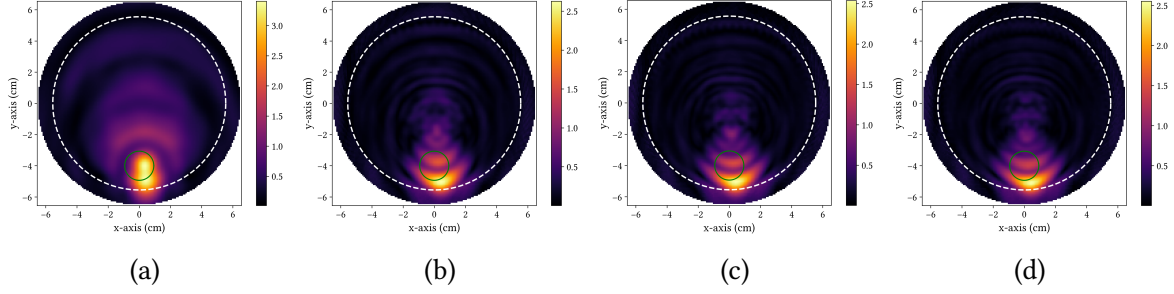


Figure 2.9: DAS reconstructions of the same ‘ball’ scan with the target present in the phantom sorted by increased complexity of physics enhancements. (a) - homogeneous DAS, (b) - binary DAS, (c) - frequency-dependent DAS ($\sigma = 0$), (d) - frequency-dependent DAS (full model).

Table 2.5: The mean localization error in mm in the ‘ball’ dataset for various reconstruction algorithms sorted by the increased complexity.

Homogeneous	Binary	Frequency-dependent ($\sigma = 0$)	Frequency-dependent (full)
5.20	7.53	8.56	9.91

are distributed within 0-20 mm range, the enhanced physics algorithms experience outliers of 40 and even 80 mm. Such errors arise from the fact that on some reconstructions, the target response is no longer a maximum intensity feature of the image, which effectively allows any arbitrary point of high intensity in the imaging domain to be labelled as the tumour.

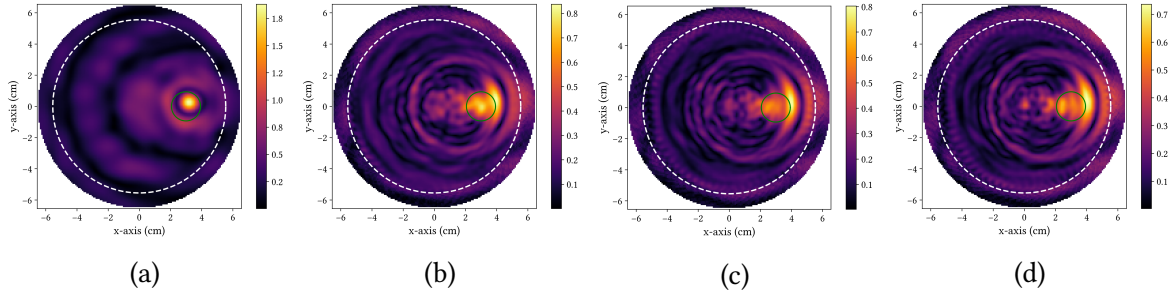


Figure 2.10: Noisy DAS reconstructions of the same ‘ball’ scan with the target present in the phantom sorted by increased complexity of physics enhancements. (a) - homogeneous DAS, (b) - binary DAS, (c) - frequency-dependent DAS ($\sigma = 0$), (d) - frequency-dependent DAS (full model).

Table 2.6 provides the values of orthogonal extents of the target response. We can see that the enhanced modelling persistently decreased the $\hat{\rho}$ -extent of the metal ball, however, this indicated an overfocusing of the signal, since the diameter of the ball was 186.7 mm. As was evident from the reconstructions, the enhanced algorithms experience significant arching of the response, which is showcased by the increase of the $\hat{\phi}$ -extent of the target response.

From Table 2.7 we can notice similar trends to the ‘rod’ dataset: the contrast is decreased with the addition of the binary partitioning, and slightly increased with the addition of the frequency dependence. The inclusion of the conductivity slightly lowered the SCR and SMR, by 10% and 1%

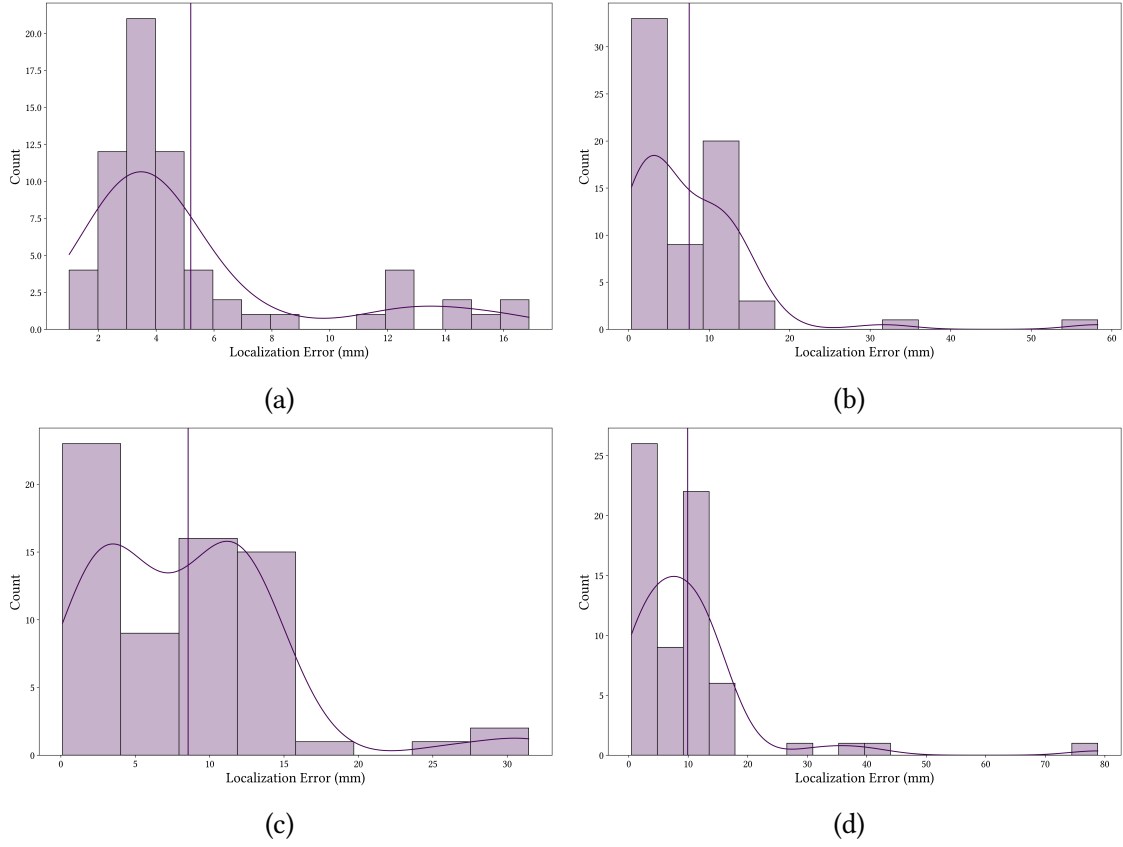


Figure 2.11: The localization error distributions in the ‘ball’ dataset for various reconstruction algorithms. (a) - homogeneous DAS, (b) - binary DAS, (c) - frequency-dependent ($\sigma = 0$), (d) - frequency-dependent (full model).

respectively. The overall contrast is decreased comparing with the ‘rod’ dataset, which is explained by the lower surface area of the ball exposed to the antenna.

Table 2.6: The mean $\hat{\rho}$ - and $\hat{\phi}$ -extents in mm in the ‘ball’ dataset for various reconstruction algorithms sorted by the increased complexity.

	Homogeneous	Binary	Frequency-dependent ($\sigma = 0$)	Frequency-dependent (full)
$\hat{\rho}$	100.4	108.0	90.28	87.8
$\hat{\phi}$	89.1	121.5	125.1	122.4

Table 2.7: The mean Signal-to-Clutter (SCR) and Signal-to-Mean (SMR) ratios in dB in the ‘ball’ dataset for various reconstruction algorithms sorted by the increased complexity.

	Homogeneous	Binary	Frequency-dependent ($\sigma = 0$)	Frequency-dependent (full)
SCR	6.42	4.25	4.56	4.14
SMR	31.06	28.65	29.11	28.93

Chapter 3

Boundary Detection

3.1 Motivation and Overview

The binary domain partitioning methods outlined in Chapter 2 rely on an analytical derivation of the ray–boundary intersection points to compute the time delay. Although this approach is tractable for idealized geometries such as circles or ellipses, it breaks down for realistic breasts, whose axial outlines are irregular and vary markedly from patient to patient, making a closed-form description virtually impossible.

A logical next step in robust modelling is to let the data itself construct the breast outline and then use that contour to constrain the interior dielectric estimation. Section 3.2 explains how this can be done with a DAS reconstruction, while Section 3.3 details another approach that operates directly on time domain microwave sinograms.

As noted in Chapter 1, the skin is the first dielectric interface the wave meets and therefore the layer at which it loses the most energy. The resulting strong early-time signal makes the air-skin boundary easy to identify and localize.

Amplifying the skin response is achieved by first acquiring a reference scan of the empty chamber and subtracting it from the breast scan. This subtraction aims to eliminate ambient reflections and system noise, leaving only the reflections produced by the wave interaction with the breast itself. We can formalize it the following way:

$$S_{11}(\mathbf{r}_a, f) = S_{11}^{\text{target}}(\mathbf{r}_a, f) - S_{11}^{\text{empty}}(\mathbf{r}_a, f), \quad (3.1)$$

where S_{11} denotes the ‘calibrated’ reflection data, S_{11}^{target} and S_{11}^{empty} are the target and reference empty chamber scans respectively.

Figure 3.1 displays the time-domain S_{11} signal after subtraction of the empty-chamber reference. A pronounced skin peak appears at roughly 1.6 ns, while the remainder of the waveform stays near the noise level. A fuller discussion of transforming frequency-domain measurements to the time domain is given in Section 3.3. Throughout the rest of this chapter, every boundary extraction step is performed on empty-chamber-calibrated measurements. Accordingly, any appearance of S_{11} without subscripts or superscripts denotes the reflection trace obtained after subtracting the empty-chamber reference, as formalized in equation (3.1).

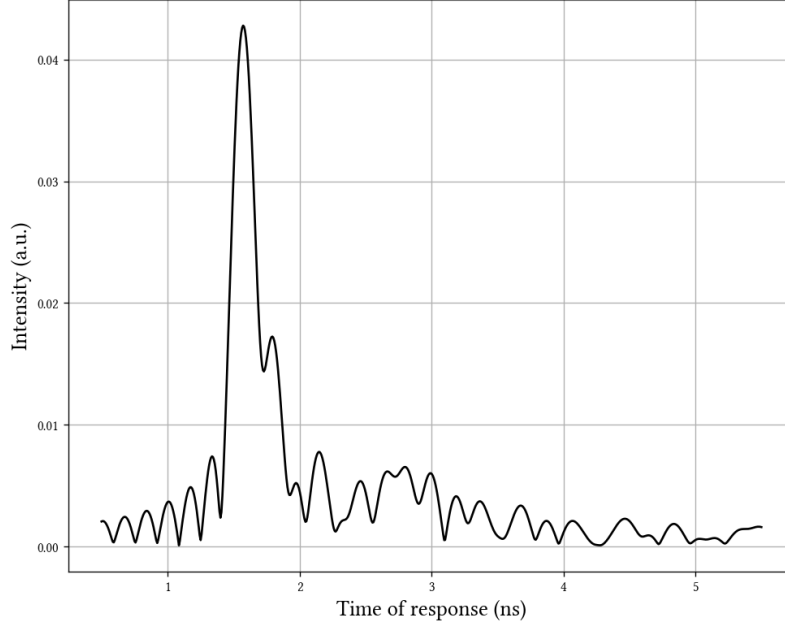


Figure 3.1: A time domain S_{11} MW signal acquired after the empty chamber reference subtraction.

3.2 Extracting the Boundary Using DAS Reconstructions

Figure 3.2 illustrates a delay-and-sum reconstruction obtained using the empty-chamber subtracted S_{11} data. The skin outline appears as a bright wide ring. The central ‘hot spot’ artifact can also be observed along with a secondary ring closer to the center.

Let the image be $I(\mathbf{r})$ reconstructed by (1.1) with an origin in the image centre. We choose N equally spaces angles

$$\varphi_k = \frac{2\pi k}{N}, \quad k = 0, \dots, N-1, \quad (3.2)$$

and define a one-dimensional slice obtained at each angle as

$$I_k(\rho) = I(\rho \cos \varphi_k, \rho \sin \varphi_k), \quad \rho \in [-\rho_{\max}, \rho_{\max}], \quad (3.3)$$

where $\rho_{\max}$ is the radial extent of the image. The full set of radial slices is then

$$\mathcal{S} = \{I_k(\rho) \mid k = 0, \dots, N-1\} \quad (3.4)$$

where every element $I_k(\rho)$ represents an intensity profile of the image along the line at an angle φ_k . Figure 3.3b shows what a typical profile looks like. The peak corresponding to the location of the air-skin interface is always the first peak above the ‘noise level’ (defined empirically). We can formalize such an extraction the following way. Let the radial grid along each slice be discretized as

$$\rho_n = n\Delta\rho, \quad n = 0, \dots, N_\rho - 1, \quad (3.5)$$

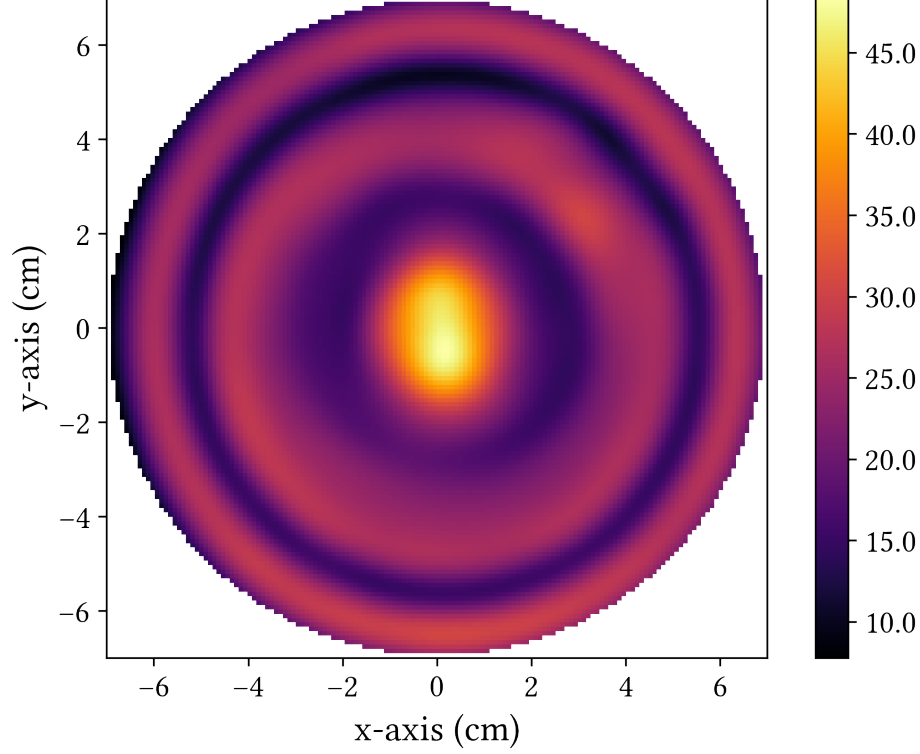


Figure 3.2: An example DAS reconstruction of the empty-chamber calibrated S_{11} data.

where $\Delta\rho$ is the sampling density, equivalent to the width of the pixel¹, and N_ρ is the length of the slice. Then we are able to sample each slice $I_k(\rho)$ from (3.3) at those points:

$$I_k[n] = I(\rho_n \cos \varphi_k, \rho_n \sin \varphi_k) . \quad (3.6)$$

Now we can define the set of local maxima (above a threshold) indices:

$$\mathcal{A}_k = \{n \in \{1, \dots, N_\rho - 2\} \mid I_k[n] > I_k[n-1] \wedge I_k[n] > I_k[n+1]\} . \quad (3.7)$$

To extract the skin peak, we must find the first index corresponding to a local maximum:

$$n_k^{\text{skin}} = \min \mathcal{A}_k \quad (3.8)$$

and the radial coordinate of the peak will be

$$\rho_k^{\text{skin}} = \rho_{n_k^{\text{skin}}} . \quad (3.9)$$

The resulting Cartesian coordinates are simply

$$(x_k, y_k) = (\rho_k^{\text{skin}} \cos \varphi_k, \rho_k^{\text{skin}} \sin \varphi_k) , \quad (3.10)$$

collecting all of which at all angles yields the boundary set

¹Such sampling is acceptable due to us taking the horizontal slices of the *rotated* image by the angle φ_k . Otherwise, the constant $\Delta\rho$ would need to be recalculated for every slice.

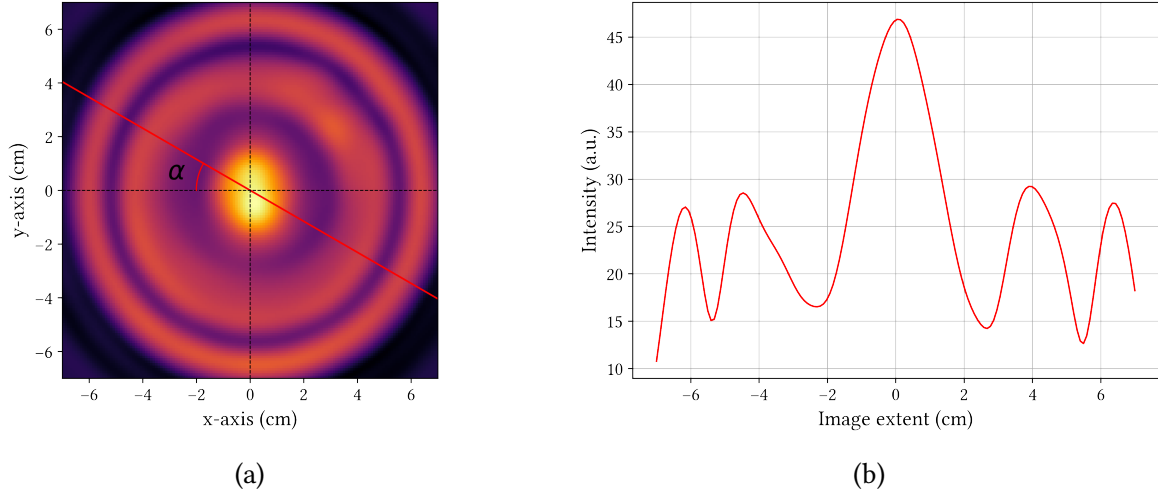


Figure 3.3: Slicing procedure. (a) DAS reconstruction with a red line marking the radial slice at angle α ; (b) intensity profile extracted along that slice.

$$\mathcal{B} = \{(x_k, y_k) \mid k = 0, \dots, N - 1\}. \quad (3.11)$$

This set of discrete points is used then to acquire a continuous function $\hat{\rho}(\varphi)$ using `CubicSpline` function from the `SciPy` library. Figure 3.4a illustrates a smooth cubic spline line going through the set of points $\mathcal{B}$ and Figure 3.4b shows this extracted skin outline on top of the DAS reconstruction.

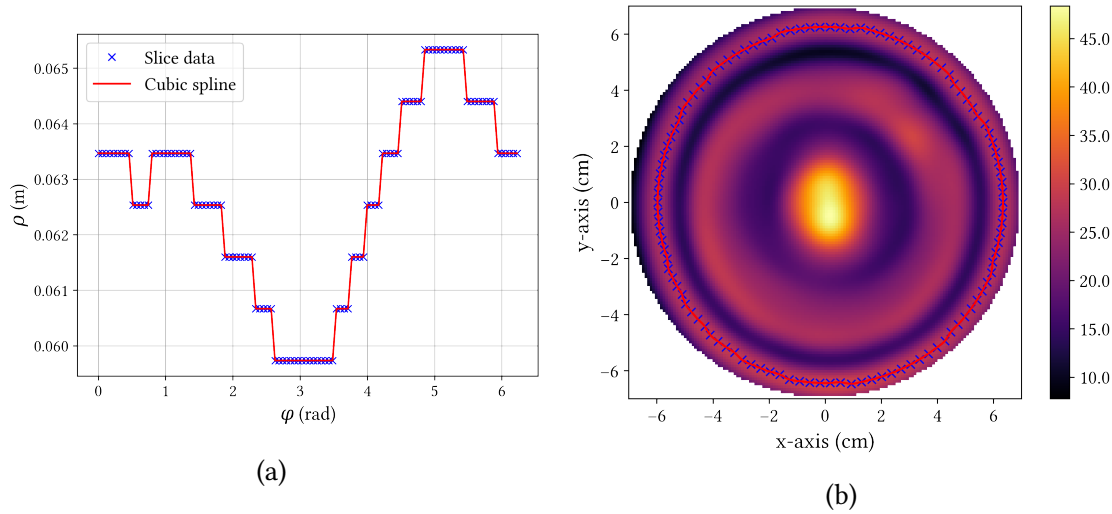


Figure 3.4: (a) - cubic spline (solid red) line through the discrete set of extracted skin peaks (blue marks), (b) - DAS reconstruction of the empty-chamber calibrated data with the extracted boundary overlaid on top of the image.

We have shown that the skin outline can be extracted from a delay-and-sum reconstruction. However, this approach has several drawbacks. It first requires a full image reconstruction, adding computational cost and inheriting all the artifacts and modelling errors discussed in earlier

chapters, such as reliance on the average propagation speed value and the algorithm’s inability to distinguish between different tissues within the breast. The necessity to reconstruct the image creates a recursive issue since the boundary detection is considered for the purpose of improving the reconstruction procedure. It also relies on an empirically chosen intensity threshold to discard ‘noisy’ peaks, a parameter that must be tuned not only for every image but often for each slice; an ill-chosen threshold causes the algorithm to pick an incorrect peak (Figure 3.5). Together with the central hot-spot artifact, these factors raise concerns about the robustness and stability of the method.

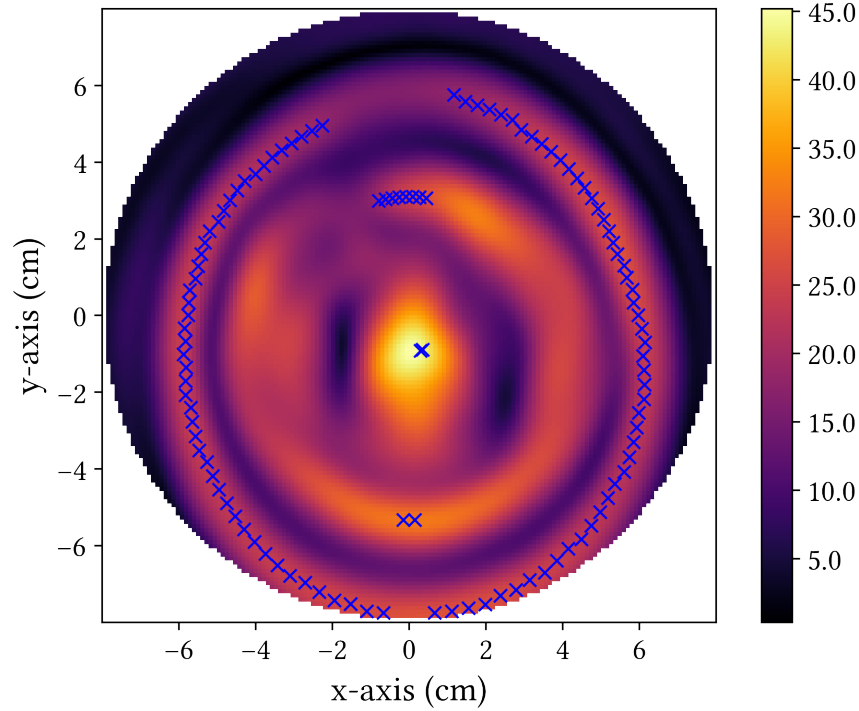


Figure 3.5: A boundary extracted from the DAS reconstruction with a poorly chosen threshold value.

3.3 Extracting the Boundary Using Sinograms

Microwave imaging employs an acquisition geometry analogous to Computed Tomography (CT). In CT, a rotating gantry directs a narrow X-ray beam through the patient, while a detector on the opposite side records the beam’s attenuation. Arranging these attenuation values against the rotation angle produces a sinogram - a two-dimensional array in which each column represents the line integral of the object’s linear attenuation coefficient along a specific projection line.

Because microwave measurements can be converted between the frequency and time domains via Fourier transforms, the data can be displayed in a sinogram-like fashion. Figure 3.6 shows a representative MBI sinogram, where the horizontal axis denotes the viewing angle of the transmitting antenna relative to the center of the imaging domain, and the vertical axis represents

the corresponding microwave propagation time. It is important to note that the intensity values in the sinogram are not arbitrary, as in images produced with the DAS beamformer. Each value is proportional to the ratio of reflected power to emitted power (see Chapter 1).

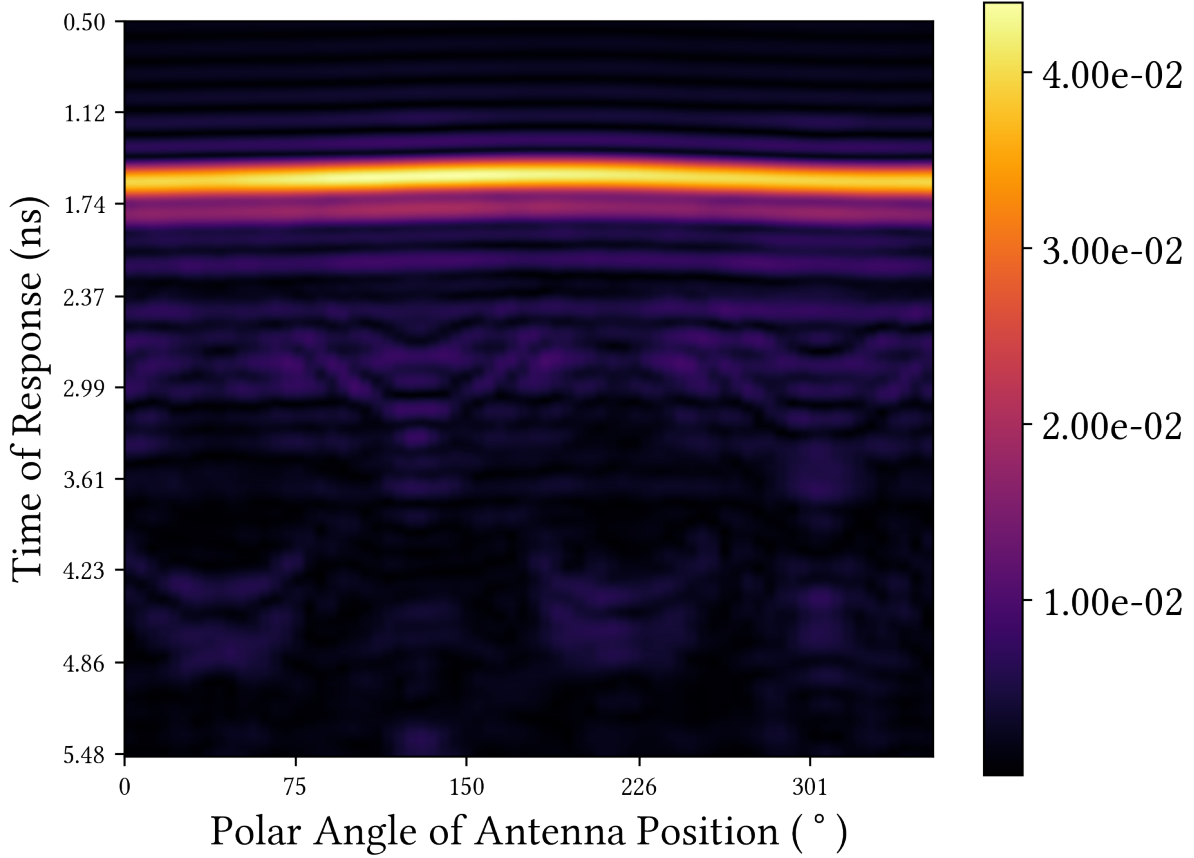


Figure 3.6: A typical MBI sinogram.

The inverse chirp z-transform (ICZT) is used in place of the standard inverse discrete Fourier transform (IDFT) because it enables arbitrarily fine sampling in the time domain, leading to more precise signal reconstruction. The algorithm and its impact on image quality are discussed in Reimer et al. [44]. Henceforth, all conversions from frequency-domain data to the time domain are assumed to be carried out with the ICZT.

The algorithm can be defined as:

$$\hat{S}(n) = \sum_{k=0}^N S_{11}(k) e^{j2\pi\theta_0 k} e^{j2\pi\varphi_0 kn}, \quad (3.12)$$

where φ_0 and θ_0 are the angle step size and the initial angle of the unit circle in the Z-plane, n corresponds to the index of the time point. For the purposes of signal processing withing this thesis we can say that $\hat{S}(n)$ is equivalent to $\hat{S}_{11}(\mathbf{r}_a, t)^2$ - the time domain reflection data.

²If the parentheses are omitted while talking about the S_{11} signal, e.g., $S_{11}(f, \mathbf{r}_a)$, S_{11} without the hat (^) symbol on

Applying the same technique as with the DAS reconstruction extraction, namely - taking an empty chamber reference from the raw data, we can notice that ICZT is able to produce the skin line on the sinogram that is noticeably sharper (Figure 3.6) compared to one of the DAS image, which helps to narrow the selection of the coordinate and increase the precision of the boundary extraction algorithm. Figure 3.7 shows the comparison between the skin peak in DAS reconstruction and the sinogram. Even though on the same scale, the sinogram peak has a slightly bigger FWHM, it is evident that as long as the signal is calibrated to the empty reference, the skin peak is going to be the highest intensity feature on the image (Figure 3.1), simplifying the signal processing and peak selection. Additionally, the accuracy of boundary extraction from sinograms is limited by the ICZT sampling rate, whose computational cost grows linearly with the chosen time resolution. Achieving comparable accuracy with DAS therefore requires increasing the image resolution, but the associated computational complexity rises quadratically with the physical sampling.

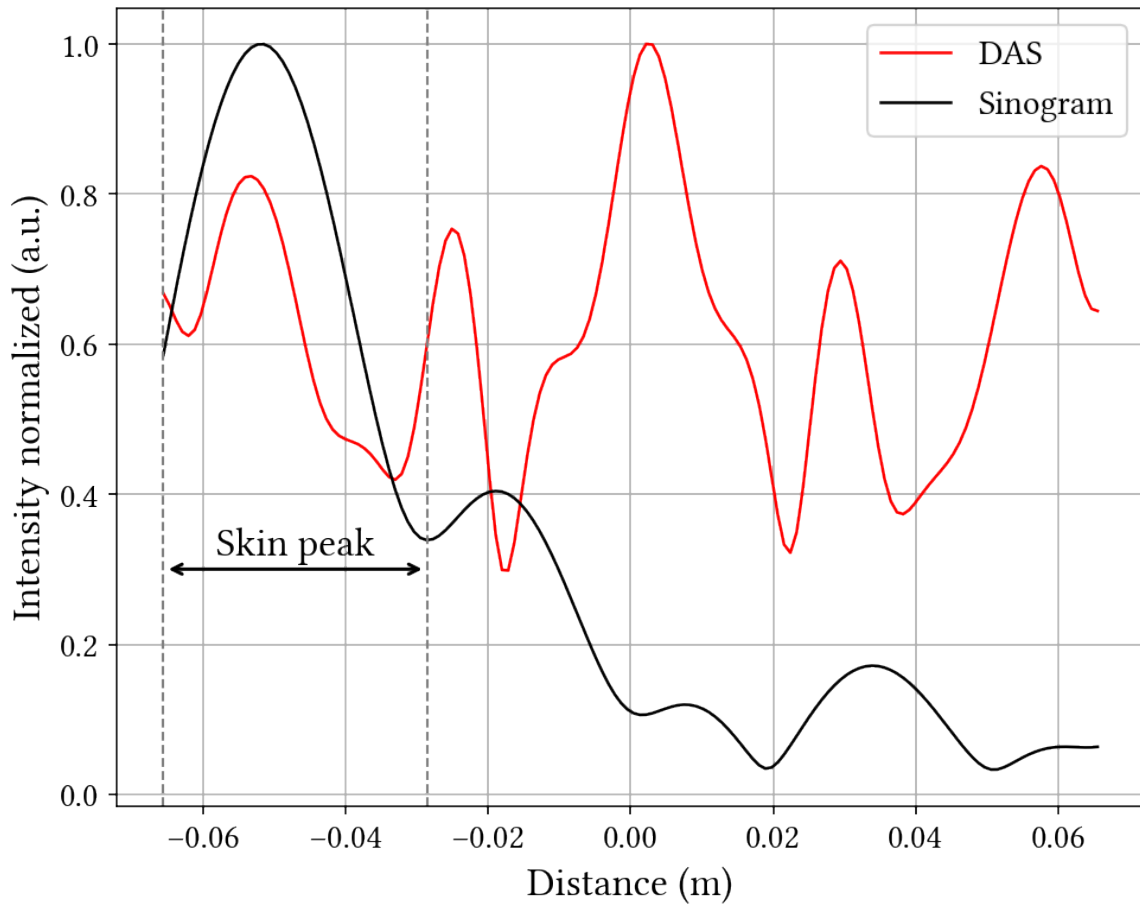


Figure 3.7: Comparison of the skin peaks between the DAS reconstruction and the sinogram.

One might also notice that the part of the image ‘above’ the skin line corresponds to the top denotes the reflection data in the frequency domain, and $\hat{S}_{11}$ corresponds to the reflection data in the time domain. The hat is included even if the parentheses are present for conciseness.

propagation through air, where the speed is known. This reduces the problem of boundary detection to finding the time of response corresponding to the skin peak, analogously with the DAS reconstruction method. Because the antenna positions and the speed of light are known, time-of-flight is sufficient to determine the position of the closest point of the skin to antenna.

The following sections describe the proposed boundary detection framework for sinogram data. We justify the adoption of correlation-based peak selection, provide evidence that this strategy suppresses specific artifacts, and integrate the resulting boundary estimates into a ray-tracing algorithm for image reconstruction. We then introduce differential imaging, using the detected boundaries as a means to align left and right breast scans allowing for the clinically possible experimental skin suppression procedure.

3.3.1 Correlation-Based Peak Selection

Peak selection can be a challenging problem in boundary extraction. In theory, the strongest peak corresponds to the skin reflection, because most of the wave's energy is lost at the air-skin interface. Yet a high-intensity '*secondary peak*' often appears in microwave sinograms, complicating this assumption and prompting the need for additional signal processing within the skin-detection routine. Usually this artifact is attributed to the shape of the phantom, i.e., a phantom with a higher eccentricity may produce a later skin response from the off-axis skin positions that constructively interfere.

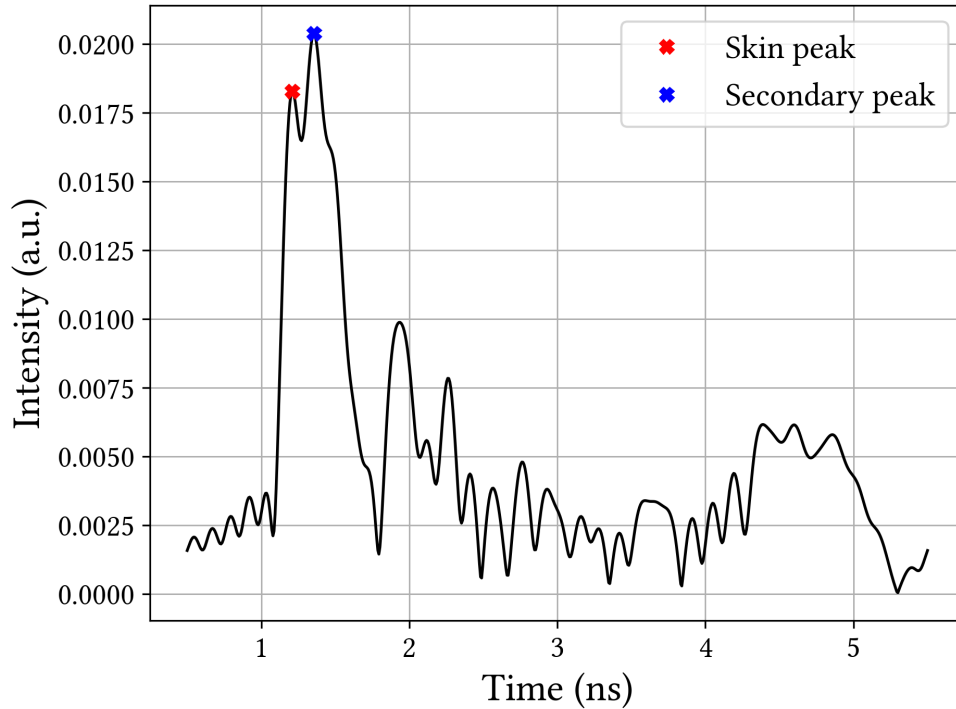


Figure 3.8: Time-domain microwave signal with a skin peak that is being overpowered by another peak later in time.

Figure 3.8 shows such a signal for a single antenna. From experiments, the secondary peak

is actually a region on the sinogram that can span almost a quarter of the angular range. Thus ignoring this phenomenon can lead to the outlines that have characteristic ‘dents’ in them, due to the secondary peak happening later in time. The ‘dent’ artifact is shown on the Figure 3.10.

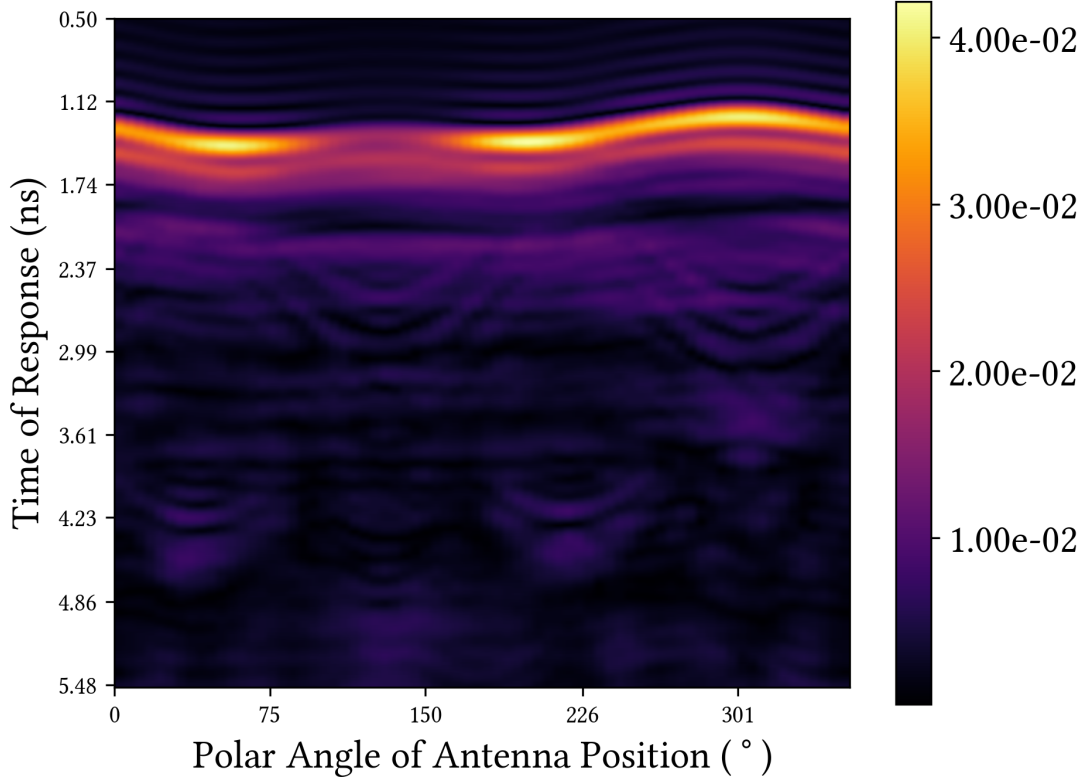


Figure 3.9: A sinogram of an image with the region of secondary peaks of higher intensity than the skin peaks. The secondary peak is overpowering the skin peak in the region corresponding to approximately 100-150 °.

One way to address this artifact is to employ a cross-correlation routine that can still identify the skin peak even when it is lower intensity than the secondary reflections. By cross-correlating each new trace with a time-aligned kernel extracted from the measurement itself, the algorithm predicts the expected position of the skin reflection for the next antenna location. Because the kernel is derived entirely from the collected data, the procedure requires no additional modelling and remains fully data-driven.

The result of the correlation is defined as follows:

$$h_i(\tau) = \hat{S}_{11}(\mathbf{r}_a^i, \tau) \star k(\tau) \triangleq \int_{-\infty}^{\infty} \hat{S}_{11}^*(\mathbf{r}_a^i, t) k(t + \tau) dt, \quad (3.13)$$

where $\hat{S}_{11}$ denotes the time-domain S_{11} data at the i -th antenna position $\mathbf{r}_a^i$ and the $*$ symbol denotes the complex conjugate, τ is conventionally called *lag*. $k(\tau)$ is the *time-aligned kernel* that is constructed to sharpen the result of the correlation $h(\tau)$ in the following manner:

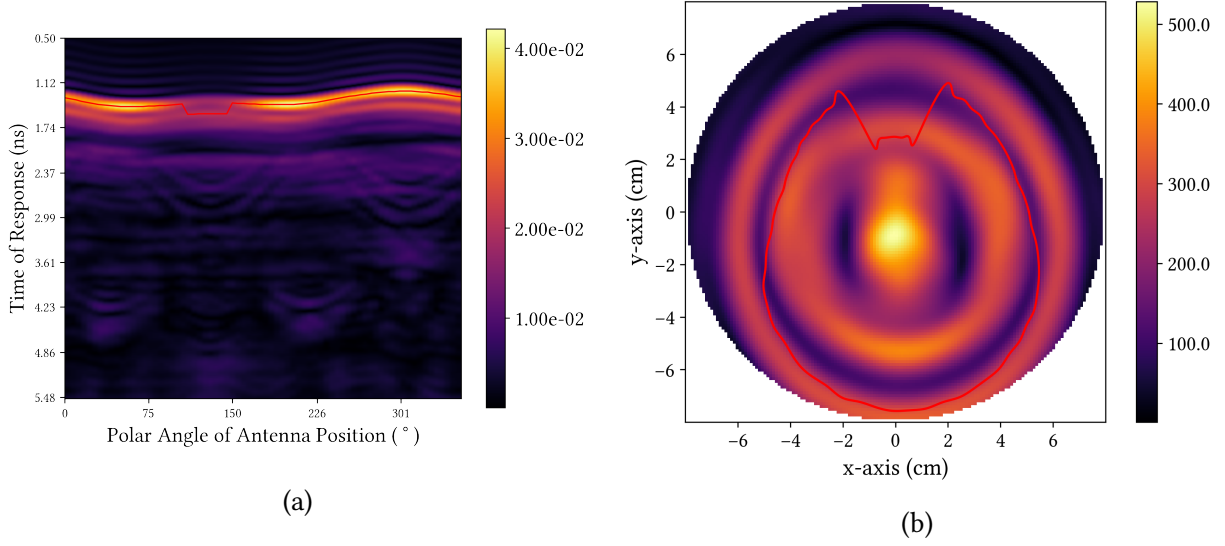


Figure 3.10: An example of the ‘dent’ artifact. (a) - sinogram with the estimated boundary (red solid line), (b) - reconstructed image with the boundary extracted from the sinogram.

$$k(t) = \frac{\sum_{i=1}^{N_{\text{ant}}} \hat{S}_{11}(\mathbf{r}_a^i, t + \Delta t_i)}{N_{\text{ant}} - 1}, \quad (3.14)$$

where Δt_i is the time interval between the consecutive maxima and N_{ant} is the total number of antenna positions. The kernel is essentially a mean reflection signal in time domain. The time-alignment is happening inside of the Δt term defined as

$$\Delta t_i = t_i^{\text{max}} - t_{i-1}^{\text{max}}, \quad (3.15)$$

where t_i^{max} denotes the time coordinate of the i -th time-domain S -parameter’s maximum:

$$t_i^{\text{max}} = \arg \max_t \hat{S}_{11}(\mathbf{r}_a^i, t). \quad (3.16)$$

Meaning that every i -th $\hat{S}_{11}$ reflection signal in the equation (3.14) is being shifted so that its highest intensity peak was positioned at the same time coordinate as the $(i - 1)$ -th.

The correlation kernel is time-aligned so that its secondary peak is retained, and its overall shape still captures the average behaviour of the time-domain traces at every antenna location. Figure 3.11 provides the comparison between the time-aligned kernel and the one that is acquired as a mean of the time-domain signal. The time-aligned kernel outputs a sharper skin response and retains more general features like the ripple visible before 1 ns and the secondary peak. Reading the time coordinate of the global maximum of the correlation output yields a first estimate of the skin peak’s shift relative to the kernel’s skin peak before any peak search is applied. This estimate is denoted $\tilde{t}_i$ for the i -th antenna:

$$\tilde{t}_i = \arg \max_t h_i(t) = \arg \max_t \hat{S}_{11}(\mathbf{r}_a^i, t) \star k(t). \quad (3.17)$$

And the kernel skin peak:

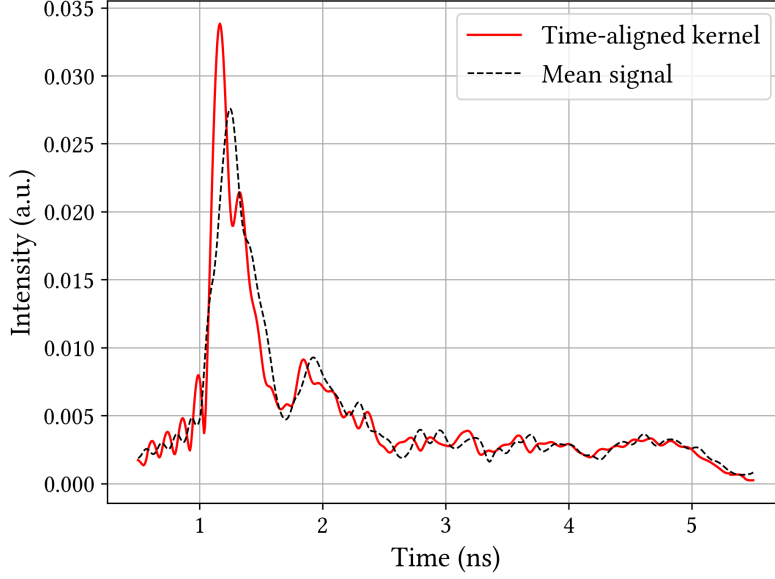


Figure 3.11: Time-aligned kernel vs the kernel acquired as the mean signal.

$$\bar{t} = \arg \max_t k(t). \quad (3.18)$$

Figure 3.12 illustrates the cross-correlation procedure, with the correlation output shown in Figure 3.12c. The global maximum of $h_i(t)$ in (3.13) marks the time shift that produces the greatest similarity between the two signals - $\hat{S}_{11}(\mathbf{r}_a^i, t)$ and $k(t)$. Extracting this maximum therefore reveals the offset between the skin peak in the measured trace and the corresponding peak in the kernel. For example, the sinogram slice in Figure 3.12a has its strongest peak at 1.29 ns, whereas the kernel in Figure 3.12b peaks at 1.17 ns. The correlation output consequently peaks at 0.18 ns, whereas the difference between the two time coordinates is approximately 0.13 ns, which means that the correlation method is able to predict the location of the skin peak within roughly 0.05 ns or ~ 1 cm.

Once we know the ‘average’ position of the skin peak from the kernel and the correlation-derived shift for the current antenna, we select peaks as follows. For the first antenna we take the average peak position (derived from the kernel) and add the measured shift to get our initial estimate. For each subsequent antenna we compare the time points corresponding to the global maxima with the peak chosen for the previous antenna. If the time gap between them is larger than a set threshold, we again take the average peak plus the current shift, which prevents a selection of the secondary peak as the true skin reflection. If the gap stays below the threshold, we assume the boundary changes smoothly and simply choose the local peak that lies closest in time to the predicted position. We formalize this algorithm in the following matter:

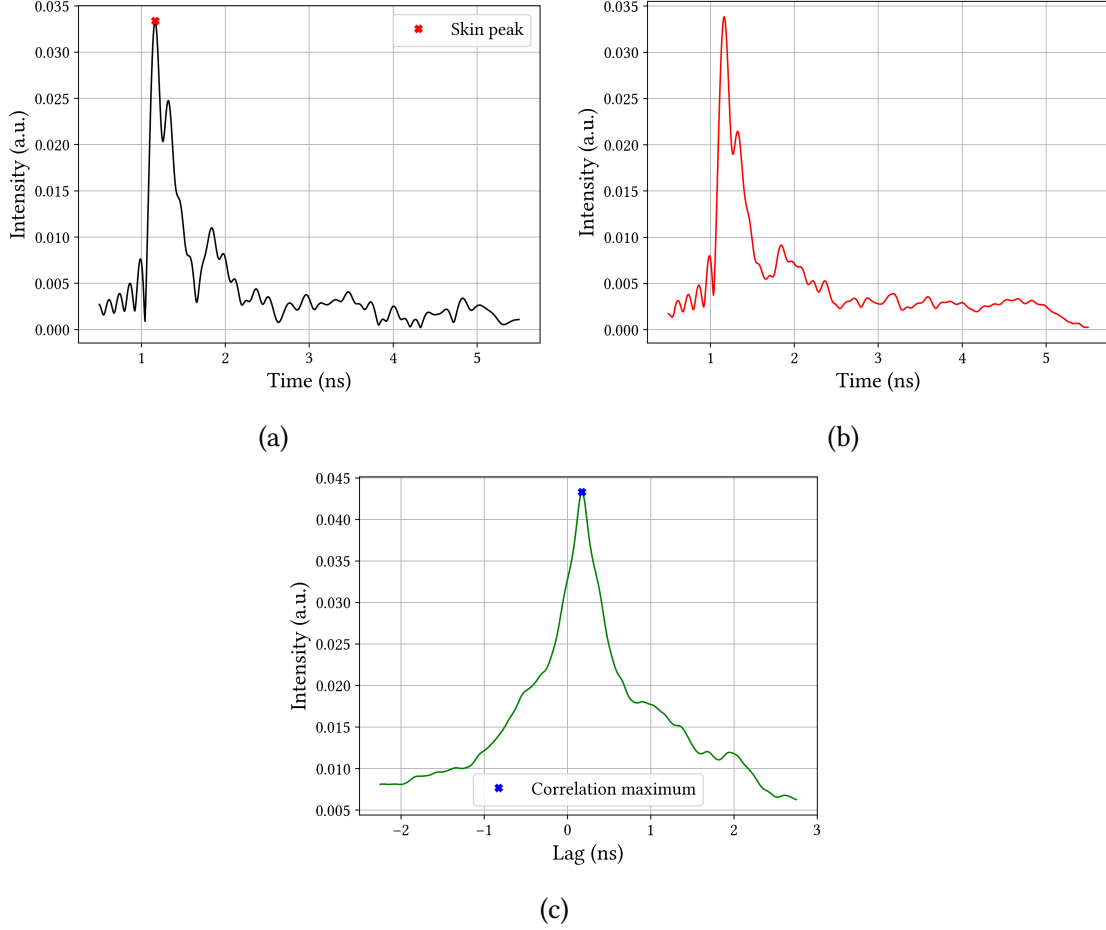


Figure 3.12: Demonstration of the cross-correlation procedure. (a) - the signal at a certain antenna position, (b) - time-aligned kernel, (c) - the result of the cross-correlation of (a) and (b).

$$t_i^{\text{skin}} = \begin{cases} \bar{t} + \tilde{t}_i, & i = 0 \\ \bar{t} + \tilde{t}_i, & |t_i^{\text{max}} - t_{i-1}^{\text{max}}| > t_{\text{threshold}}, \\ \arg \min_{t \in \mathcal{T}_i} |t - (\bar{t} + \tilde{t}_i)|, & |t_i^{\text{max}} - t_{i-1}^{\text{max}}| < t_{\text{threshold}} \end{cases} \quad \begin{matrix} (3.19a) \\ (3.19b) \\ (3.19c) \end{matrix}$$

where $\bar{t}$ is the time coordinate of the skin peak in the kernel $k(t)$ defined by equation (3.18), $\tilde{t}_i$ is the lag or the shift for the i -th antenna position determined by the correlation defined by (3.17), t_i^{max} is the time coordinate of the global maximum of the i -th trace defined by (3.16), $\mathcal{T}_i$ is the set of the all local maxima of the signal from the i -th antenna position, and $t_{\text{threshold}}$ is an arbitrarily small time threshold that determines the acceptable deviation from the previous antenna position. It was empirically chosen to be ~ 0.07 ns.

After applying the peak-selection routine to every antenna trace, the resulting skin-reflection times form the set $\mathcal{S} = \{t_i^{\text{skin}} \mid i = 1, \dots, N_{\text{ant}}\}$. Since the sinogram is constructed using the S_{11} data, these time points correspond to the time of flight of the wave from the antenna to the air-skin barrier and back to the antenna phase center. In order to obtain a smooth outline, we chose to perform the calculations in the polar coordinates.

The set $\mathcal{S}$ can be converted to the set of polar distances from the center of the imaging domain:

$$\mathcal{P} = \left\{ \rho_i = r'_a - \frac{ct_i^{\text{skin}}}{2} \mid i = 1, \dots, N_{\text{ant}} \right\}, \quad (3.20)$$

where r'_a is the corrected radius (i.e., radius that corresponds to the antenna phase center) of the antenna in [m] and c is the vacuum speed of light [m/seconds]. We can use c because the propagation from the antenna to the skin happens in air as we are not using any coupling liquids.

To obtain a smooth boundary estimate, we first convert all antenna positions $\mathbf{r}_a^i$ from Cartesian (x_a^i, y_a^i) to polar coordinates (ρ_a^i, ϕ_a^i) . Next, the extracted radii ρ_i corresponding to the skin reflection are interpolated as a function of the antenna angles ϕ_a^i with a cubic spline. The spline is implemented using the `CubicSpline` function from the *SciPy* library, producing a continuously differentiable curve $\hat{\rho}(\phi)$ that represents the smoothed outline.

Figure 3.13 illustrates the boundary detection procedure. The top and bottom rows correspond to two phantoms with different adipose shells. In the left panels (Figures 3.13a and 3.13c), the red crosses mark the skin-peak positions extracted from the sinogram, while the black line is the cubic spline that smoothly interpolates these points. The right panels (Figures 3.13b and 3.13d) show the corresponding DAS reconstructions with the detected boundary overlaid in red.

3.3.2 Performance Against Phantom STL Data

The UM-BMID dataset comprises 320 MW scans taken using the bed system and the collection of realistic breast phantoms. Such an array of data provides enough information to verify the performance of the boundary detection algorithm against the ground truths. Since the 3D printed breast phantoms are MRI-derived, we can access the STL data and compare it with the extracted boundary data.

UM-BMID dataset employs four distinct adipose shells indexed ‘A2’, ‘A3’, ‘A14’, and ‘A16’. The following section attempts to quantify the quality of the boundary detection methods as well as their repeatability and consistency across different scans of the similar shells.

Due to the breast phantoms being three-dimensional objects, the ‘skin peak’ signal may come from a reflection outside the antenna plane. Thus, we define two axial slices: the ‘best’ slice corresponds to the STL-slice at the z-coordinate for which the Mean-Squared-Error (MSE) between itself and the extracted boundary; the ‘real’ slice corresponds to the STL-slice at the actual z-coordinate of the antenna which is -6.5 cm from the bed system aperture. The difference in the algorithm’s performance at these slices will provide insight about the shape of the phantom in the z-direction and its influence on our ability to extract the boundary.

For every adipose shell we compare the extracted boundary to the STL-slice at z-coordinated ranging from the nipple to the chest wall with the increment of 0.5 mm and calculate the MSE. The slice corresponding to the minimal MSE is assigned to be the best for this particular shell. The value of this z-slice is then averaged across all same-shell images and used in the analysis. Table 3.1 provides the values of the z-coordinated for the four shells of interest. It is notable that all the phantoms have a higher z-coordinate associated with the lowest MSE. Since the signal is recorded in the near field and the antennas have a three-dimensional beam pattern, a big variance in shape of the shell along the z-axis contributes to an earlier signal in time domain being recorded.

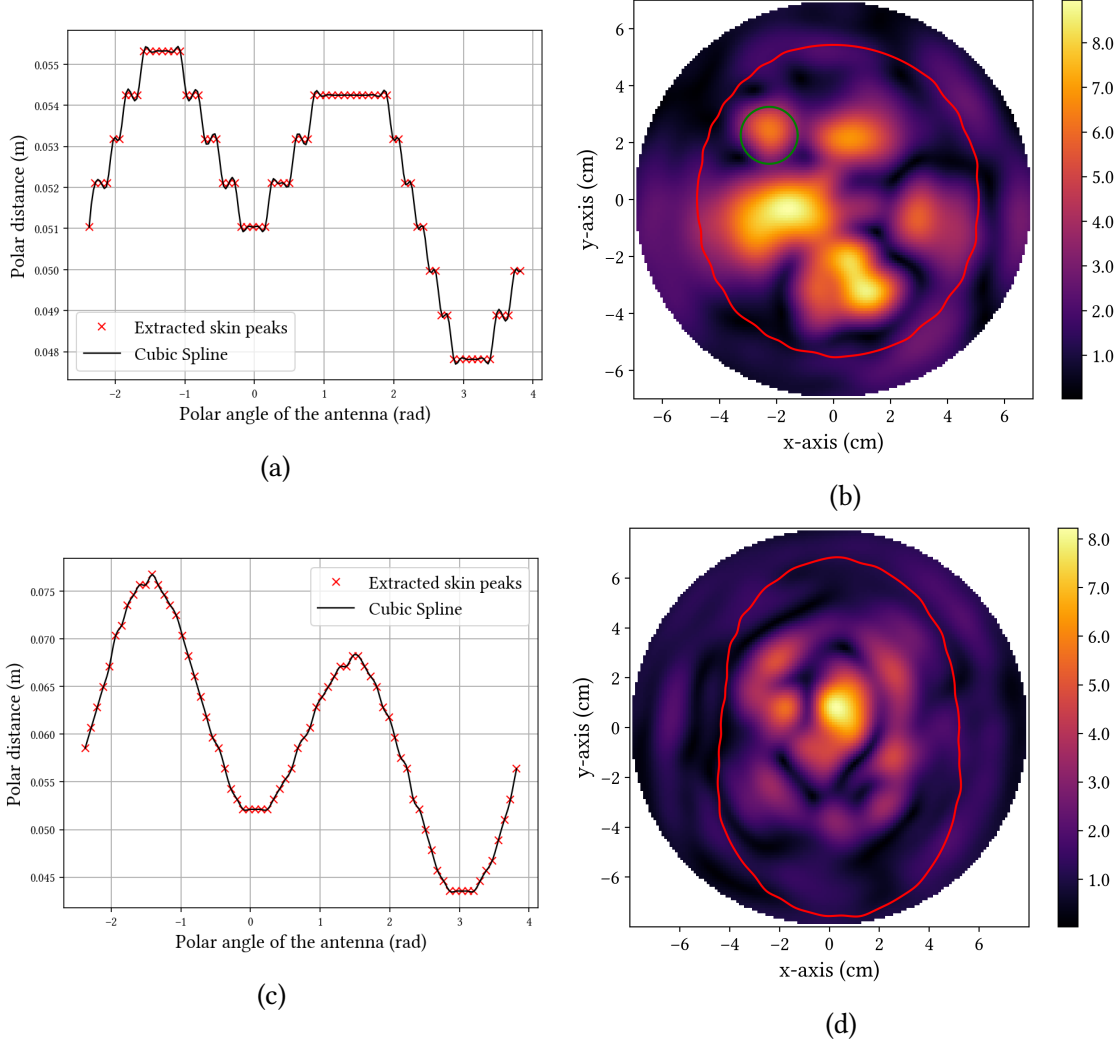


Figure 3.13: Example of the boundary extraction procedure. (a & c) - the extracted (ρ_i, φ_i) coordinates vs the cubic spline $\hat{\rho}(\varphi)$, (b & d) - the boundary (red) overlaid on top of the DAS reconstruction.

And since the breast phantom is placed in the aperture simulating a ‘lying prone’ examination, the ‘best’ STL-slice will be biased towards the chest wall.

Figure 3.14 illustrates the comparison between the extracted boundary (red) and the ‘best’ STL-slice (blue) on both the ρ - φ graphs and on the reconstructed images. Upon visual inspection the boundary detection algorithm is able to extract the shape of the skin outline and produce unique boundary outlines that have excellent alignment with the ground truths.

In order to quantify the performance we employ two metrics: the Pearson Correlation Coefficient (PCC), which measures the similarity in shape between two curves, and the Concordance Correlation Coefficient (CCC), proposed by Lin [86], which accounts for both precision and accuracy and is considered a more robust metric. The metrics range from -1 (perfect disagreement) and 1 (perfect agreement). Table 3.2 provides the values of CCC and PCC for the four adipose shells. Excellent agreement was achieved for ‘A3’, ‘A14’ and ‘A16’ shells with both PCC - surpassing

Table 3.1: z -coordinates from the bed system aperture corresponding to the ‘best’ STL-slice for various adipose shells.

A2	A3	A14	A16
(-4.99 ± 0.04) cm	(-2.3 ± 0.1) cm	(-2.60 ± 0.07) cm	(-3.70 ± 0.01) cm

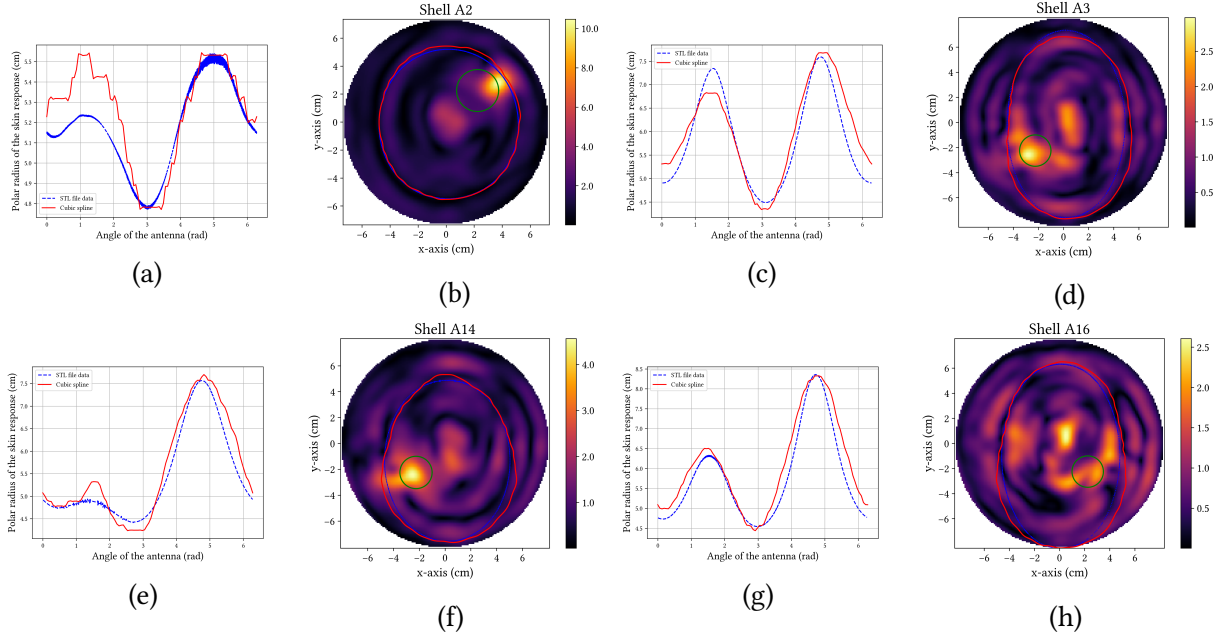


Figure 3.14: Comparison between the extracted boundary (red) and the axial slice of the STL model of the corresponding adipose shell at the z -coordinate with the lowest MSE between the boundary and the slice. The shells are presented in the following order: (a) & (b) - A2, (c) & (d) - A3, (e) & (f) - A14, (g) & (h) - A16.

0.94 and CCC - surpassing 0.93. The ‘A2’ shell produced boundaries with good agreement with the ground truth (PCC of 0.86 and CC of 0.81), however performed notably worse than the other shells. The difference can be noted on the Figures 3.14b and 3.14a, where the extracted boundary has an evident elongated shape in the y -axis direction.

Table 3.2: Values of PCC and CCC between the extracted boundary and the STL slice at the ‘best’ z -coordinate.

	A2	A3	A14	A16
PCC	0.859	0.942	0.979	0.982
CCC	0.807	0.930	0.961	0.960

Figure 3.15 illustrates the exacted boundary as compared to the STL-data at the -6.5 cm z -coordinate and Table 3.3 provides the metrics. Shells ‘A2’, ‘A3’, and ‘A16’ remain visually very similar to the true boundary, however, using the lower value of z predictably corresponded to physically smaller true boundary. The visual similarity is supported by the PCC and CCC values

in shells ‘A3’ and ‘A16’ yielding moderate agreement, with ‘A16’ shell performing very similarly to the ‘best’ slice case. We can attribute this shell retaining the quality of the extracted boundary to its low variability in curvature in the z-direction.

The shell ‘A2’ even though produced visually convincing boundary performed the worst - CCC of 0.1 and PCC of 0.6. This can be attributed to the fact the ‘real’ STL slice of this particular adipose shell is very flat on the ρ - φ graph (Figure 3.15a). Thus any extracted boundary that happens to be off-center or slightly elongated in the image coordinate system, will have low agreement with the ground truth.

The shell ‘A14’ experienced an opposite effect of comparing the two shapes in the polar coordinates. Even though ‘A14’ performed the worst visually due to the rapid change in shape with the change in the z-coordinate, the boundary detection algorithm has achieved the PCC of 0.96 and CCC of 0.68. On Figure 3.15e we can notice that the algorithm was able to match the later half of the curve very well with a slight vertical shift, which was predictably penalized by the CCC metric.

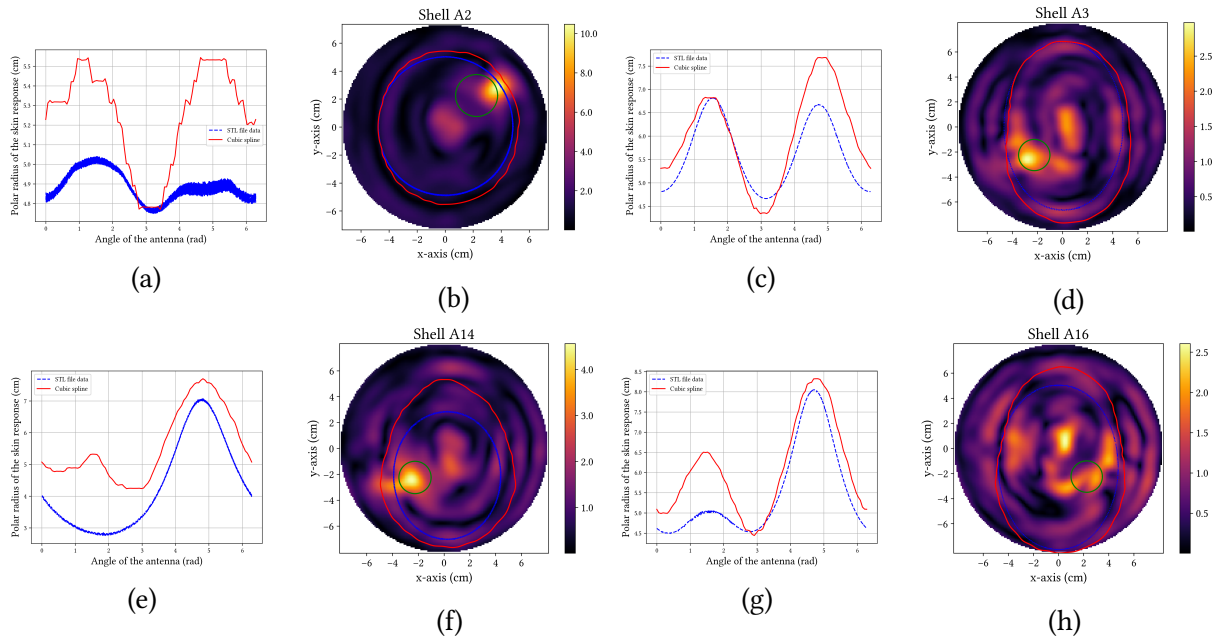


Figure 3.15: Comparison between the extracted boundary (red) and the axial slice of the STL model of the corresponding adipose shell at the z-coordinate that corresponds to the actual antenna height. The shells are presented in the following order: (a) & (b) - A2, (c) & (d) - A3, (e) & (f) - A14, (g) & (h) - A16.

Table 3.3: Values of PCC and CCC between the extracted boundary and the STL slice at the ‘real’ z-coordinate.

	A2	A3	A14	A16
PCC	0.564	0.871	0.964	0.930
CCC	0.102	0.771	0.676	0.818

3.4 Ray Tracing

So far we have developed a robust algorithm that reconstructs the geometric position of the skin boundary. The next step is to incorporate this extracted outline into an image-formation scheme. DAS reconstruction relies on accurate time-delay calculation, which can be written as line integral - equation (2.1). Chapter 2 outlined how the imaging domain can be partitioned analytically so that these integrals can be evaluated efficiently. In the following section we apply Siddon's raytracing algorithm, combined with the sinogram-based boundary detection, to compute the required delays and produce a boundary-aware DAS image. A complete derivation of the algorithm is provided in Siddon [75]; here we restrict the discussion to its practical application and omit the underlying theory.

3.4.1 Formulation of the Algorithm

One of the principal advantages of Siddon's raytracing algorithm is its ability to determine the exact indices of all voxels intersected by a given ray. In our workflow we use these indices to locate the precise point where each antenna-to-pixel ray crosses the extracted skin boundary, providing the intersection coordinates needed for accurate time-delay calculations. We attempt to follow the same computational logic as presented in the Chapter 2.

First, we rewrite Siddon's ray-tracing steps using the same symbols as in the earlier chapters so the ray direction, voxel indices, path lengths, and intersection points follow our existing notation.

The set of orthogonal planes [75, eq. (3)] is defined as:

$$\begin{aligned} X_{\text{plane}}(i) &= X_{\text{plane}}(1) + (i - 1)d_x \quad (i = 1, \dots, N_x), \\ Y_{\text{plane}}(j) &= Y_{\text{plane}}(1) + (j - 1)d_y \quad (j = 1, \dots, N_y), \end{aligned} \quad (3.21)$$

where d_x and d_y are the x - and y -extents of the individual pixels and N_x and N_y correspond to the numbers of pixels per x - and y -axes. The parametric values that correspond to the sides [75, eq. (4)] are:

$$\begin{aligned} \alpha_x(1, a_x, p_x) &= \frac{X_{\text{plane}}(1) - a_x}{p_x - a_x}, \\ \alpha_x(N_x, a_x, p_x) &= \frac{X_{\text{plane}}(N_x) - a_x}{p_x - a_x}, \end{aligned} \quad (3.22)$$

where p_x and a_x are the x -coordinate of the pixel and the antenna respectively. We emphasize that α_x is a function of the antenna position and the pixel coordinates. An identical equation to (3.22) can be derived for the y -coordinate as well. [75, eq. (5)] is left the same:

$$\begin{aligned} \alpha_{\min}(\mathbf{r}_a, \mathbf{p}) &= \max\{0, \min[\alpha_x(1, a_x, p_x), \alpha_x(N_x, a_x, p_x)], \min[\alpha_y(1, a_y, p_y), \alpha_y(N_y, a_y, p_y)]\}, \\ \alpha_{\max}(\mathbf{r}_a, \mathbf{p}) &= \min\{0, \max[\alpha_x(1, a_x, p_x), \alpha_x(N_x, a_x, p_x)], \max[\alpha_y(1, a_y, p_y), \alpha_y(N_y, a_y, p_y)]\}, \end{aligned} \quad (3.23)$$

where $\mathbf{r}_a$ is the antenna position point (a_x, a_y) and $\mathbf{p}$ are the pixel coordinates (p_x, p_y) . The edge points of the intersected planes' indices [75, eq. (6)] if $p_x - a_x > 0$:

$$\begin{aligned}
i_{\min}(a_x, p_x) &= N_x - \frac{X_{\text{plane}}(N_x) - \alpha_{\min}(p_x - a_x) - a_x}{d_x}, \\
i_{\max}(a_x, p_x) &= 1 + \frac{a_x + \alpha_{\max}(p_x - a_x) - X_{\text{plane}}(1)}{d_x},
\end{aligned} \tag{3.24}$$

and if $p_x - a_x \leq 0$:

$$\begin{aligned}
i_{\min}(a_x, p_x) &= N_x - \frac{X_{\text{plane}}(N_x) - \alpha_{\max}(p_x - a_x) - a_x}{d_x}, \\
i_{\max}(a_x, p_x) &= 1 + \frac{a_x + \alpha_{\min}(p_x - a_x) - X_{\text{plane}}(1)}{d_x},
\end{aligned}$$

with similar equations for $(j_{\min}, j_{\max})$. For a given range $(i_{\min}, i_{\max})$, $(j_{\min}, j_{\max})$ the sets of $\{\alpha_x\}$ and $\{\alpha_y\}$ if $p_x - a_x > 0$ are given as [75, eq. (7)]

$$\{\alpha_x(a_x, p_x)\} = \{\alpha_x(i_{\min}(a_x, p_x), a_x, p_x), \dots, \alpha_x(i_{\max}(a_x, p_x), a_x, p_x)\}$$

and

$$\{\alpha_x(a_x, p_x)\} = \{\alpha_x(i_{\max}(a_x, p_x), a_x, p_x), \dots, \alpha_x(i_{\min}(a_x, p_x), a_x, p_x)\}$$

if $p_x - a_x \leq 0$. Where

$$\alpha_x(i, a_x, p_x) = \frac{X_{\text{plane}}(i) - a_x}{p_x - a_x}$$

with a similar equation for $\alpha_y(i)$. Lastly we must merge the sets [75, eq. (8)]:

$$\{\alpha(\mathbf{r}_a, \mathbf{p})\} = \{\alpha_{\min}(\mathbf{r}_a, \mathbf{p}), \text{merge}[\{\alpha_x(a_x, p_x)\}, \{\alpha_y(a_y, p_y)\}], \alpha_{\max}(\mathbf{r}_a, \mathbf{p})\}, \tag{3.25}$$

and the indices of the intersected pixels are given by [75, eq. (12)]:

$$\begin{aligned}
i(m, a_x, p_x) &= 1 + \frac{a_x + \alpha_{\text{mid}}(m, \mathbf{r}_a, \mathbf{p})(p_x - a_x) - X_{\text{plane}}(1)}{d_x}, \\
j(m, a_y, p_y) &= 1 + \frac{a_y + \alpha_{\text{mid}}(m, \mathbf{r}_a, \mathbf{p})(p_y - a_y) - Y_{\text{plane}}(1)}{d_y},
\end{aligned} \tag{3.26}$$

where α_{mid} is defined as

$$\alpha_{\text{mid}}(m, \mathbf{r}_a, \mathbf{p}) = \frac{\alpha(m, \mathbf{r}_a, \mathbf{p}) + \alpha(m-1, \mathbf{r}_a, \mathbf{p})}{2}. \tag{3.27}$$

Now we can define the set $\{\mathcal{I}(\mathbf{r}_a, \mathbf{p})\}$ that corresponds to the set of coordinates of the pixels intersected by the ray coming from the antenna position $\mathbf{r}_a$ to the pixel $\mathbf{p}$

$$\{\mathcal{I}(\mathbf{r}_a, \mathbf{p})\} = \{(P_x[i(m, a_x, p_x), j(m, a_y, p_y)], P_y[i(m, a_x, p_x), j(m, a_y, p_y)]) \mid m = 1, \dots, M\}, \tag{3.28}$$

where P_x and P_y are corresponding mesh-grids for the x - and y -coordinates of the pixels in the imaging domain. One benefit of the Siddon's algorithm is in the way the intersections are sorted.

The resulting set of intersected pixels is sorted so that the first element corresponds to the point the closest to the antenna and the last element corresponds to the pixel itself. This directionality of $\{\mathcal{S}(\mathbf{r}_a, \mathbf{p})\}$ can be used to find the intersection coordinate between the said ray and the extracted boundary.

The boundary $\hat{\rho}(\varphi)$ extracted using the Correlation-Based Peak Selection algorithm allows us to construct a 2-dimensional mask of the image:

$$\mathcal{M}(\mathbf{r}) = \begin{cases} 0, & \hat{\rho}(\varphi_p) < \rho_p \\ 1, & \hat{\rho}(\varphi_p) \geq \rho_p \end{cases}, \quad (3.29a)$$

$$(3.29b)$$

where (φ_p, ρ_p) are the polar coordinates of the pixel $\mathbf{r}$. The usage of the cubic spline allows us to sample the imaging domain arbitrarily densely and the Siddon's ray tracing algorithm will not need to be changed, because its precision is driven by the size of d_x and d_y - parameters that reflect how finely the imaging grid is sampled.

Figure 3.16 showcases how the Siddon's algorithm works. An arbitrarily chosen ray on Figure 3.16a is propagating through the imaging grid. By finding the indices of the intersected pixels, we are able to get a 1-dimensional representation of the ray with respect to the boundary presented on the Figure 3.16c. On the x -axis we denote the indices m of the array of indices of the intersected pixels. This can be interpreted the following way: the y -value on the Figure 3.16c corresponds to the value of the mask $\mathcal{M}$ at the point $(P_x[i(m, a_x, p_x), j(m, a_y, p_y)], P_y[i(m, a_x, p_x), j(m, a_y, p_y)])$.

We note two of these indices, m_{front} and m_{back} :

$$m_{\text{front}} = \min\{m \mid s_m = 1\}, \quad (3.30)$$

$$m_{\text{back}} = \max\{m \mid s_m = 1\}, \quad (3.31)$$

where s_m is the m -th element of the binary sequence shown in Figure 3.16c, with $m = 1, \dots, M$. The index m_{front} is the first position at which $s_m = 1$; because the intersection indices are ordered by increasing distance from the antenna, this pixel is the ray's entry point into the breast. Likewise, m_{back} is the last position with $s_m = 1$ and marks the pixel where the ray leaves the breast. Thus we can define an array of pairs of intersection points analogously to the equation (2.10):

$$\mathbf{R}(\mathbf{r}_a, \mathbf{r}) = (\mathbf{r}_{\text{front}}(\mathbf{r}_a, \mathbf{r}), \mathbf{r}_{\text{back}}(\mathbf{r}_a, \mathbf{r})), \quad (3.32)$$

where the pixel coordinates are

$$\mathbf{r}_{\text{front}}(\mathbf{r}_a, \mathbf{r}) = (P_x[i(m_{\text{front}}, a_x, p_x), j(m_{\text{front}}, a_y, p_y)], P_y[i(m_{\text{front}}, a_x, p_x), j(m_{\text{front}}, a_y, p_y)]), \quad (3.33)$$

$$\mathbf{r}_{\text{back}}(\mathbf{r}_a, \mathbf{r}) = (P_x[i(m_{\text{back}}, a_x, p_x), j(m_{\text{back}}, a_y, p_y)], P_y[i(m_{\text{back}}, a_x, p_x), j(m_{\text{back}}, a_y, p_y)]). \quad (3.34)$$

3.4.2 Image Quality Performance

To evaluate the performance of the ray-tracing algorithm, we applied the same quality metrics introduced in Section 2.5 to the identical datasets used previously. By computing each metric on the same data, we ensure a direct and fair comparison of ray tracing against the literature-standard methods and the reconstruction algorithms presented in this thesis.

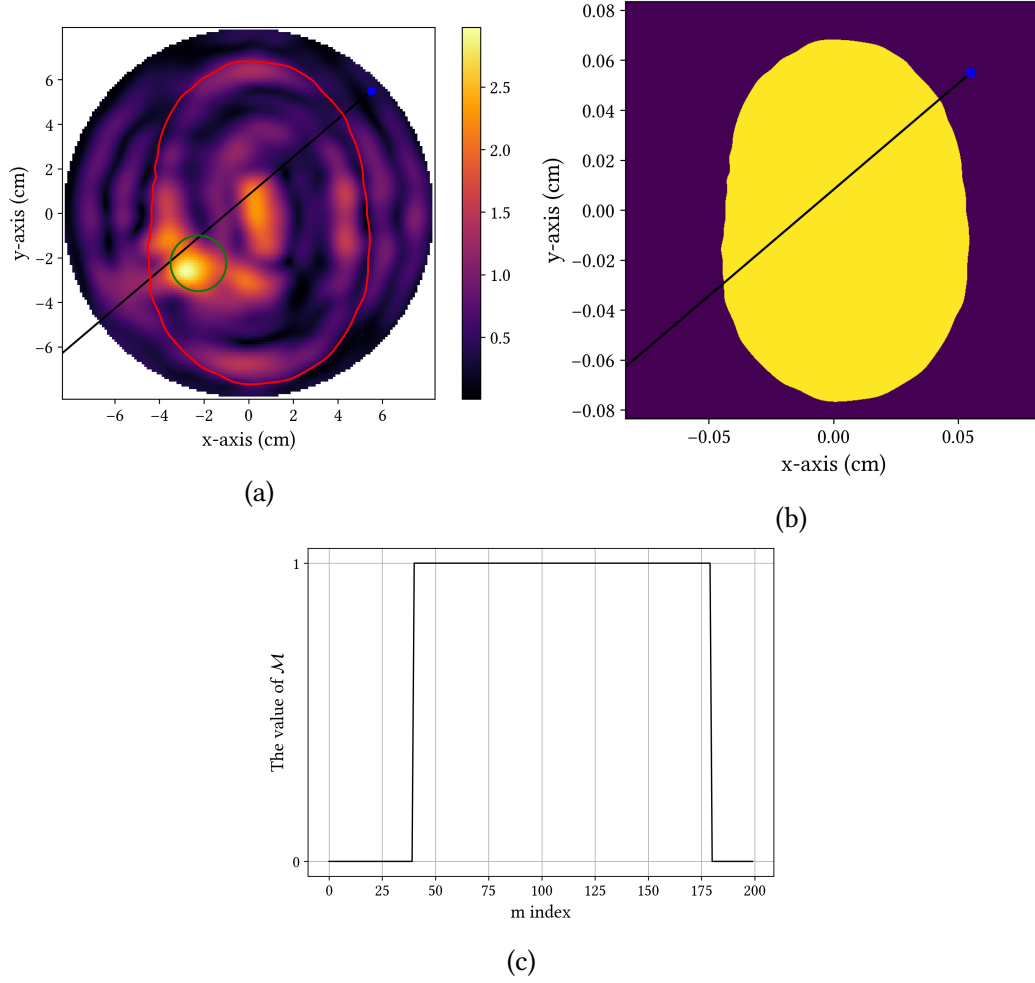


Figure 3.16: (a) - the DAS reconstruction with an arbitrarily chosen ray (red line) from an antenna position (outside of the imaging domain) to the pixel (blue mark), (b) - an abstract representation of the configuration in (a) with a binary mask, (c) - unraveled values of the mask $\mathcal{M}$ that the ray encounters.

Figure 3.17 presents an image reconstructed using the ray-tracing algorithm with the inclusion of the frequency-dependence. The red line outlines the extracted boundary of the cylindrical phantom. The ray tracing algorithm introduces the same benefit as the other physics enhancements for the ‘rod’ dataset - the reduction of the $\hat{\rho}$ -stretch for positions closer to the plastic boundary (Figure 2.7). And the algorithm behaves similarly to the enhanced versions of DAS presented in Chapter 2 in the ‘ball’ dataset - the target experiences arching in the $\hat{\varphi}$ -direction and positions closer to the center produce images with higher noise and lower contrast (Figure 3.19).

Table 3.4 provides the quality metrics for the ‘rod’ dataset performance of the ray tracing algorithm. The localization error is slightly higher compared to the homogeneous and enhanced versions of DAS, however, the algorithm still produces a symmetrical target that is significantly smaller than in the homogeneous case. The inclusion of the boundary does not seem to affect the contrast of the image in any major way.

Binary and frequency-dependent image reconstruction methods employ a circular domain

partitioning that exactly matches the adipose shell geometry of the cylindrical phantom. In contrast, the ray tracing algorithm infers the boundary shape from data, inheriting uncertainties from the boundary detection process. Consequently, this added uncertainty leads to a slight increase in localization error.

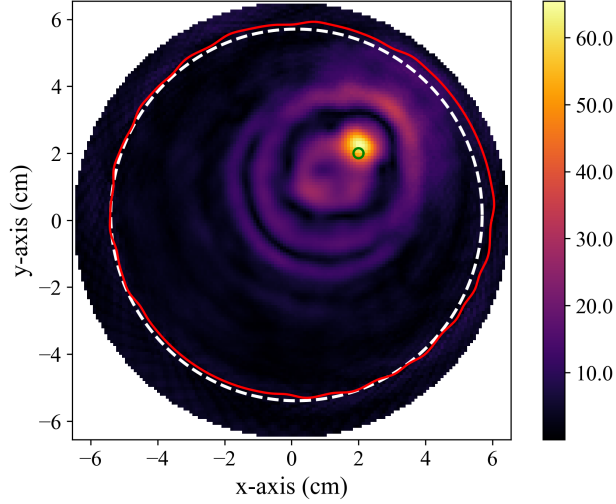


Figure 3.17: Image reconstructed using the frequency-dependent DAS with the extracted boundary (red).

Table 3.4: Image quality metrics evaluating the performance of the frequency-dependent ray-tracing algorithm obtained using the ‘rod’ dataset.

Localization error, mm	$\hat{\rho}$ -extent, mm	$\hat{\phi}$ -extent, mm	SCR, dB	SMR, dB
3.81	59.9	63.1	7.57	32.42

As with the enhanced physics modelling, the ‘ball’ dataset produces worse reconstructions. Table 3.5 shows the quality metrics. The mean localization error of 13.0 mm is not only attributed to the uncertainties in the boundary detection, but also to the outliers in the distribution on the Figure 3.20b. The algorithm produces a smaller target response in the $\hat{\rho}$ -direction and experiences arching which drives the value of the $\hat{\phi}$ to be as high as 141.6 mm. The inclusion of the boundary detection does not seem to influence the contrast in the ball dataset as well.

Table 3.5: Image quality metrics evaluating the performance of the frequency-dependent ray-tracing algorithm obtained using the ‘ball’ dataset.

Localization error, mm	$\hat{\rho}$ -extent, mm	$\hat{\phi}$ -extent, mm	SCR, dB	SMR, dB
13.0	89.0	141.6	3.72	28.81

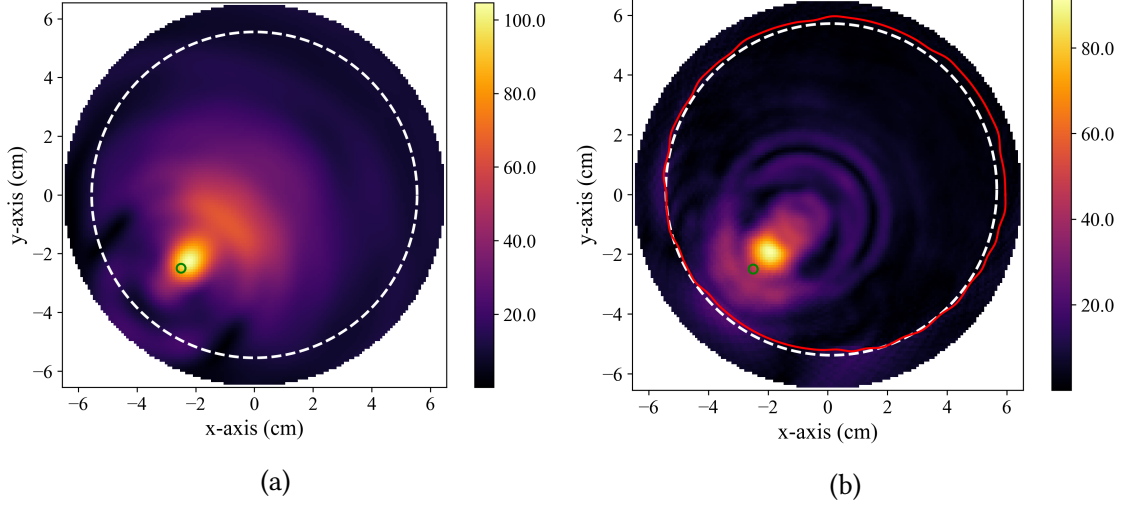


Figure 3.18: The reduction of the $\hat{\rho}$ -stretch at the positions farther from the center of the imaging domain. (a) - homogeneous DAS, (b) - ray-tracing algorithm using the extracted boundary (red).

3.5 Differential Microwave Imaging

As was stated in the introduction, MBI has a benefit of resolving the subtle contrast between the fibroglandular and the malignant tissues due to differences in their dielectric properties. However, the fundamental design of MBI is limited by the fact that most of the incident power of the wave is reflected on the air-skin interface, and consequently, the further penetration is considerably attenuated. The ‘skin peak’ has been used in this thesis to extract the boundary information of the breast, but the reconstruction of the tissues inside the breast requires sophisticated skin suppression.

Phantom studies performed at the University of Manitoba use the ‘adipose reference’ approach, which is impossible in the clinical settings, but show promising results [40], [42], [44]. It is important to note that this approach operates under the assumption that there will be an available reference object in the clinical setting - the other patient’s breast. It is extremely rare for the patient to have malignancies in both breasts [87], which would allow us to perform the *differential imaging procedure*.

Differential imaging follows the same logic as the empty-chamber or adipose calibrations presented earlier: acquire two frequency-domain scans, one of a healthy breast and one of the suspect breast, and subtract them to isolate pathological differences under the assumption of similar fibroglandular structure across the two breast. Because real breasts are asymmetrical, the skin surfaces do not align perfectly, so an additional signal processing step is required to suppress the high-intensity skin-reflection peak before performing the subtraction. The skin-response sinograms and boundary detection methods presented in Section 3.3 can serve as powerful tools for aligning the target and the reference breasts.

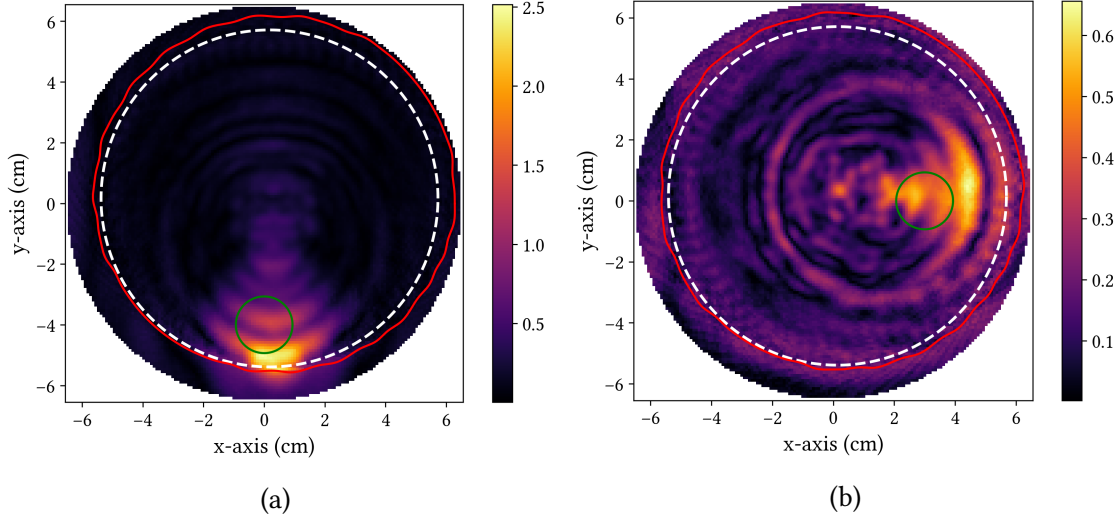


Figure 3.19: ‘Ball’ dataset reconstructions using the frequency-dependent DAS with ray tracing. The extracted boundary is outlined in red. (a) - higher contrast image, (b) - lower contrast, higher noise image.

3.5.1 Alignment Based on the Time Shift

Suppressing the skin response begins with temporally aligning the left and right scans. For each antenna, the exact arrival time of the skin echo is obtained from the sinogram via the peak-selection routine in equation (3.19) (Section 3.3), yielding two ordered sets of timestamps, $\mathcal{S}^{(L)} = \{t_i^{\text{skin},L}\}$ and $\mathcal{S}^{(R)} = \{t_i^{\text{skin},R}\}$. The antenna-wise differences $\Delta t_i = t_i^{\text{skin},L} - t_i^{\text{skin},R}$ then specify how far one trace must be shifted relative to the other before subtraction.

In order to perform a shift in the time domain, we can use the Fourier pair:

$$f(t - \Delta t) \xleftrightarrow{\mathcal{F}} \hat{f}(\xi) e^{-j2\pi\xi\Delta t}, \quad (3.35)$$

where ξ is the spatial frequency. A clear benefit of performing such a phase shift is due to $\hat{f}$ being equivalent to the measured microwave data in the frequency domain, meaning that all the manipulations can be performed on the data itself prior to the reconstruction. We rewrite (3.35):

$$\hat{S}_{11}(\mathbf{r}_a^i, t - \Delta t_i) \xleftrightarrow{\text{CZT}} S_{11}(\mathbf{r}_a^i, f) e^{-j2\pi f \Delta t_i}, \quad (3.36)$$

which reduces the problem of aligning the two breast to finding the correct phase shift in the frequency domain and applying it to the S_{11} data. The differential procedure is formalized as following. First we define two signals, the one of the left $S_{11}^{(L)}$ and the right $S_{11}^{(R)}$ breasts. Because the reconstructed image represents an absolute value of the reflectivity, we can perform the phase shift on either breast. For the remainder of this chapter we choose to modify the signal of the right breast keeping the signal of the left one untouched. The signal from the right breast temporally aligned with the left one is denoted

$$S_{11}^{(R \rightarrow L), \text{time}}(\mathbf{r}_a^i, f) = S_{11}^R(\mathbf{r}_a^i, f) e^{-j2\pi f \Delta t_i}. \quad (3.37)$$

And the calibrated (or differential) signal is then:

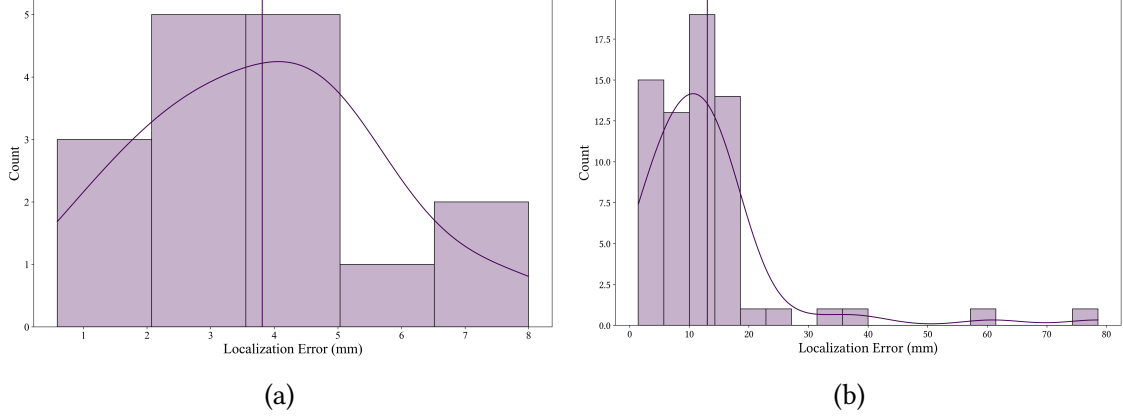


Figure 3.20: The localization error distributions for the (a) ‘rod’ and (b) ‘ball’ datasets acquired using the frequency-dependent ray-tracing DAS.

$$S_{11}^{\text{cal,time}}(\mathbf{r}_a^i, f) = S_{11}^L(\mathbf{r}_a^i, f) - S_{11}^{(R \rightarrow L),\text{time}}(\mathbf{r}_a^i, f). \quad (3.38)$$

3.5.2 Alignment Based on the Spatial Shift

Previous section investigated the alignment of the skin responses purely in time, neglecting breast geometry. Such estimation of time shifts can distort later-time reflections and compromise the reconstructed shape. We therefore introduce a skin-alignment method that first registers the extracted boundaries geometrically and then derives the corresponding temporal shifts, preserving both the internal reflections and the true breast contour.

We start with the usual boundary extraction procedure. We acquire the cubic splines for the left and the right breasts $\hat{\rho}^{(L)}(\varphi)$ and $\hat{\rho}^{(R)}(\varphi)$. The corresponding Cartesian position vectors:

$$\mathbf{r}^{(L)}(\varphi) = \hat{\rho}^{(L)}(\varphi) \begin{bmatrix} \cos \varphi \\ \sin \varphi \end{bmatrix}, \quad \mathbf{r}^{(R)}(\varphi) = \hat{\rho}^{(R)}(\varphi) \begin{bmatrix} \cos \varphi \\ \sin \varphi \end{bmatrix}. \quad (3.39)$$

Because alignment depends only on the relative transform, either breast could serve as the reference; here we simply fix the left boundary and translate-rotate the right one. The transformation of the right breast

$$T_{\theta} \mathbf{r}^{(R)}(\varphi) = \begin{bmatrix} \cos \delta\varphi & -\sin \delta\varphi \\ \sin \delta\varphi & \cos \delta\varphi \end{bmatrix} \mathbf{r}^{(R)}(\varphi) + \begin{bmatrix} \delta x \\ \delta y \end{bmatrix}, \quad \theta = (\delta x, \delta y, \delta\varphi) \quad (3.40)$$

allows us to define the mean squared error (MSE) between the two shapes:

$$\text{MSE}(\theta) = \frac{1}{N} \sum_{k=1}^N \left\| \mathbf{r}^{(L)}(\varphi_k) - T_{\theta} \mathbf{r}^{(R)}(\varphi_k) \right\|^2, \quad (3.41)$$

where $\|\cdot\|$ denotes the Euclidean norm. MSE serves as a metric that quantifies the geometrical similarity between the outlines of the right and the left breasts after the linear shift and rotation of the right one. Here, $\varphi_k = k\Delta\varphi$ and $\Delta\varphi = 5^\circ$ corresponding to the angular spacing between the antenna positions, $k = 0, \dots, N_{\text{ant}} - 1$. Now we formulate an optimization problem:

$$\boldsymbol{\theta}^* = \arg \min_{\delta x, \delta y \in \mathbb{R}, \delta \varphi \in (-\pi, \pi]} \text{MSE}(\boldsymbol{\theta}), \quad (3.42)$$

where $\boldsymbol{\theta}^* = (\delta x^*, \delta y^*, \delta \varphi^*)$ is the combination of the linear shift and rotation required to align the two outlines. The aligned right boundary with respect to the left one

$$\hat{\rho}^{(R \rightarrow L)}(\varphi) = \hat{\rho}^{(R)}(\varphi - \delta \varphi^*) + \delta x^* \cos \varphi + \delta y^* \sin \varphi, \quad \varphi \in [0, 2\pi) \quad (3.43)$$

is then used to find the set of temporal coordinates of the skin peaks

$$\mathcal{S}^{(R \rightarrow L)} = \left\{ t_i^{\text{skin}, (R \rightarrow L)} = \frac{2[r_a' - \hat{\rho}^{(R \rightarrow L)}(\varphi_i)]}{c} \middle| \varphi_i = i\Delta\varphi, i = 0, \dots, N_{\text{ant}} - 1 \right\} \quad (3.44)$$

sampled at the same angles as the antenna positions on the sinogram. This way we can calculate the antenna-wise time differences $\Delta t_i^{\text{spatial}}$ using the aligned boundaries:

$$\Delta t_i^{\text{spatial}} = t_i^{\text{skin}, L} - t_i^{\text{skin}, (R \rightarrow L)}. \quad (3.45)$$

Finally, transforming the frequency domain data of the right breast

$$S_{11}^{(R \rightarrow L), \text{spatial}}(\mathbf{r}_a^i, f) = S_{11}^R(\mathbf{r}_a^i, f) e^{-j2\pi f \Delta t_i^{\text{spatial}}} \quad (3.46)$$

we can perform the subtraction:

$$S_{11}^{\text{cal}, \text{spatial}}(\mathbf{r}_a^i, f) = S_{11}^L(\mathbf{r}_a^i, f) - S_{11}^{(R \rightarrow L), \text{spatial}}(\mathbf{r}_a^i, f). \quad (3.47)$$

3.5.3 Fourier Window Alignment

Section 3.5.1 presents a purely temporal approach that aligns the skin responses by applying a phase shift equal to the delay between their peaks; this correction can distort both the breast outline and the later reflections. Section 3.5.2 investigates an approach based on breast geometry: it first translates and rotates the extracted boundaries, then derives the phase shifts, thereby preserving the overall shape and internal reflections, yet it can leave residual misalignment because the two breasts are intrinsically different. This section introduces a skin-suppression method for differential imaging that simultaneously matches the skin peaks and retains the temporal position of internal reflections, combining the two previous strategies.

In order to minimize the skin reflections, we define a ‘window’ approach. The time domain microwave signal can be separated into three temporal regions: the region of propagation earlier in time - before the skin peak, the skin peak itself (due to the fact that the bandwidth is finite, the skin peak is not a delta function, but has a non-zero time span), and the remainder of the signal later in time. We can formalize it by separating the time domain signal into the three regions using the rect function:

$$\hat{S}_{11}(\mathbf{r}_a^i, t) = \underbrace{\text{rect}\left(\frac{t-t_0}{a_0}\right) \hat{S}_{11}(\mathbf{r}_a^i, t)}_{\text{before the skin peak}} + \underbrace{\text{rect}\left(\frac{t-t_1}{a_1}\right) \hat{S}_{11}(\mathbf{r}_a^i, t)}_{\text{skin peak}} + \underbrace{\text{rect}\left(\frac{t-t_2}{a_2}\right) \hat{S}_{11}(\mathbf{r}_a^i, t)}_{\text{after the skin peak}}, \quad (3.48)$$

where the time points and the widths of the rect functions are defined as follows:

$$t_0 = \frac{t_{\text{start}}}{2}, \quad a_0 = t_{\text{start}}, \quad (3.49)$$

$$t_1 = t_{\text{start}} + \frac{t_{\text{end}} - t_{\text{start}}}{2}, \quad a_1 = t_{\text{end}} - t_{\text{start}}, \quad (3.50)$$

$$t_2 = t_{\text{end}} + \frac{t_{\text{fin}} - t_{\text{end}}}{2}, \quad a_2 = t_{\text{fin}} - t_{\text{end}}, \quad (3.51)$$

where $t \in [0, t_{\text{fin}}]$ and the skin peak lies in $[t_{\text{start}}, t_{\text{end}}]$ time interval. The latter interval can be defined empirically, but we will present a signal-based way of skin peak's width determination later in this section. Figure 3.21 illustrates this split and the composite signal acquired using the equation (3.48). It is evident that the original time domain signal and the composite one are identical. We proceed to the frequency domain. Fourier pair of the signal in the equation (3.48) is:

$$S_{11}(\mathbf{r}_a^i, f) = \mathcal{F}\{\hat{S}_{11}(\mathbf{r}_a^i, t)\} = a_0 \text{sinc}(a_0 f) e^{-2\pi i f t_0} * S_{11}(\mathbf{r}_a^i, f) + \underbrace{a_1 \text{sinc}(a_1 f) e^{-2\pi i f t_1} * S_{11}(\mathbf{r}_a^i, f)}_{\text{skin peak}} + a_2 \text{sinc}(a_2 f) e^{-2\pi i f t_2} * S_{11}(\mathbf{r}_a^i, f), \quad (3.52)$$

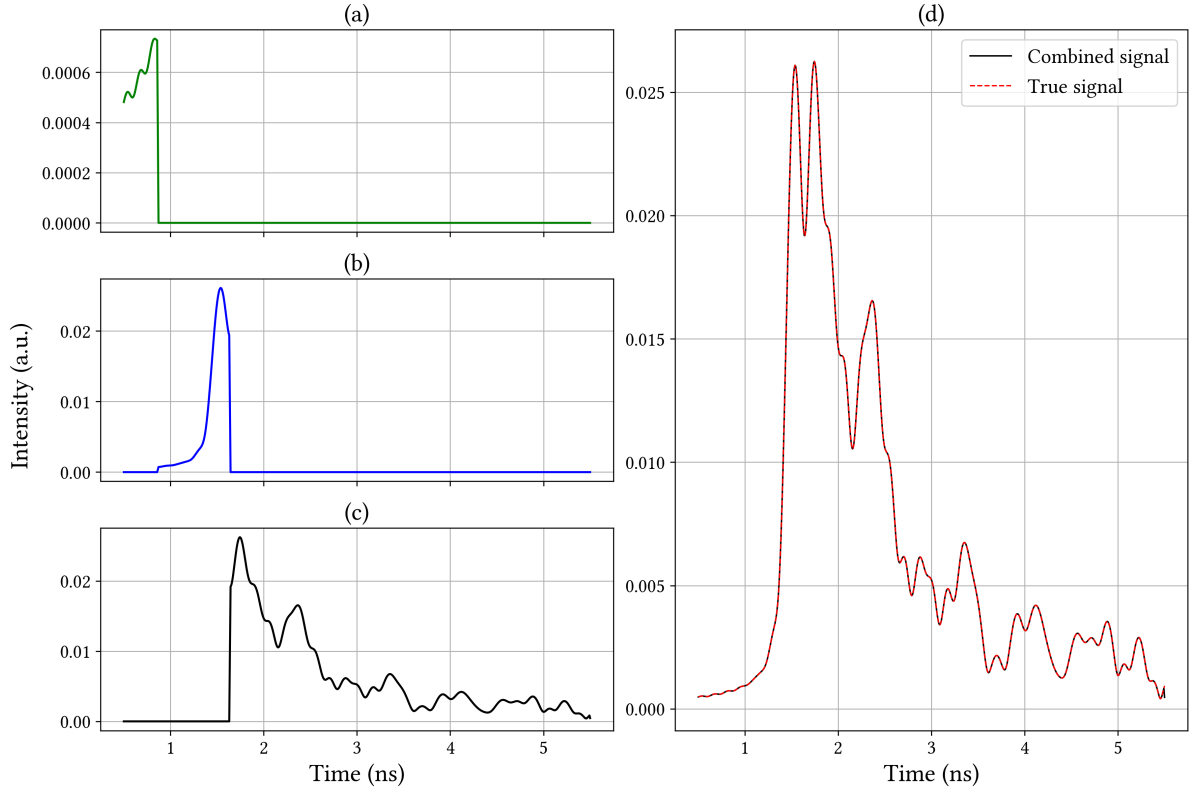


Figure 3.21: Time-domain $\hat{S}_{11}$ signal divided into three regions: (a) before the skin, (b) skin peak, (c) after the skin, (d) - combined signal using the equation (3.48) compared to the original time domain signal.

where $*$ denotes the convolution operation and sinc is the normalized $\text{sinc}(x) = \sin(\pi x)/\pi x$. With the skin peak isolated, we are able to perform the time shift similar to Section 3.5.1. We employ the results of the boundary detection and again extract the time delays between the right and the left breasts:

$$\Delta t_i = t_i^{\text{skin},L} - t_i^{\text{skin},R}. \quad (3.53)$$

and we apply this shift to the portion of the signal in (3.48) that corresponds to the skin peak:

$$\hat{S}_{11}^{(R \rightarrow L), \text{window}}(\mathbf{r}_a^i, t) = \text{rect}\left(\frac{t - t_0}{a_0}\right) \hat{S}_{11}(\mathbf{r}_a^i, t) + \text{rect}\left(\frac{t - t_1}{a_1}\right) \underbrace{\hat{S}_{11}(\mathbf{r}_a^i, t - \Delta t_i)}_{\text{shifted skin peak}} + \text{rect}\left(\frac{t - t_2}{a_2}\right) \hat{S}_{11}(\mathbf{r}_a^i, t). \quad (3.54)$$

And the Fourier transform of (3.54) is

$$\begin{aligned} S_{11}^{(R \rightarrow L), \text{window}}(\mathbf{r}_a^i, f) &= a_0 \text{sinc}(a_0 f) e^{-2\pi i f t_0} * S_{11}(\mathbf{r}_a^i, f) \\ &\quad + \left[a_1 \text{sinc}(a_1 f) e^{-2\pi i f t_1} \right] * \underbrace{\left[S_{11}(\mathbf{r}_a^i, f) e^{-2\pi i f \Delta t_i} \right]}_{\text{shifted skin peak}} \\ &\quad + a_2 \text{sinc}(a_2 f) e^{-2\pi i f t_2} * S_{11}(\mathbf{r}_a^i, f), \end{aligned} \quad (3.55)$$

Note that the time shifts Δt_i in (3.54) and (3.55) is identical to the ones used in equation (3.37). Due to us gating the skin peak with a rect function, we are able to align the peaks precisely without compromising the internal reflections.

In order to carry out such skin suppression, the time interval $[t_{\text{start}}, t_{\text{end}}]$ must be determined for every single antenna position. We propose a method of calculation of this interval that does not involve guesswork of empirical measurements. We acquire the endpoints of the interval as follows:

$$t_{\text{start}} = \arg \max_{t \in \mathcal{T}_i^{-1}} (t - t_i^{\text{skin}}), \quad t - t_i^{\text{skin}} < 0, \quad (3.56)$$

$$t_{\text{end}} = \arg \min_{t \in \mathcal{T}_i^{-1}} (t - t_i^{\text{skin}}), \quad t - t_i^{\text{skin}} > 0, \quad (3.57)$$

where $\mathcal{T}_i^{-1}$ is the set of all the *antipeaks* or local minima of the time-domain signal at the antenna position $\mathbf{r}_a^i$. Meaning that t_{start} corresponds to the closest antipeak preceding the skin peak determined due to correlation-based peak selection boundary detection procedure. And t_{end} is the time of the closest antipeak succeeding the skin peak. Figure 3.22 shows the resulting window. Such a method has a benefit of flexibly defined window based on the signal itself as opposed to arbitrarily chosen thresholds.

3.6 Incorporation of the Skin Suppression Techniques in Differential Imaging

This section presents preliminary results of images reconstructed using the D2 dataset omitted in [41], which is generated from the UM-BMID breast phantom dataset by synthetically creating

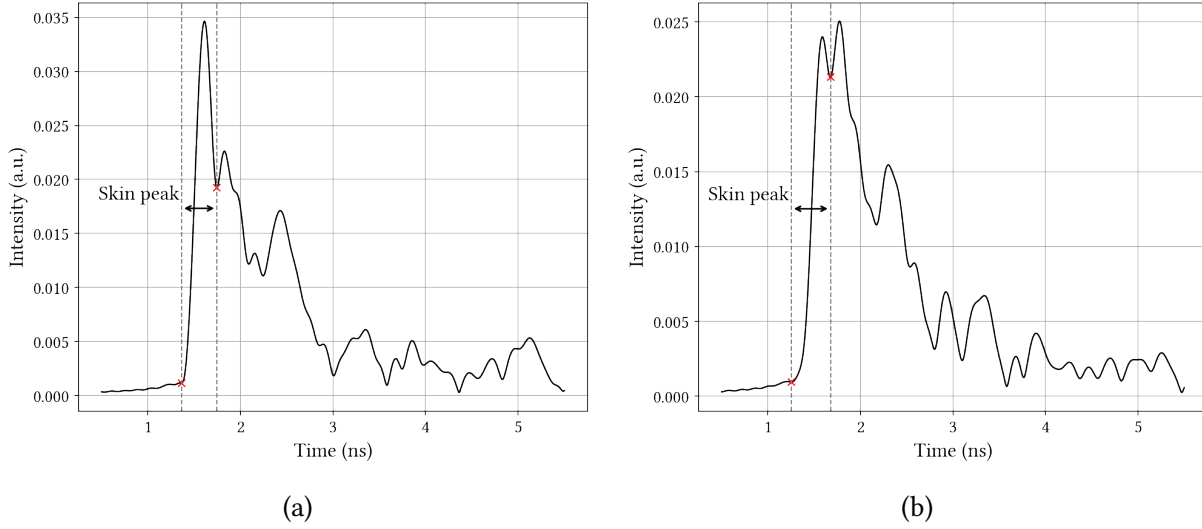


Figure 3.22: Skin peak window width determination. The starting and the ending points correspond to the two antipeaks (red marks) on either side of the skin peak. (a) - the primary peak with the highest intensity, (b) - secondary peak overpowering the primary peak, but still excluded from the skin window due to boundary detection procedure.

left-right breast pairs. As the second-most complex dataset, D2 supports both perfectly symmetric healthy-tissue configurations and left-right mirroring with translation (that can occur due to the possible off-centre position of the phantom), the latter being included to simulate realistic inconsistencies between the two breasts.

Figure 3.23 illustrates the impact of the skin alignment on a regular DAS reconstruction produced using the breast pairs with perfect healthy tissue symmetry but the two breasts are mirrored with respect to one another. The top row (3.23a-3.23c) corresponds to the DAS reconstruction of the images with no skin suppression present. The bottom row (3.23d-3.23f) corresponds to the reconstruction of the same breast pairs but with the Fourier window skin alignment applied.

Upon visual inspection the images acquired using the skin suppression technique are able to improve the tumour localization - a high intensity tumour response can be visible at the expected position with decent contrast, compared to the ‘no alignment’ case, where the tumour response is not visible at all. Figures on top have noticeably higher maximal intensity due to the skin reflections that are not accounted for during the data processing phase.

However, the tumour can be concealed by the clutter or the remaining skin reflections and imperfections in the fibroglandular alignment on the images with the Fourier window skin alignment applied. Figure 3.24 illustrates such reconstructions.

To quantify the diagnostic improvement provided by the skin suppression techniques, we employ the sensitivity and specificity estimation procedure previously adopted by our group in multiple publications [41], [42]. The image is labelled true positive if the tumour containing reconstruction’s SCR surpassed a certain threshold and the location error of the response is within its known radius plus the uncertainty in the polar position. If this criterion is met by the healthy scan, it was considered a false positive. The ROC curves for the D2 dataset are shown on the Figure 3.25. The ‘no alignment’ case has achieved the AUC of 29.6% and the reconstructions acquired using the Fourier window alignment has achieved the AUC of 31.5%. Even though both

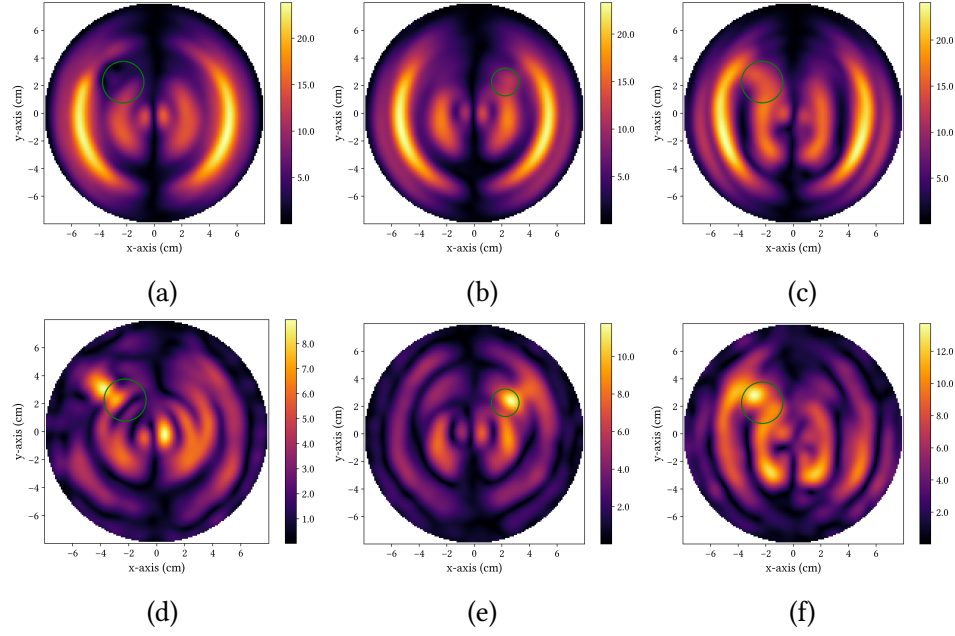


Figure 3.23: Comparison of reconstructions without alignment (top) and with Fourier window alignment (bottom).

methods did not surpass the random classifier, based on the curves, marginal improvement in the AUC and the images presented in this chapter, the skin alignment methods manage to suppress the skin in the phantoms with slightly different shapes of the boundary outline and improve our ability to localize tumours using the differential imaging approach.

It is important to note that all three methods of boundary alignment presented in this chapter apply a pure phase correction to one of the breasts, resulting in time-only alignment. However, the match in the amplitude is not guaranteed, leaving the possibility of residual skin peak of non-negligible intensity that might shadow the tumour response. Using the equation (3.55), it is possible to simply apply an intensity correction to the skin region the following way:

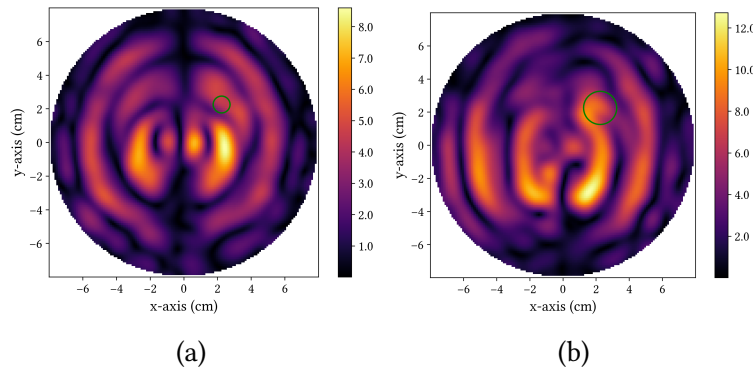


Figure 3.24: Examples of reconstructions with skin alignment, where the tumour is not visible.

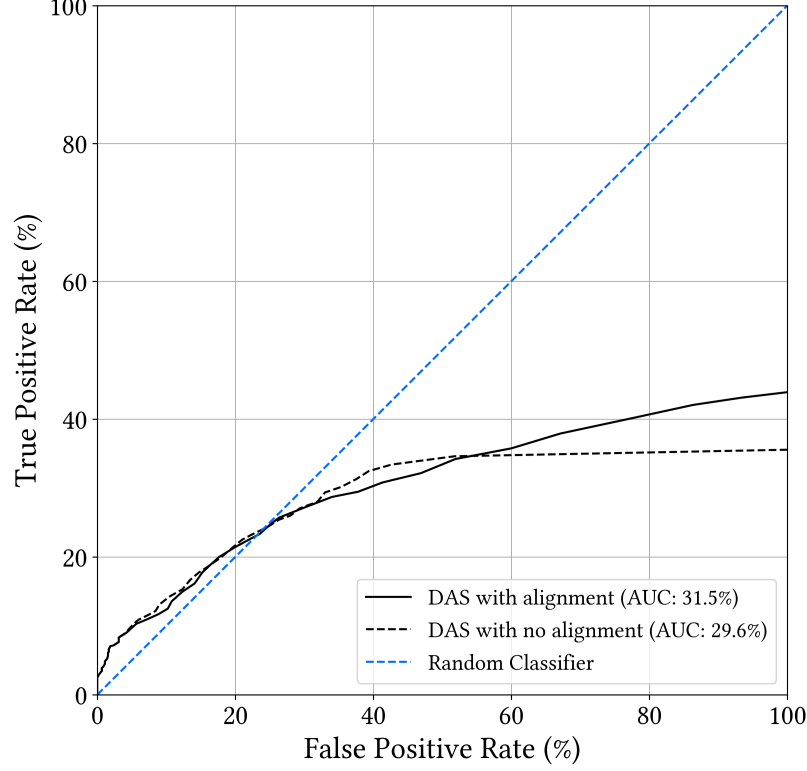


Figure 3.25: The ROC curves and the values of area under the curve (AUC) acquired using the dataset D2.

$$\begin{aligned}
S_{11}^{(R \rightarrow L), \text{window}}(\mathbf{r}_a^i, f) = & a_0 \text{sinc}(a_0 f) e^{-2\pi i f t_0} * S_{11}(\mathbf{r}_a^i, f) \\
& + \left[a_1 \text{sinc}(a_1 f) e^{-2\pi i f t_1} \right] * \left[I \cdot S_{11}(\mathbf{r}_a^i, f) e^{-2\pi i f \Delta t_i} \right] \\
& + a_2 \text{sinc}(a_2 f) e^{-2\pi i f t_2} * S_{11}(\mathbf{r}_a^i, f),
\end{aligned} \tag{3.58}$$

where I is the correction factor that equalizes the amplitudes of the skin response between the two breasts. Such an algorithm requires careful modelling of the intensity modulation based on the relative amplitude difference for signals from each antenna position across the scan. However, the shape of the skin peak, the noise profile, and the edge transitions in equation (3.58) are not taken into the account and would require more sophisticated modelling, which falls outside of the scope of this thesis and is reserved for future work.

Chapter 4

Propagation Speed Extraction

As has been stated in the Chapters 1 and 2, accurate estimation of the propagation speed of the microwave radiation in various breast tissues is the most important factor influencing the time-delay calculation, which thus determines the focusing ability of the reconstruction algorithm.

The reconstruction algorithms shown in most of the literature relies on the estimate of the average propagation speed in the whole imaging domain, assuming homogeneous nature of the propagation. Chapter 2 presented enhanced techniques of propagation speed modelling and its effects on the resulting images. However, the modelling was associated with a major drawback of requiring a priori information, specifically the exact values of the dielectric properties of the tissues through which the ‘rays’ are assumed to be propagating.

Such an approach is clinically impossible without surgical intervention for an accurate examination of the patient-specific tissues with a dielectric probe or incorporation of previously measured dielectric properties [74]. The latter requires further modelling based on the BI-RADS category and the tissue distribution.

The following chapter introduces an attempt to exclude a priori information from the imaging chain by employing transition (S_{21}) data.

4.1 Transition Data

To find a way of estimating the propagation speed through the unknown material, we need to establish a wave model. We can use equations (2.41)-(2.43) the same way it was used in the Section 2.3:

$$U(x) = Ae^{-\gamma x} + Be^{+\gamma x},$$

$$S_{21} = Ae^{-\gamma x} = Ae^{-(\alpha+i\beta)x},$$

$$\beta = \frac{2\pi}{\lambda} = \frac{2\pi f}{v} = \frac{\omega}{v}.$$

It is important to note that when the microwave signal is being recorded, we have the access to its *intensity* and *phase*. The phase of the wave in a dispersive material is:

$$\varphi(\omega) = -\beta x. \quad (4.1)$$

Combining this equation with (2.43), we can find the relation between the propagation speed of the wave and its phase in the dielectric:

$$v(\omega) = -\frac{\omega x}{\varphi(\omega)}. \quad (4.2)$$

From equation (4.2) we can see that by measuring the physical separation between the antennas x , and using the measured phase $\varphi(\omega)$ we can extract the effective propagation speed along the transition line.

However, acquiring a smooth propagation speed curve as a function of frequency poses several challenges. Mainly the challenge of unwrapping the phase signal and denoising it.

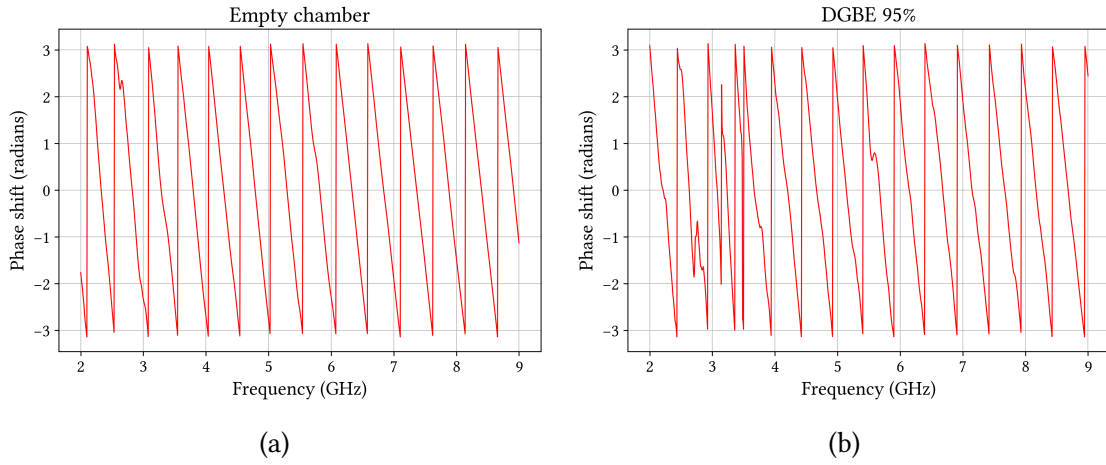


Figure 4.1: Wrapped microwave phase signal of the: (a) - empty chamber, (b) - cylindrical phantom filled with a dielectric material (95% solution of DGBE).

Figure 4.1 shows a sample wrapped phase signal as function of frequency. One can notice a substantial level of noise, specifically in the region of 2-4 GHz that appears with the insertion of the dielectric material when compared to an empty chamber.

4.1.1 Unwrapping the Phase

The main challenge associated with the unwrapping of the phase is the initial shift. By simply unwrapping the signal one acquires the curve shown on the Figure 4.2.

By applying the equation (4.2) to the extracted phase, we get a very poor propagation speed spectrum with asymptotes (Figure 4.3). This happens due to the fact that the initial wrapped phase signal is always constrained to the $[-\pi, \pi]$ range and does not take into account the number of multiples of 2π the wave has shifted in addition to the recorded phase shift at the lowest frequency. If the initial recorded frequency happens to be a positive angle, the unwrapped signal will pass through zero, not only creating a small region of the spectrum with a negative propagation speed, but also creating the asymptote.

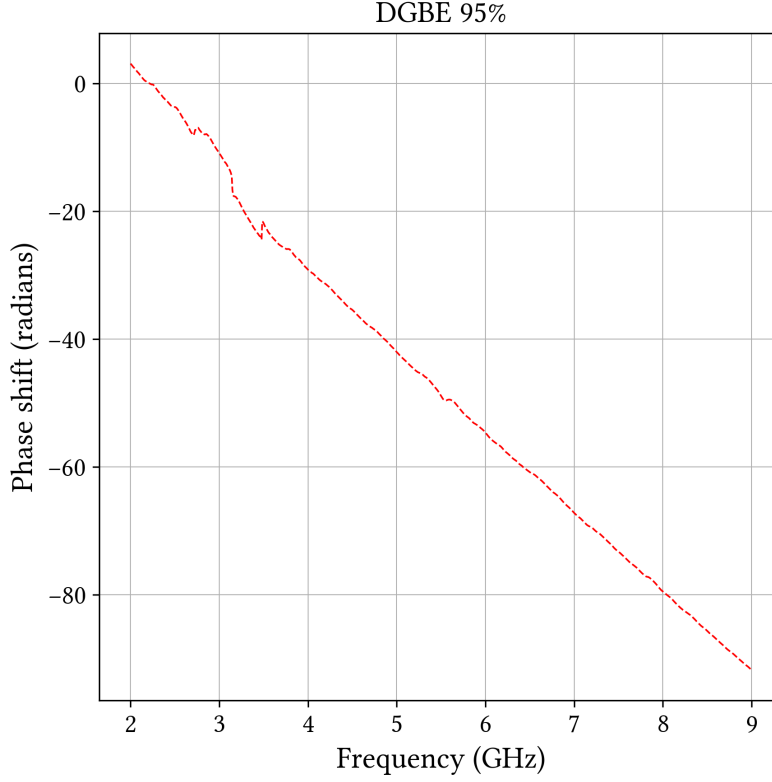


Figure 4.2: Unwrapped phase without the initial shift.

We propose a method of estimation of the initial shift in phase based on the simplistic model of the experiment and the propagation speed through the material with the known dielectric properties.

The experiments conducted within this chapter exclusively use the cylindrical phantom to ensure the radial symmetry of the imaging domain and the antennas are separated by 180° . Figure 4.4 shows the experimental setup in the chamber.

Based on the setup and the knowledge of the dielectric properties of the liquid we can derive the initial phase shift. The general idea of the method is to compare the experimentally extracted phase shift with the theoretically predicted at the lowest frequency.

We start with defining a theoretical phase shift:

$$\varphi_{\text{th}}(\omega) = -\frac{\omega L}{\bar{v}(\omega)}, \quad (4.3)$$

where $\bar{v}$ is the average propagation speed along the transition line and L is the physical separation between the two antennas in meters.

We define the average propagation speed $\bar{v}$ according to the simple model presented on the Figure 4.5. It is important to note that here we neglect the effects of multiple scattering, creeping waves or the antenna beam pattern.

We define two regions of propagation much like in Chapter 2: d - propagation through the dielectric and d_{air} - propagation through air. The time-of-flight associated with these regions are:

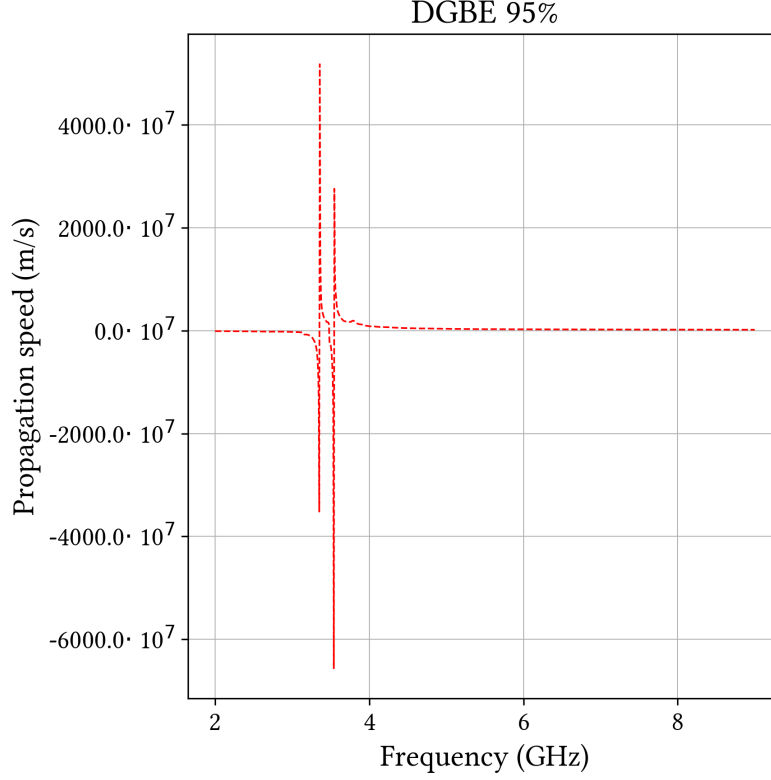


Figure 4.3: Propagation speed spectrum based on the unwrapped phase from the Figure 4.2.

$$t_{\text{air}} = \frac{d_{\text{air}}}{c}, \quad (4.4)$$

$$t_{\text{in}} = \frac{d}{v_{\text{in}}}, \quad (4.5)$$

where v_{in} is the propagation speed inside the breast. Since the separation between the antennas is known, we can derive an expression for the average speed along the line:

$$\bar{v}(\omega) = \frac{L}{2 \frac{d_{\text{air}}}{c} + \frac{d}{v_{\text{in}}(\omega)}}. \quad (4.6)$$

The value of the propagation speed inside the dielectric was derived in Section 2.3.1:

$$v_{\text{in}}(\omega) = \left\{ \frac{\mu_0 \varepsilon'(\omega)}{2} \left[\sqrt{1 + \left(\frac{\varepsilon''(\omega)}{\varepsilon'(\omega)} \right)^2} + 1 \right] \right\}^{-1/2} = \left\{ \frac{\mu_0 \varepsilon_0 \varepsilon_r(\omega)}{2} \left[\sqrt{1 + \left(\frac{\sigma(\omega)}{\omega \varepsilon_0 \varepsilon_r(\omega)} \right)^2} + 1 \right] \right\}^{-1/2}. \quad (4.7)$$

This model operates under the following simplifying assumptions: we can approximate the transmitted wave as a pencil-beam, the propagation speed in air is exactly c , and the phase center of the antenna does not change its position with frequency. The consequence of reducing the realistic

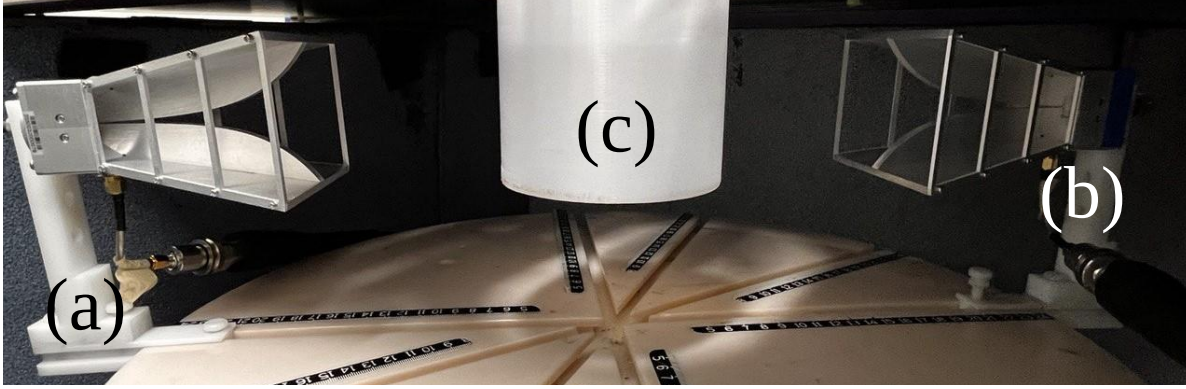


Figure 4.4: Experimental setup. (a) & (b) - antennas, (c) - cylindrical phantom filled with the dielectric liquid.

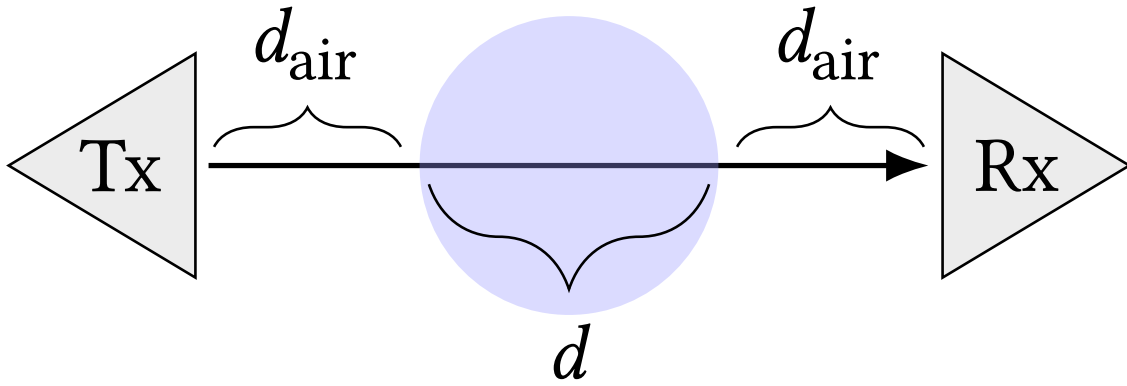


Figure 4.5: Geometric model of the propagation path.

beam to a pencil-beam is the inability of the model to distinguish between the signal transmitted through the dielectric and the signal received as a creeping wave. Simplifying the propagation speed in air to c might carry a systematic error due to the possibility of the chamber acting as a waveguide, practically reducing the propagation speed. And neglecting the frequency-dependence of the phase center of the wideband horn antenna can lead to incorrect estimation of the separation L in (4.6). A full discussion of the effects of such modelling is reserved for the Discussion section of this chapter.

From this point forward, the propagation speed as determined by the dielectric properties of the material will be referred to as the *true* or *actual* propagation speed. In contrast, the propagation speed extracted from the transition measurement using the phase-shift method will be referred to as *experimental* or *extracted*. The propagation speed inside the dielectric material is denoted v_{in} when we refer to the true value based on the known dielectric properties and $v_{\text{in}}^{\text{exp}}$ when we refer to the experimentally extracted value based on the phase shift and the underlying model. The average propagation speed along the transition line is denoted $\bar{v}$ when we refer to the theoretically predicted value based on the model and $\bar{v}_{\text{exp}}$ when we refer to the experimentally extracted values.

Now we have everything to model the initial phase shift. Assume that the theoretical phase shift based on the average propagation speed defined by the equation (4.3) is equivalent to the

experimentally measured phase shift with an integer multiple n of 2π shift:

$$\varphi_{\text{th}}(\omega) = \varphi_{\text{exp}}(\omega) - 2\pi n. \quad (4.8)$$

The benefit of using this particular model is in the fact that the resulting phase must retain its wrapped and unshifted value to be equivalent to the experimentally measured one. Thus, the shift is frequency independent and can be calculated at one frequency of choice, e.g., at the initial one. From this we can observe that the value of n is:

$$n = \frac{|\varphi_{\text{th}}(\omega_0) - \varphi_{\text{exp}}(\omega_0)|}{2\pi}, \quad (4.9)$$

where ω_0 is the initial angular frequency at which the measurement is performed.

Correcting the phase this way is beneficial because it only requires a single-frequency estimation of the shift, reducing the computation and reliance on a priori information. However, this is fragile if the system's SNR (signal-to-noise ratio) is poor at the initial frequency. Future research might feature a similar correction based on multiple frequencies to improve the robustness and maintain a relatively low reliance on a priori data.

Table 4.1 presents values of n at 2 GHz for Glycerin and different concentrations of DGBE, which serve as different tissue mimicking materials. As expected, the liquids with higher dielectric properties are associated with a higher value of n because of the decreased propagation speed in the medium - equation (4.7).

Table 4.1: Values of n and theoretically predicted $\bar{v}$ at 2 GHz.

	Glycerin	DGBE 95%	DGBE 90%	DGBE 70%
$\bar{v} (10^8 \text{m/s})$	2.17	2.04	1.97	1.56
n , rounded	4	4	4	6

4.1.2 Denoising the Signal

Figure 4.1b illustrates another imperfection of the method that is to be addressed - the noise. We propose a simple theoretical model to reduce the noise in the data without compromising the quality or the underlying physics.

It was decided to fit the experimentally extracted unwrapped phase to a model to further use to calculate the propagation speed spectrum. We begin by looking at the equation (4.2), which we can rewrite as:

$$\varphi(\omega) = -\frac{\omega x}{\bar{v}(\omega)}. \quad (4.10)$$

Here we emphasize that the phase is dependent on the *average* propagation speed through the transition region. And as we have already shown, we are able to model the propagation speed using equations (4.6) and (4.7). At this point to complete the model we need to designate parameters for the fit. A Cole-Cole model [88] provides the necessary means to express the complex permittivity in terms of several parameters. The equation is as follows:

$$\varepsilon(\omega) = \varepsilon_\infty + \frac{\varepsilon_s - \varepsilon_\infty}{1 + (i\omega\tau)^{1-\alpha}}, \quad (4.11)$$

where ε_∞ and ε_s are the ‘infinite’ and ‘static frequency’ dielectric constants, τ is a generalized relaxation time and α is a parameter that can take the value between 0 and 1. For the purposes of denoising the signal however, all these four variables are treated as parameters in the fit. The constraints of the fit used were based on [84] due to the similarity of materials used during the experiment. The system (4.12) summarizes the algorithm. By fitting the experimental phase to the analytical expression φ_{fit} , we are able to achieve a smoother phase curve.

$$\begin{cases} \varphi_{\text{fit}}(\omega) = -\frac{\omega x}{\bar{v}(\omega)} \\ \bar{v}(\omega) = \frac{L}{2\frac{d_{\text{air}}}{c} + \frac{d}{v_{\text{in}}(\omega)}} \\ v_{\text{in}}(\omega) = \left\{ \frac{\mu_0 \varepsilon'(\omega)}{2} \left[\sqrt{1 + \left(\frac{\varepsilon''(\omega)}{\varepsilon'(\omega)} \right)^2} + 1 \right] \right\}^{-1/2} \\ \varepsilon'(\omega) = \Re\{\varepsilon(\omega)\}, \varepsilon''(\omega) = \Im\{\varepsilon(\omega)\} \\ \varepsilon(\omega) = \varepsilon_\infty + \frac{\varepsilon_s - \varepsilon_\infty}{1 + (i\omega\tau)^{1-\alpha}} \end{cases} \quad (4.12)$$

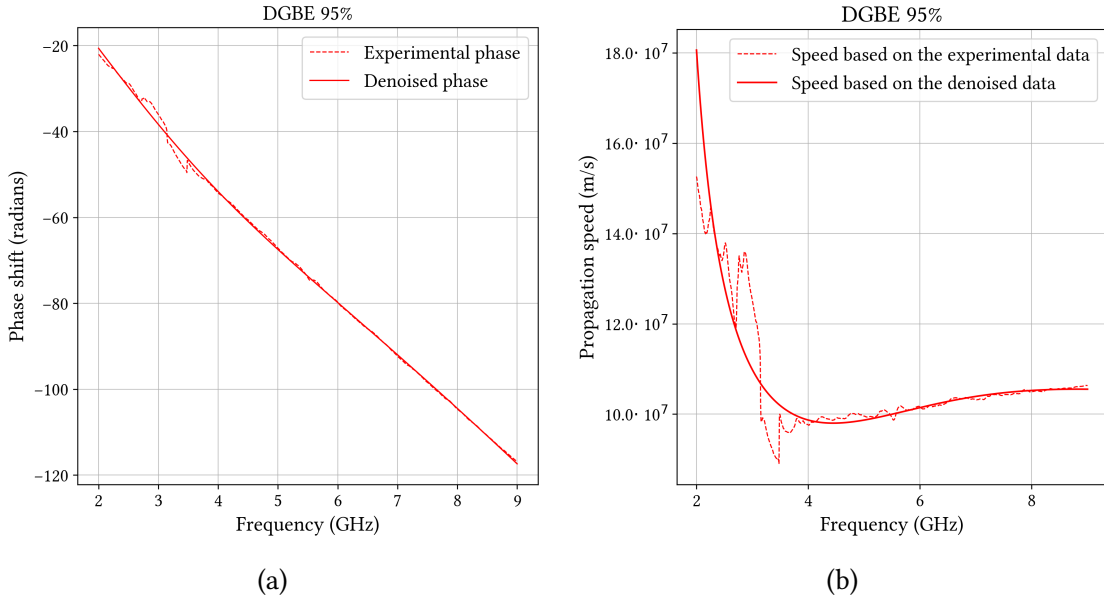


Figure 4.6: (a) - Experimentally extracted phase (dashed) and its denoised counterpart (solid). (b) - Average propagation speed calculated using the extracted phase (dashed) and the smoothed (solid).

As can be seen from Figure 4.6, the seemingly minor difference in the phase constituted a significant improvement in terms of the propagation speed. It is still apparent that the low-frequency part of the spectrum does not behave as predicted (the comparison between the experimental

propagation speed and the ground truths are going to be presented later in this chapter) despite our attempt to mitigate the noise in the signal.

$$v_{\text{in}}^{\text{exp}}(\omega) = \frac{d}{\frac{L}{\bar{v}_{\text{exp}}(\omega)} - 2\frac{d_{\text{air}}}{c}}, \quad (4.13)$$

where $\bar{v}_{\text{exp}}$ is the experimentally extracted average propagation speed after applying all the corrections: initial phase shift and denoising.

4.2 Experiment

A simple experimental setup, as illustrated in Figure 4.4, was used to facilitate the use of the transition theory presented in this section. Two horn antennas operating on frequencies from 2 to 9 GHz are positioned in front of each other at a distance of 0.42 m edge-to-edge. The antennas are connected to a Vector Network Analyzer (VNA) that collects S_{21} signals. An 11 cm diameter cylindrical breast phantom was used to provide a circular symmetry of the imaging system. Four dielectric liquids were used: Glycerin – commonly used as an adipose mimicking material, and three different solutions of Diethylene Glycol Butyl Ether (DBGE) with water in the following percent-by-weight concentrations: 70%, 90% and 95%.

4.3 Results

Figure 4.7 presents the phase-derived propagation speed spectra, computed using (4.13), in comparison with the actual values. Below 4 GHz, curves with higher mean values and lower n were significantly overestimated. Owing to the hyperbolic relation between speed and phase, noise in the data for materials with higher propagation speeds results in greater distortion. The method tends to underestimate propagation speed across all tested dielectrics. Nonetheless, the frequency dependence of the discrepancy between measured and actual propagation speeds was assessed, excluding data below 4 GHz via a 4 GHz cutoff, for potential correlation.

Visual inspection of Figure 4.7 reveals that all experimental curves fall below the actual propagation speed values beyond 4 GHz, indicating a systematic effect. The least squares fit of $k \cdot v_{\text{in}}^{\text{exp}}$ to $v_{\text{in}}^{\text{true}}$ serves to estimate k , representing the ratio of theoretical to experimental propagation speed. Table 4.2 lists the estimated values of k for the tested dielectrics, along with their uncertainties (one standard deviation). A decreasing trend in k with increasing mean propagation speed suggests a dependence on the dielectric properties.

After applying the curve shift correction and establishing the cutoff, the experimental and theoretical profiles can be compared. Figure 4.8 displays the adjusted experimental spectra of propagation speed alongside the known values. Two statistical metrics were employed: PCC and CCC, analogously to the Section 3.3.2. Table 4.3 reports the PCC and CCC values for the corrected spectra from 4 to 9 GHz. High agreement was observed for DGBE 70% (PCC 0.995, CCC 0.953) and 95% (PCC 0.983, CCC 0.920), with DGBE 90% also showing strong concordance (PCC 0.981, CCC 0.877). Glycerin yielded the lowest metrics - PCC of 0.906 and CCC of 0.849 - though the match between experimental and theoretical results remained acceptable.

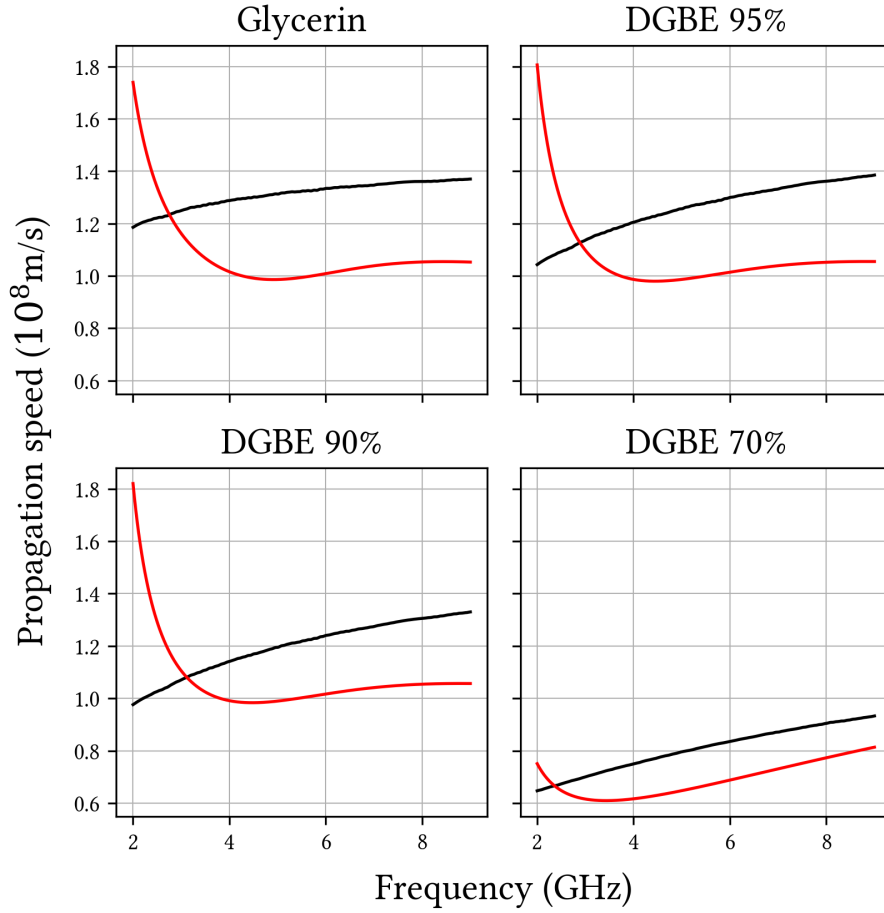


Figure 4.7: Extracted propagation speed inside the breast phantom (red) versus the known propagation speed (black) in different tissue-mimicking liquids.

4.4 Discussion

The theory presented here neglects creeping waves - waves that propagate along the phantom's surface. If one assumes a creeping wave travels at the speed of light, then the model of Fig. 4.5 no longer holds, since the phase data include an extra high speed component. Moreover, the values of k in Table 4.2 display a systematic trend as the mean propagation speed decreases, indicating that creeping-wave contributions may depend on the dielectric properties. Enhanced geometric and physical modelling should increase the extracted propagation speed and bring it closer to its theoretical value.

The cylindrical phantom used in Section 4.2 does not accurately mimic the shape or composition of real breast tissue. Subsequent work could consider evaluating the method's ability to discriminate dielectric variations induced by tumours.

The fitting procedure in Section 4.1.2 is sensitive to outliers and noise, producing the "tail" artifact visible in Fig. 4.7. Adopting a more constrained model - either by excluding problematic data or by applying algorithmic weighting - could suppress this artifact, improve accuracy, and

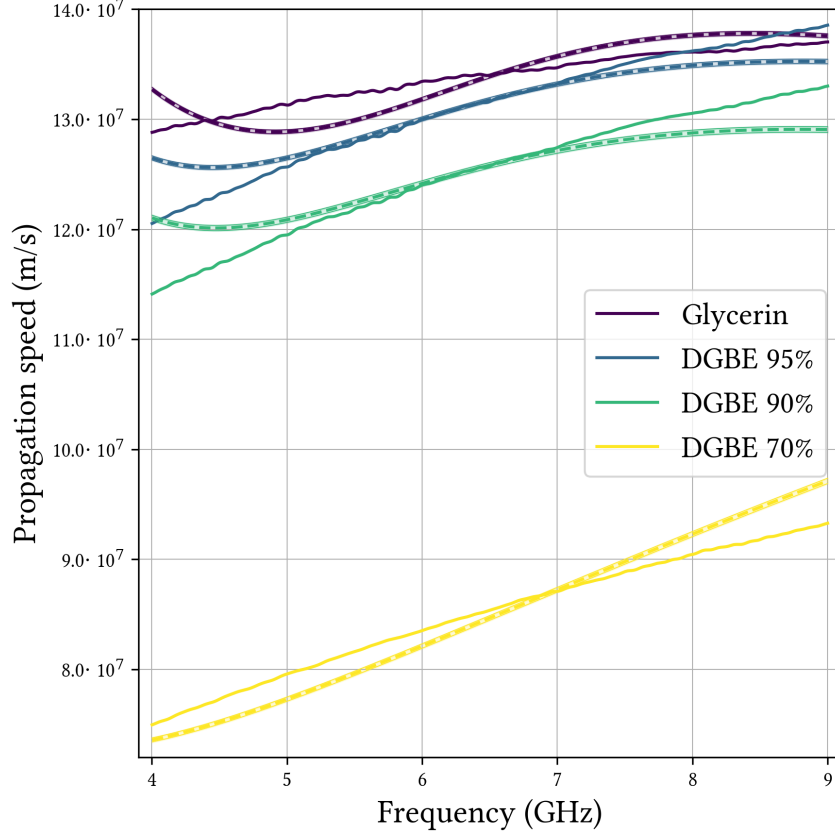


Figure 4.8: Corrected propagation speed in various dielectric liquids (dashed) with the 99% confidence interval (filled) versus the known values (solid).

Table 4.2: Values of k correction parameter for various dielectric liquids.

	Glycerin	DGBE 95%	DGBE 90%	DGBE 70%
k (a.u.)	1.306 ± 0.001	1.282 ± 0.001	1.221 ± 0.002	1.194 ± 0.002

broaden the statistical analysis bandwidth.

We implicitly assume that the propagation speed in the chamber's air equals c , but this may be influenced by the chamber's size and shape. It would be of interest to include measurements and analysis of empty chambers to validate this assumption.

The main systematic errors stem from antenna misalignment and using the front-edge separation rather than the phase-center separation, effectively reducing L in equation (4.6) and underestimating the propagation speed. Correcting L to reflect the true phase-center distance will raise the measured speed but will also alter the curve shape, since the phase-center location is frequency dependent.

Some VNAs are equipped with the ability to measure the time delay at a given port. Such measurements may provide additional experimental data, eliminating the need to model the initial phase shift n . However, this topic falls outside the scope of this thesis.

The data and methods presented in this chapter can be used to create an image corresponding

Table 4.3: Values of CCC and PCC for the corrected extracted values of the propagation speed from 4 GHz to 9 GHz.

	Glycerin	DGBE 95%	DGBE 90%	DGBE 70%
CCC	0.849	0.920	0.877	0.953
PCC	0.906	0.983	0.981	0.995

to the distribution of propagation speed in the imaging domain by employing an algorithm such as fan-beam back projection [89]. Figure 4.9 shows a simulated example generated with a MATLAB function from the Image Processing Toolbox using 200 synthetic antennas and precomputed propagation speed values based on the assumption of a homogeneous circular medium at the domain center and speed-of-light propagation outside the medium. Due to the ill-posed nature of CT-type image reconstruction, achieving a sharp image requires a very large number of projections, which current microwave systems cannot accommodate. One way to address this limitation is to apply controlled rotation of the object to synthetically increase the number of unique projections. However, examination of this topic lies beyond the scope of this thesis.

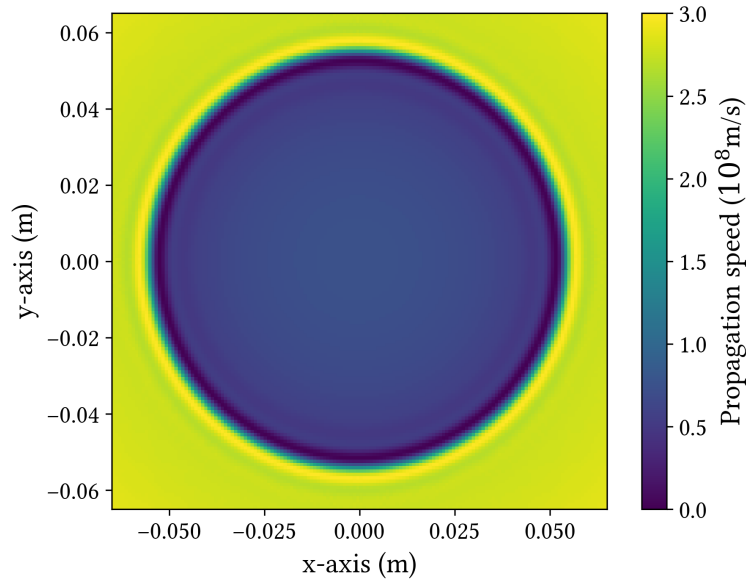


Figure 4.9: Fan-beam reconstruction of synthetically generated propagation speed values.

Chapter 5

Conclusions

In the introduction, three key challenges were identified: the homogeneous-medium assumption that ignores breast tissue heterogeneity, the neglect of frequency-dependent dielectric properties, and the unknown true propagation speed.

5.1 Enhanced Physics

To address tissue heterogeneity and unknown speed, a binary-partitioning model was developed. Each ray from antenna to pixel is intersected analytically with a circular breast outline, splitting the propagation path into air and breast segments and enabling piecewise time-delay calculations with distinct propagation speeds.

Building on this, a full frequency-dependent propagation speed model was derived from Maxwell's equations in lossy media. By expressing the complex propagation constant in terms of permittivity and conductivity, the model applies the true, frequency-varying speed $v(\omega)$ along each ray with the possibility of the domain partitioning.

Image enhancements were assessed using three metrics: localization error, response size, and contrast to quantify both feasibility and image quality improvements across reconstruction methods. Two datasets were designed and collected to facilitate the statistical analysis. Cylindrical phantom was used as the adipose shell and a long steel rod and a metal ball attached to a glass rod were employed as targets.

For the steel rod, binary and frequency-dependent models reduced mean localization error from 2.96 mm to as low as 1.91 mm. Both $\hat{\rho}$ and $\hat{\phi}$ extents shrank by roughly 40 % with enhanced physics, yielding more symmetric, tightly focused responses. Contrast decreased under binary partitioning but recovered with frequency dependence, confirming that modelling propagation speed refocuses energy and mitigates hot-spot clutter present around the target response.

For the small metal ball, images were noisier and localization error increased from 5.20 mm to nearly 10 mm with greater model complexity, driven by outlier mislocalizations when non-tumour hotspots dominated. Enhanced methods over-focused radially ($\hat{\rho}$ smaller than actual diameter) and introduced angular arching ($\hat{\phi}$ increased). Contrast again fell under binary DAS and rose slightly with frequency dependence, though overall signal-to-background contrast remained lower than in the 'rod' case.

Poorer performance of the enhanced physics methods of image reconstruction in the ball

dataset can be attributed to lower return power of the ball as the target and to the x - y -extent of the ball. The latter influences the way we compute the time-delays inside the breast. Since physically there can't be any propagation through the ball, the algorithms presented in Chapter 2 are susceptible to uncertainties caused by the calculation of the time-delays of the rays that go through the ball.

5.2 Boundary Detection

A data-driven boundary extraction algorithm was implemented to replace the idealized circular breast outline. For each antenna measurement, the received signal is subtracted from the empty chamber image to highlight reflections from the skin interface.

Next, along each radial direction from the antenna center, the peak corresponding to the skin is identified. These peak locations are converted into Cartesian coordinates, yielding a set of boundary points distributed around the phantom.

Finally, a cubic spline is performed on the acquired data to achieve a smooth and analytically defined boundary. This boundary is then used in all subsequent ray tracing calculations to ensure that propagation paths accurately account for the true breast outline.

5.2.1 Performance Against STL Data

Boundary detection was evaluated on the UM-BMID dataset of 320 scans using four MRI-derived adipose shells ('A2', 'A3', 'A14', 'A16'). For each shell, the extracted skin outline was compared against STL-model axial slices over a range of z -coordinates. The slice minimizing the mean squared error ('best' slice) and the anatomically correct slice at $z = -6.5$ cm ('real' slice) were used for performance assessment.

On the 'best' slice, shells 'A3', 'A14', and 'A16' achieved excellent agreement with ground truth ($PCC > 0.94$, $CCC > 0.93$), while shell 'A2' showed good but lower concordance ($PCC = 0.86$, $CCC = 0.81$). At the 'real' slice, shape agreement decreased modestly: 'A3', 'A14', and 'A16' maintained moderate-to-high PCC (0.87-0.96) and CCC (0.68-0.82), whereas 'A2' fell to $PCC = 0.56$ and $CCC = 0.10$.

These results confirm that the sinogram-based boundary detection accurately reconstructs realistic breast outlines when the optimal z -position is used, and remains robust to vertical variability for most shells, supporting its integration into boundary-aware ray tracing. However, they are also indicating that a more robust similarity metric needs to be developed to better quantify the performance on the Cartesian plane.

5.2.2 Differential Imaging

Differential imaging acquires paired frequency-domain scans of a healthy and suspect breast, then subtracts them to isolate pathological differences. To suppress the dominant skin reflection, three alignment strategies were developed: time-shift alignment (applying antenna-wise phase shifts in frequency domain), spatial-shift alignment (geometric registration of extracted boundaries prior to phase correction), and Fourier-window alignment (gating the skin-peak region with rect functions to preserve internal reflections while aligning skin responses after the spatial-shift alignment).

These skin-suppression techniques were integrated into the differential imaging. The time-shift and spatial-shift methods each are associated with possible distortions. The time-shift method distort anatomy and the spatial-shift method might leave residual misalignment; the Fourier-window approach combines their strengths by simultaneously matching skin peaks and retaining true tissue reflections. Thus, it was chosen to be evaluated.

Performance was evaluated on the D2 phantom dataset, with sensitivity-specificity ROC analysis. Without alignment, the AUC was 29.6 %; Fourier-window alignment modestly increased AUC to 31.5 %, demonstrating a slight but consistent improvement in tumour detectability through skin suppression.

Together, these methods bring differential microwave imaging closer to clinical viability by reducing skin response and enhancing contrast of pathological features, addressing the challenge of reliable tumour detection in the presence of strong skin reflections.

5.3 Propagation Speed Extraction

Chapter 4 introduced a data-driven method to extract propagation speed directly from measured S_{21} phase data. The raw wrapped phase signal $\varphi(\omega)$ was first unwrapped by estimating an integer 2π shift n at the lowest frequency, then denoised via a Cole-Cole model fit to produce a smooth phase suitable for speed computation.

Using the unwrapped, denoised phase and the known antenna separation L , the experimental average speed was computed from (4.6) and the interior propagation speed was isolated by subtracting the air path contribution (4.13). Four tissue-mimicking liquids (glycerin, DGBE 95%, 90%, 70%) were tested in a cylindrical phantom over 2-9 GHz.

Results showed that the extracted speed spectra consistently underestimated the true speed above 4 GHz. A simple least-squares fit was proposed to correct for the underestimation and to examine the shape similarity. The correction factors decreased from 1.306 for glycerin to 1.194 for DGBE 70%, indicating stronger underestimation in faster media. After applying k and a 4 GHz cutoff, corrected spectra achieved reasonable concordance with theory (PCC 0.983-0.995, CCC 0.920-0.953 for DGBE, PCC 0.906, CCC 0.849 for glycerin).

Despite this success, systematic errors arising from creeping-wave contributions, antenna misalignment, and use of edge-to-edge separation rather than phase-center distance, limit absolute accuracy. Addressing these via improved geometric modeling, more sophisticated scattering models, and direct VNA time-delay measurements could bring experimental speeds closer to theoretical values and enable spatial mapping of $v(\mathbf{r})$ for boundary-aware ray tracing.

Appendix A

Enhanced Physics Code Listings

The appendices provide the code snippets of most mentioned novel algorithms or methods. A full functioning repository that includes the reconstruction scripts and the asynchronous versions of the functionalities can be found on the authors *GitHub* page: <https://github.com/Djllesh>.

A.1 Domain Partitioning: Circle

```
1 import numpy as np
2
3
4 def get_pix_ts(
5     ant_rad,
6     m_size,
7     roi_rad,
8     air_speed,
9     *,
10    n_ant_pos=72,
11    ox=0.0,
12    oy=0.0,
13    ini_ant_ang=-136.0,
14    breast_speed=0.0,
15    adi_rad=0.0,
16 ):
17     """Get one-way pixel response times
18
19     Parameters
20     -----
21     ant_rad : float
22         Antenna radius, after correcting for the antenna time delay
23     m_size : int
24         Size of image-space along one dimension
25     roi_rad : float
26         Radius of the region of interest that will define the spatial
27         extent of the image-space
```

```

28     air_speed : float
29         The estimated propagation speed of the signal in air
30     n_ant_pos : int
31         Number of antenna positions used in the scan
32     ox : float
33         x_coord of the centre of the circle
34     oy : float
35         y_coord of the centre of the circle
36     ini_ant_ang : float
37         Polar angle of initial antenna position
38     breast_speed : float
39         The estimated propagation speed of the signal in phantom
40     adi_rad : float
41         Approximate radius of a phantom slice
42     Returns
43     -----
44     pix_ts : array_like, n_ant_pos x m_size x m_size
45         One-way response times of all pixels in the NxN image-space.
46         M is the number of antenna positions.
47     int_f_xs : array-like n_ant_pos x m_size x m_size
48         x-coordinates of each front intersection
49     int_f_ys : array-like n_ant_pos x m_size x m_size
50         y-coordinates of each front intersection
51     int_b_xs : array-like n_ant_pos x m_size x m_size
52         x-coordinates of each back intersection
53     int_b_ys : array-like n_ant_pos x m_size x m_size
54         y-coordinates of each back intersection
55     """
56
57     # Get antenna x/y positions during scan
58     ant_xs, ant_ys = get_ant_scan_xys(
59         ant_rad=ant_rad, n_ant_pos=n_ant_pos, ini_ant_ang=ini_ant_ang
60     )
61
62     # Create arrays of pixel x/y positions
63     pix_xs, pix_ys = get_xy_arrs(m_size=m_size, roi_rad=roi_rad)
64
65     int_f_xs, int_f_ys, int_b_xs, int_b_ys = find_xy_ant_bound_circle(
66         ant_xs,
67         ant_ys,
68         n_ant_pos,
69         pix_xs[0, :],
70         pix_ys[:, 0],
71         adi_rad,
72         ox=ox,
73         oy=oy,
74     )

```



```

75
76     return (
77         calculate_time_delays(
78             n_ant_pos,
79             m_size,
80             ant_xs,
81             ant_ys,
82             pix_xs,
83             pix_ys,
84             int_f_xs,
85             int_f_ys,
86             int_b_xs,
87             int_b_ys,
88             air_speed,
89             breast_speed,
90         ),
91         int_f_xs,
92         int_f_ys,
93         int_b_xs,
94         int_b_ys,
95     )
96
97
98 def calculate_time_delays(
99     n_ant_pos,
100     m_size,
101     ant_xs,
102     ant_ys,
103     pix_xs,
104     pix_ys,
105     int_f_xs,
106     int_f_ys,
107     int_b_xs,
108     int_b_ys,
109     air_speed,
110     breast_speed,
111 ):
112     """Calculates time delays for given set of intersections
113     for all antenna positions
114
115     Parmeters:
116     -----
117     n_ant_pos : int
118         Number of antenna positions used in the scan
119     m_size : int
120         Size of image-space along one dimension
121     ant_xs : array_like 1 x n_ant_pos

```

```

122     The x-positions in meters of each antenna position used in the
123     scan
124     ant_ys : array_like 1 x n_ant_pos
125     The y-positions in meters of each antenna position used in the
126     scan
127     pix_xs : array_like m_size x m_size
128     A 2D arr. Each element in the arr contains the x-position of
129     that pixel in the model, in meters
130     pix_ys : array_like m_size x m_size
131     A 2D arr. Each element in the arr contains the y-position of
132     that pixel in the model, in meters
133     int_f_xs : array-like n_ant_pos x m_size x m_size
134     x-coordinates of each front intersection
135     int_f_ys : array-like n_ant_pos x m_size x m_size
136     y-coordinates of each front intersection
137     int_b_xs : array-like n_ant_pos x m_size x m_size
138     x-coordinates of each back intersection
139     int_b_ys : array-like n_ant_pos x m_size x m_size
140     y-coordinates of each back intersection
141     air_speed : float
142     The estimated propagation speed of the signal in air
143     breast_speed : float
144     The estimated propagation speed of the signal in phantom
145
146     Returns:
147     -----
148     pix_ts : array_like n_ant_pos x m_size x m_size
149     One-way response times of all pixels in the NxN image-space.
150     M is the number of antenna positions.
151     """
152
153     # Init array for storing pixel time-delays
154     pix_ts = np.zeros([n_ant_pos, m_size, m_size])
155     ant_pos_idx = np.arange(n_ant_pos)
156
157     for a_pos, ts_ant_pos in zip(ant_pos_idx, range(np.size(pix_ts, axis=0))):
158         pix_to_back_xs = pix_xs - int_b_xs[a_pos]
159         pix_to_back_ys = pix_ys - int_b_ys[a_pos]
160
161         back_to_front_xs = int_b_xs[a_pos] - int_f_xs[a_pos]
162         back_to_front_ys = int_b_ys[a_pos] - int_f_ys[a_pos]
163
164         front_to_ant_xs = int_f_xs[a_pos] - ant_xs[a_pos]
165         front_to_ant_ys = int_f_ys[a_pos] - ant_ys[a_pos]
166
167         air_td_back = np.sqrt(pix_to_back_xs**2 + pix_to_back_ys**2) /
            air_speed

```

```

168     breast_td = (
169         np.sqrt(back_to_front_xs**2 + back_to_front_ys**2) / breast_speed
170     )
171     air_td_front = (
172         np.sqrt(front_to_ant_xs**2 + front_to_ant_ys**2) / air_speed
173     )
174
175     all_td = air_td_front + breast_td + air_td_back
176
177     # Calculate one-way time-delay of propagation from antenna to
178     # each pixel
179     pix_ts[ts_ant_pos, :, :] = all_td
180
181     return pix_ts
182
183
184 def find_xy_ant_bound_circle(
185     ant_xs, ant_ys, n_ant_pos, pix_xs, pix_ys, adi_rad, *, ox=0.0, oy=0.0
186 ):
187     """Finds breast boundary intersection coordinates
188     with propagation trajectory from antenna position
189     to corresponding pixel
190
191     Parameters
192     -----
193     ant_xs : array_like Mx1
194         Antenna x-coordinates
195     ant_ys : array_like Mx1
196         Antenna y-coordinates
197     n_ant_pos : int
198         Number of antenna positions
199     pix_xs : array_like
200         Positions of x-coordinates of each pixel
201     pix_ys : array_like
202         Positions of y-coordinates of each pixel
203     adi_rad : float
204         Approximate radius of a phantom
205     ox : float
206         x_coord of the centre of the circle
207     oy : float
208         y_coord of the centre of the circle
209
210     Returns
211     -----
212     int_f_xs : array-like NxN
213         x-coordinates of each front intersection
214     int_f_ys : array-like NxN

```

```

215     y-coordinates of each front intersection
216     int_b_xs : array-like NxN
217     x-coordinates of each back intersection
218     int_b_ys : array-like NxN
219     y-coordinates of each back intersection
220     """
221
222     # initializing arrays for storing intersection coordinates
223     # front intersection - closer to antenna
224     int_f_xs = np.empty([len(ant_xs), len(pix_xs), len(pix_ys)], dtype=float)
225     int_f_ys = np.empty_like(int_f_xs)
226
227     # back intersection - farther from antenna
228     int_b_xs = np.empty_like(int_f_xs)
229     int_b_ys = np.empty_like(int_f_xs)
230
231     for a_pos in range(n_ant_pos):
232         # singular antenna position
233         ant_pos_x = ant_xs[a_pos]
234         ant_pos_y = ant_ys[a_pos]
235
236         # for each pixel
237         for px_x, x in zip(pix_xs, range(len(pix_xs))):
238             for px_y, y in zip(pix_ys, range(len(pix_ys))):
239                 # calculating coefficients of polynomial
240                 k = (ant_pos_y - px_y) / (ant_pos_x - px_x)
241                 a = k**2 + 1
242                 b = 2 * (k * px_y - k**2 * px_x - ox - k * oy)
243                 c = (
244                     px_x**2 * k**2
245                     - 2 * k * px_x * px_y
246                     + px_y**2
247                     - adi_rad**2
248                     + ox**2
249                     + 2 * k * px_x * oy
250                     - 2 * px_y * oy
251                     + oy**2
252                 )
253
254                 # calculating the roots
255                 x_roots = np.roots([a, b, c])
256                 y_roots = k * (x_roots - px_x) + px_y
257
258                 # flag to determine whether there are two real roots
259                 are_roots = np.logical_and(
260                     ~np.iscomplex(x_roots)[0], ~np.iscomplex(x_roots)[1]
261                 )

```

```

262
263     if not are_roots: # if no roots
264         # pixel coords are stored at both front and back
265         int_f_xs[a_pos, y, x], int_f_ys[a_pos, y, x] = px_x, px_y
266         int_b_xs[a_pos, y, x], int_b_ys[a_pos, y, x] = px_x, px_y
267
268     else: # if two real roots
269         # distance from centre to pixel
270         d_centre_pix = np.sqrt((px_x - ox) ** 2 + (px_y - oy) ** 2)
271
272         distances_root_ant = np.sqrt(
273             (x_roots - ant_pos_x) ** 2 + (y_roots - ant_pos_y) ** 2
274         )
275         # initializing the list of tuples for easier sorting
276         dtype = [("x", float), ("y", float), ("distance", float)]
277         values = [
278             (x_roots[0], y_roots[0], distances_root_ant[0]),
279             (x_roots[1], y_roots[1], distances_root_ant[1]),
280         ]
281         roots = np.array(values, dtype=dtype)
282
283         # sort in ascending order wrt distance from antenna
284         roots = np.sort(roots, order="distance")
285
286         is_inside = d_centre_pix <= adi_rad
287
288         if is_inside: # if pixel is inside the breast
289             # store one intersection point
290
291             int_f_xs[a_pos, y, x], int_f_ys[a_pos, y, x], _ = roots
292             [
293                 0
294             ]
295             # store pixel coords as back intersection
296             int_b_xs[a_pos, y, x], int_b_ys[a_pos, y, x] = (
297                 px_x,
298                 px_y,
299             )
300
301         else: # if pixel is outside the breast
302             # calculate distance from antenna to pixel
303             d_pix_ant = np.sqrt(
304                 (ant_pos_x - px_x) ** 2 + (ant_pos_y - px_y) ** 2
305             )
306             # distance from antenna to adjacent point on circle
307             d_ant_adj = np.sqrt(
308                 (ant_pos_x - ox) ** 2

```

```

308         + (ant_pos_y - oy) ** 2
309         - adi_rad**2
310     )
311
312     # flag to determine whether the pixel is
313     # in front of the breast
314     is_front = d_ant_adj >= d_pix_ant
315
316     if is_front: # if pixel is in front
317         # store the same way as for no roots
318         int_f_xs[a_pos, y, x], int_f_ys[a_pos, y, x] = (
319             px_x,
320             px_y,
321         )
322         int_b_xs[a_pos, y, x], int_b_ys[a_pos, y, x] = (
323             px_x,
324             px_y,
325         )
326
327     else: # if pixel is past the breast
328         int_f_xs[a_pos, y, x], int_f_ys[a_pos, y, x], _ = (
329             roots[0]
330         )
331         int_b_xs[a_pos, y, x], int_b_ys[a_pos, y, x], _ = (
332             roots[1]
333         )
334
335     return int_f_xs, int_f_ys, int_b_xs, int_b_ys
336
337
338 def get_ant_scan_xys(ant_rad, n_ant_pos, *, ini_ant_ang=-136.0):
339     """Returns the x,y positions of each antenna position in the scan
340
341     Returns two vectors, containing the x- and y-positions in meters of
342     the antenna during a scan.
343
344     Parameters
345     -----
346     ant_rad : float
347         The radius of the trajectory of the antenna during the scan,
348         in meters
349     n_ant_pos : int
350         The number of antenna positions used in the scan
351     ini_ant_ang : float
352         The initial angle offset (in deg) of the antenna from the
353         negative x-axis
354

```

```

355 Returns
356 -----
357 ant_xs : array_like
358     The x-positions in meters of each antenna position used in the
359     scan
360 ant_ys : array_like
361     The y-positions in meters of each antenna position used in the
362     scan
363 """
364
365 # Find the polar angles of each of the antenna positions used in the
366 # scan
367 ant_angles = np.linspace(
368     0, (355 / 360) * 2 * np.pi, n_ant_pos
369 ) + np.deg2rad(ini_ant_ang)
370 ant_angles = np.flip(ant_angles)
371
372 ant_xs = np.cos(ant_angles) * ant_rad # Find the x-positions
373
374 ant_ys = np.sin(ant_angles) * ant_rad # Find the y-positions
375
376 return ant_xs, ant_ys
377
378
379 def get_xy_arrs(m_size, roi_rad):
380     """Finds the x/y position of each pixel in the image-space
381
382     Returns arrays that contain the x-distances and y-distances of every
383     pixel in the model.
384
385     Parameters
386     -----
387     m_size : int
388         The number of pixels along one dimension of the model
389     roi_rad : float
390         Radius of the region of interest that will define the spatial
391         extent of the image-space
392
393     Returns
394     -----
395     x_dists : array_like
396         A 2D arr. Each element in the arr contains the x-position of
397         that pixel in the model, in meters
398     y_dists : array_like
399         A 2D arr. Each element in the arr contains the y-position of
400         that pixel in the model, in meters
401     """

```

```

402
403     # X arrays are horizontal, Y arrays are vertical
404     # (transposition discrepancy fixed)
405     x_dists = np.linspace(-roi_rad, roi_rad, m_size)
406     x_dists = np.tile(x_dists, (m_size, 1))
407     y_dists = np.linspace(-roi_rad, roi_rad, m_size)
408     y_dists = np.tile(np.flip(y_dists), (m_size, 1)).T
409
410     return x_dists, y_dists

```

Listing A.1: Implementation of the intersection points calculation for the binary partitioning. The shape of the breast is assumed to be a circle.

Appendix B

Boundary Detection Code Listings

B.1 Boundary Detection from DAS Reconstruction

```
1 import numpy as np
2 from scipy import ndimage
3 from scipy.signal import find_peaks, correlate, correlation_lags
4 from scipy.interpolate import CubicSpline
5 from scipy.constants import speed_of_light
6
7 __VAC_SPEED = speed_of_light
8
9
10 def rot(theta):
11     """Returns a 2-D rotation matrix
12
13     Parameters:
14     -----
15     theta : float
16         Radian angle of rotation (counter clockwise)
17
18     Returns:
19     -----
20     rot_matr : array_like 2x2
21         Rotation matrix
22     """
23     return np.array(
24         [[np.cos(theta), -np.sin(theta)], [np.sin(theta), np.cos(theta)]]
25     )
26
27
28 def find_boundary(img, roi_rad, n_slices=50, threshold=0.005):
29     """Finds the approximate outline of a breast phantom.
30     Search is based on a highest intensity peaks that are the closest to
31     the antenna
```

```

32
33 Parameters
34 -----
35 img : array_like, NxN
36     Reconstructed reflectivity profile, breast phantom image.
37     Works best if the reconstruction was performed in reference to
38     an empty chamber scan
39 roi_rad : float
40     Radius of region of interest of the scan
41 n_slices : int
42     Number of slices that will be taken of the image
43 threshold : float
44     Precision value
45 Returns
46 -----
47 bound_x, bound_y : array_like n_slices x 1
48     x and y coordinate arrays of breast boundary
49 """
50 # unit rotation
51 theta = 360 / n_slices
52
53 # initialize arrays
54 bound_x, bound_y = np.array([]), np.array([])
55 # one pixel distance in meters
56 dx = 2 * roi_rad / np.size(img, axis=0)
57
58 for i in range(n_slices):
59     # create a temporary rotated image
60     img_to_slice = ndimage.rotate(
61         img, i * theta, reshape=False, prefilter=False
62     )
63
64     # take a slice right in the middle that corresponds to y = 0
65     slice = img_to_slice[np.size(img, axis=0) // 2, :]
66     # normalize the slice
67     max_val = np.amax(slice[~np.isnan(slice)])
68     slice /= max_val
69
70     # find two peaks
71     peaks, _ = find_peaks(slice, height=0.4)
72
73     # find corresponding x coordinates
74     x = (peaks[0] - 74) * dx
75
76     # temporary matrix of coordinates with no rotation
77     to_rot = np.array([[x], [0]])
78

```

```

79     # rotate back
80     to_store = np.matmul(rot(np.deg2rad(-theta * i)), to_rot)
81
82     if i != 0:
83         distance = np.sqrt(
84             (to_store[0, 0] - bound_x[i - 1]) ** 2
85             + (to_store[1, 0] - bound_y[i - 1]) ** 2
86         )
87
88         if distance > threshold:
89             prev_peak = np.array([[bound_x[i - 1]], [bound_y[i - 1]]])
90             new_idx = find_peak_threshold(
91                 slice, -i * theta, dx, prev_peak, threshold=threshold
92             )
93
94             x = (new_idx - 74) * dx
95             to_store = np.matmul(rot(np.deg2rad(-i * theta)), [[x], [0]])
96
97             bound_x = np.append(bound_x, to_store[0])
98             bound_y = np.append(bound_y, to_store[1])
99
100     return bound_x, bound_y
101
102
103 def find_peak_threshold(slice, theta, dx, prev_peak, threshold):
104     """Finds a peak distance from which to previous isn't surpassing
105     given threshold
106
107     Parameters:
108     -----
109     slice : array_like m_size x 1
110         One-dimensional signal of reconstructed image
111         along x-axis
112     theta : float
113         Rotation angle of a slice
114     dx : float
115         Transformation factor, one pix distance in meters
116     prev_peak : array_like 2 x 1
117         Coordinates of a previous peak in space domain
118
119     threshold : float
120         Maximal acceptable deviation
121
122     Returns:
123     -----
124     idx : int
125         Index of a new peak

```

```

126     """
127     # decrease the height to find undetected peaks
128
129     # get idx array to iterate through
130     peaks, _ = find_peaks(slice)
131     # for a case that several peaks are chosen
132     under_threshold = np.array([], dtype=int)
133
134     for peak_idx in peaks: # for each index
135         # find x_coordinate in spacial units
136         x = (peak_idx - 74) * dx
137         # find coordinates of the current peak with rotation
138         peak_xy = np.matmul(rot(np.deg2rad(theta)), [[x], [0]])
139
140         current_distance = np.sqrt(
141             (peak_xy[0, 0] - prev_peak[0, 0]) ** 2
142             + (peak_xy[1, 0] - prev_peak[1, 0]) ** 2
143         )
144
145         # append to a list of peaks that satisfy threshold
146         if current_distance < threshold:
147             under_threshold = np.append(under_threshold, peak_idx)
148
149     # if only 1 found - return
150     if np.size(under_threshold) == 1:
151         return under_threshold[0]
152
153     # if not, find a peak with minimal distance
154     min_dist = 100
155     idx_to_return = 0
156     # iterate over all found indices
157     for idx in under_threshold:
158         peak_xy = np.matmul(rot(np.deg2rad(theta)), [[slice[idx]], [0]])
159         current_distance = np.sqrt(
160             (peak_xy[0, 0] - prev_peak[0, 0]) ** 2
161             + (peak_xy[1, 0] - prev_peak[1, 0]) ** 2
162         )
163
164         if current_distance < min_dist: # update minimal distance index
165             min_dist = current_distance
166             idx_to_return = idx
167
168     return idx_to_return

```

Listing B.1: Implementation of the boundary detection algorithm using the DAS reconstruction data.

B.2 Boundary Detection from Sinograms

```
1 import numpy as np
2 from scipy.signal import find_peaks, correlate, correlation_lags
3 from scipy.interpolate import CubicSpline
4 from scipy.constants import speed_of_light
5 from umbms.beamform.iczt import iczt
6
7 __VAC_SPEED = speed_of_light
8
9
10 def get_boundary_iczt(
11     adi_emp_cropped,
12     ant_rad,
13     *,
14     adi_rad=0,
15     n_ant_pos=72,
16     ini_ant_ang=-136.0,
17     ini_t=0.5e-9,
18     fin_t=5.5e-9,
19     n_time_pts=700,
20     ini_f=2e9,
21     fin_f=9e9,
22     peak_threshold=10,
23 ):
24     """Returns a CubicSpline interpolation
25     function that approximates phantom boundary from a time-domain
26     converted data
27
28     Parameters:
29     -----
30     adi_emp_cropped : array_like n_freqs X n_ant_pos
31         Frequency-domain data of a scan minus empty chamber reference
32     ant_rad : float
33         Radius of antenna position AFTER all the corrections in [m]
34     adi_rad : float
35         Approximate radius of the breast in [m]
36     n_ant_pos : int
37         Number of antenna positions during one scan
38     ini_ant_ang : float
39         Initial polar angle of an antenna, in degrees
40     ini_t : float
41         The starting time-of-response to be used for computing the ICZT,
42         in seconds
43     fin_t : float
44         The stopping time-of-response to be used for computing the ICZT,
45         in seconds
```

```

46     n_time_pts : int
47         The number of points in the time-domain at which the transform
48         will be evaluated
49     ini_f : float
50         The initial frequency used in the scan, in Hz
51     fin_f : float
52         The final frequency used in the scan, in Hz
53     peak_threshold : int
54         The maximal allowed index jump in time points array
55         (recommended not to change)
56     Returns:
57     -----
58     cs : PPoly
59         Cubic spline interpolation of a boundary
60     x_cm, y_cm : float
61         Cartesian coordinates of a centre of mass
62     """
63
64     # Prepare the data to obtain time-domain scan data, time points and time
65     # aligned kernel for cross-correlation
66     td, ts, kernel = prepare_fd_data(
67         adi_emp_cropped=adi_emp_cropped,
68         ini_t=ini_t,
69         fin_t=fin_t,
70         n_time_pts=n_time_pts,
71         ini_f=ini_f,
72         fin_f=fin_f,
73         ant_rad=ant_rad,
74         adi_rad=adi_rad,
75     )
76     # find all rho and ToR (time-of-response) values
77     # on each antenna position
78     rho, ToR = rho_ToR_from_td(
79         td=td,
80         ts=ts,
81         kernel=kernel,
82         ant_rad=ant_rad,
83         peak_threshold=peak_threshold,
84     )
85
86     # polar angle data
87     angles = np.linspace(0, np.deg2rad(355), n_ant_pos) + np.deg2rad(
88         ini_ant_ang
89     )
90     # CubicSpline interpolation on a given set of data
91     cs = polar_fit_cs(rho, angles)
92

```

```

93     # calculate the center of mass fo this shape
94     x_cm, y_cm = find_centre_of_mass(rho, angles)
95
96     return cs, x_cm, y_cm
97
98
99 def prepare_fd_data(
100     adi_emp_cropped,
101     ini_t,
102     fin_t,
103     n_time_pts,
104     ini_f,
105     fin_f,
106     ant_rad=0,
107     adi_rad=0,
108 ):
109     """Prepares unorganized data for boundary detection
110
111     Parameters:
112     -----
113     adi_emp_cropped : array_like n_freqs X n_ant_pos
114         Frequency-domain data of a scan minus empty chamber reference
115     ini_t : float
116         The starting time-of-response to be used for computing the ICZT,
117         in seconds
118     fin_t : float
119         The stopping time-of-response to be used for computing the ICZT,
120         in seconds
121     n_time_pts : int
122         The number of points in the time-domain at which the transform
123         will be evaluated
124     ini_f : float
125         The initial frequency used in the scan, in Hz
126     fin_f : float
127         The final frequency used in the scan, in Hz
128     peak_threshold : int
129         The maximal allowed index jump in time points array
130         (recommended not to change)
131     ant_rad : float
132         Radius of antenna position AFTER all the corrections in [m]
133     adi_rad : float
134         Approximate radius of the breast in [m]
135     Returns:
136     -----
137     td : array_like
138         Time-domain signal
139     ts : array_like

```

```

140     The array of time points that correspond to the ICZT
141     kernel : array_like
142     One-dimensional time-aligned kernel
143     """
144
145     # convert frequency-domain data to time-domain
146     td = iczt(
147         adi_emp_cropped,
148         ini_t=ini_t,
149         fin_t=fin_t,
150         n_time_pts=n_time_pts,
151         ini_f=ini_f,
152         fin_f=fin_f,
153     )
154     # time response data
155     ts = np.linspace(ini_t, fin_t, n_time_pts)
156     # Time gating the data to strip away the early noise
157     if adi_rad != 0:
158         tor_min = ((ant_rad + 0.01 - adi_rad) * 2) / __VAC_SPEED
159         td_mask = td >= tor_min
160         td = td[td_mask]
161         ts = ts[td_mask]
162
163     # find the kernel
164     kernel = time_aligned_kernel(td)
165     return td, ts, kernel
166
167
168 def time_aligned_kernel(td):
169     """Produces a kernel for cross-correlation by time-aligning most
170     intense peaks
171
172     Parameters
173     -----
174     td : array_like
175         Skin response array in time domain
176
177     Returns
178     -----
179     kernel : array_like
180         Kernel for cross-correlation
181     """
182
183     # Initialize the array to store aligned responses
184     time_aligned_signals = np.zeros_like(td, dtype=float)
185     # Aligning wrt to the first antenna position
186     time_aligned_signals[:, 0] = np.abs(td[:, 0])

```



```

187 # Find the time of response for the first antenna position
188 first_peak, _ = find_peaks(
189     time_aligned_signals[:, 0],
190     height=np.max(time_aligned_signals[:, 0]) - 1e-9,
191 )
192
193 # for each antenna position
194 for ant_pos in range(1, np.size(td, axis=1), 1):
195     # find the max intensity ToR
196     signal_peak, _ = find_peaks(
197         np.abs(td[:, ant_pos]), np.max(np.abs(td[:, ant_pos])) - 1e-9
198     )
199     # if the ToR is later
200     if signal_peak > first_peak:
201         shift = signal_peak - first_peak
202         # then on this position fill from the start of the array to
203         # the position *shift* units back from the end
204         time_aligned_signals[
205             : np.size(time_aligned_signals, axis=0) - shift[0], ant_pos
206         ] = np.abs(td[shift[0] :, ant_pos])
207     # if the ToR is earlier
208     else:
209         shift = first_peak - signal_peak
210         # then on this position fill from the *shift* index to the
211         # end of the array
212         time_aligned_signals[shift[0] :, ant_pos] = np.abs(
213             td[: np.size(time_aligned_signals, axis=0) - shift[0], ant_pos]
214         )
215
216 # obtain the kernel by averaging
217 kernel = np.average(time_aligned_signals, axis=1)
218 return kernel
219
220
221 def rho_ToR_from_td(td, ts, kernel, ant_rad, peak_threshold):
222     """Completes the CBPS routine, returns the breast phantom boundary
223     as an array of rho and time responses
224
225     Parameters
226     -----
227     td : array_like
228         Scan data in time domain
229     ts : array_like
230         Time points used in the sinogram
231     kernel : array_like
232         Kernel for cross-correlation
233     ant_rad : float

```

```

234     Radius of antenna position AFTER all the corrections
235 peak_threshold : int
236     The maximal allowed index jump in time points array
237     (recommended not to change)
238
239 Returns
240 -----
241 rho : array_like
242     Array of rho values at each antenna position (m)
243 ToR : array_like
244     Array of values of the time-of-response for every antenna
245     position (s)
246 """
247 # creating an array of polar distances for storing
248 rho = np.array([])
249 # initializing an array of time-responses
250 ToR = np.array([])
251
252 # average peak index for correlation data interpretation
253 max_avg = np.max(kernel)
254 avg_peak, _ = find_peaks(kernel, height=max_avg - 1e-9)
255 previous_peak_idx = 0
256
257 for ant_pos in range(np.size(td, axis=1)):
258     # -----PEAK SEARCH----- #
259
260     # corresponding intensities
261     position = np.abs(td[:, ant_pos])
262     # correlation
263     corr = correlate(position, kernel, "same")
264     # resizing correlation back corresponding to the
265     # antenna position array length
266     lags = correlation_lags(len(position), len(kernel), "same")
267     max_corr = np.max(corr)
268     corr_peaks, _ = find_peaks(corr, height=max_corr - 1e-9)
269
270     # -----PEAK SELECTION----- #
271
272     # positive index - average signal is "shifted" to the right wrt
273     # the actual signal
274     # negative - to the left
275     indx_lag = lags[corr_peaks]
276     # approximate anticipated peak index
277     approx_peak_idx = avg_peak + indx_lag
278     # find the closest actual peak index to approximate
279     peaks, _ = find_peaks(position)
280     peak = peaks[np.argmin(np.abs(peaks - approx_peak_idx))]

```

```

281     # Correlation-based peak selection (CBPS)
282     if (
283         previous_peak_idx == 0
284         or np.abs(peak - previous_peak_idx) > peak_threshold
285     ):
286         peak = approx_peak_idx
287
288     # -----POLAR RADIUS----- #
289
290     # store the time response obtained from CBPS method
291     ToR = np.append(ToR, ts[peak])
292     # polar radius of a corresponding highest intensity response
293     # (corrected radius - radius of a time response)
294     rad = ant_rad - ts[peak] * __VAC_SPEED / 2
295     rho = np.append(rho, rad)
296
297     # for next iteration
298     previous_peak_idx = peak
299
300     # the rotation is counter-clockwise
301     rho = np.flip(rho)
302
303     return rho, ToR
304
305
306 def polar_fit_cs(rho, phi):
307     phi_ext = phi + np.pi * 2
308     phi = np.concatenate((phi, phi_ext))
309     rho = np.concatenate((rho, rho))
310     return CubicSpline(phi, rho)
311
312
313 def find_centre_of_mass(rho, phi):
314     """Finds x,y coordinates of the centre of mass of a uniform 2d shape
315
316     Parameters:
317     -----
318     rho : array_like
319         Array of polar radii
320     phi : array_like
321         Array of polar angles
322
323     Returns:
324     -----
325     x_cm, y_cm : float
326         Cartesian coordinates of a centre of mass
327     """

```

```
328
329     x = rho * np.cos(phi)
330     y = rho * np.sin(phi)
331
332     x_cm = np.sum(x) / np.size(x)
333     y_cm = np.sum(y) / np.size(y)
334
335     return x_cm, y_cm
```

Listing B.2: Implementation of the boundary detection algorithm with the correlation-based peak selection using the MW sinograms.

Appendix C

Differential Imaging Code Listings

C.1 Alignment Based on the Time Shift

```
1 import numpy as np
2 from scipy.constants import speed_of_light
3
4 __VAC_SPEED = speed_of_light
5
6
7 def phase_shift(fd, delta_t, freqs):
8     """Preforms a phase shift on the frequency domain data
9
10     Parameters
11     -----
12     fd : array_like
13         Frequency domain data of the scan
14     delta_t : array_like
15         Time shifts for every antenna position
16     freqs : array_like
17         Frequencies used in the scan (tiled for more efficient
18         computation)
19
20     Returns
21     -----
22     shifted_fd : array_like
23         Frequency domain data after phase shifting
24     """
25
26     # exponential factor for Fourier transform
27     exp_conversion = np.exp(-2j * np.pi * delta_t * freqs)
28     # conversion
29     shifted_fd = fd * exp_conversion
30
31     return shifted_fd
```

```

32
33
34 def align_skin_on_time_diff(
35     fd_emp_ref_left,
36     fd_emp_ref_right,
37     ant_rad=0.0,
38     ini_t=0.5e-9,
39     fin_t=5.5e-9,
40     n_time_pts=700,
41     ini_f=2e9,
42     fin_f=9e9,
43     peak_threshold=10,
44     scan_ini_f=1e9,
45     scan_fin_f=9e9,
46     n_fs=1001,
47 ):
48     """Converts aligned time-responses into frequency domain
49
50     https://en.wikipedia.org/wiki/Fourier\_transform
51     Performs a phase shift wrt the time shift per antenna position
52
53     Assuming the left breast is fixed
54
55     Parameters
56     -----
57     fd_emp_ref_left : array_like
58         FD data of the left breast (empty chamber reference)
59     fd_emp_ref_right : array_like
60         FD data of the right breast (empty chamber reference)
61     ant_rad : float
62         Radius of antenna position AFTER all the corrections
63     ini_t : float
64         The starting time-of-response to be used for computing the ICZT,
65         (s)
66     fin_t : float
67         The stopping time-of-response to be used for computing the ICZT,
68         (s)
69     n_time_pts : int
70         The number of points in the time-domain at which the transform
71         will be evaluated
72     ini_f : float
73         The smallest frequency to be retained, (Hz)
74     fin_f : float
75         The largest frequency to be retained, (Hz)
76     peak_threshold : int
77         The maximal allowed index jump in time points array
78         (recommended not to change)

```

```

79 scan_ini_f : int
80     The first frequency of the scan (Hz)
81 scan_fin_f : int
82     The last frequency of the scan (Hz)
83 n_fs : int
84     Number of frequency steps
85 Returns
86 -----
87 s11_aligned_right : array_like
88     FD data that corresponds to spatial alignment of the right
89     breast wrt to the left
90 """
91
92 # Number of antenna positions
93 n_ant_pos = np.size(fd_emp_ref_left, axis=1)
94 # Get frequencies for phase shifting
95 freqs = retain_and_tile_freqs(
96     scan_ini_f=scan_ini_f,
97     scan_fin_f=scan_fin_f,
98     ini_f=ini_f,
99     n_fs=n_fs,
100     n_ant_pos=n_ant_pos,
101 )
102 # convert FD to TD
103 td_left = iczt(
104     fd_emp_ref_left,
105     ini_t=ini_t,
106     fin_t=fin_t,
107     n_time_pts=n_time_pts,
108     ini_f=ini_f,
109     fin_f=fin_f,
110 )
111 td_right = iczt(
112     fd_emp_ref_right,
113     ini_t=ini_t,
114     fin_t=fin_t,
115     n_time_pts=n_time_pts,
116     ini_f=ini_f,
117     fin_f=fin_f,
118 )
119
120 # time response data
121 ts = np.linspace(ini_t, fin_t, n_time_pts)
122
123 # find the kernels
124 kernel_left = time_aligned_kernel(td_left)
125 kernel_right = time_aligned_kernel(td_right)

```

```

126
127 # find all ToR values on each antenna position
128 _, ToR_left = rho_ToR_from_td(
129     td=td_left,
130     ts=ts,
131     kernel=kernel_left,
132     ant_rad=ant_rad,
133     peak_threshold=peak_threshold,
134     plt_slices=False,
135     out_dir="",
136 )
137 _, ToR_right = rho_ToR_from_td(
138     td=td_right,
139     ts=ts,
140     kernel=kernel_right,
141     ant_rad=ant_rad,
142     peak_threshold=peak_threshold,
143     plt_slices=False,
144     out_dir="",
145 )
146 # time shifts
147 delta_t = ToR_left - ToR_right
148
149 # Phase shift
150 s11_aligned_right = phase_shift(
151     fd=fd_emp_ref_right, delta_t=delta_t, freqs=freqs
152 )
153
154 return s11_aligned_right
155
156
157 def retain_and_tile_freqs(scan_ini_f, scan_fin_f, ini_f, n_fs, n_ant_pos):
158     """Creates a tiled array of frequencies for phase shifting.
159
160     The frequencies are created in the range [scan_ini_f, scan_fin_f]
161     with a step size n_fs.
162
163     The frequencies are retained in the range [ini_f, scan_fin_f] on a
164     condition ini_f >= scan_ini_f
165
166     The frequencies are tiled n_ant_pos times.
167
168     Parameters
169     -----
170     scan_ini_f : float
171         Starting frequency of the scan
172     scan_fin_f : float

```



```

173         Finishing frequency of the scan
174     ini_f : float
175         Frequency to retain (higher than)
176     n_fs : int
177         Step size
178     n_ant_pos : int
179         Number of antenna positions during the scan
180
181     Returns
182     -----
183     freqs : array_like
184         The tiled array
185     """
186
187     # Obtain frequency array for phase shifting
188     fs = np.linspace(scan_ini_f, scan_fin_f, n_fs)
189     fs = fs[fs >= ini_f]
190     freqs = np.tile(fs, (n_ant_pos, 1)).T
191
192     return freqs

```

Listing C.1: Alignment implementation based on the temporal differences between the skin peaks of the left and the right breasts.

C.2 Alignment Based on the Spatial Shift

```

1 def extract_delta_t_from_boundary(
2     tor_right, cs_right_shifted, ant_rad, n_ant_pos=72, ini_ant_ang=-136.0
3 ):
4     """
5
6     Parameters
7     -----
8     tor_right : array_like
9         An array of times-of-response for an unshifted right boundary
10    cs_right_shifted : PPoly
11        Shifted CubicSpline of the right breast to align with the left
12    ant_rad : float
13        Corrected antenna radius
14
15    Returns
16    -----
17    delta_t : array_like
18        An array of time differences for further phase shift
19    """
20
21    # angles - real angles of antenna
22    ant_angs = np.linspace(0, np.deg2rad(355), n_ant_pos) + np.deg2rad(

```

```

23     ini_ant_ang
24 )
25 ant_angs = np.flip(ant_angs)
26
27 cs_angs = np.linspace(0, np.deg2rad(360), 1000)
28 rhos = cs_right_shifted(cs_angs)
29
30 # antenna positions
31 ant_xs = ant_rad * np.cos(ant_angs)
32 ant_ys = ant_rad * np.sin(ant_angs)
33
34 # coordinates of the breast outline
35 breast_xs = rhos * np.cos(cs_angs)
36 breast_ys = rhos * np.sin(cs_angs)
37
38 # distances from antennas to the phantom
39 distances = np.sqrt(
40     (ant_xs[:, None] - breast_xs) ** 2 + (ant_ys[:, None] - breast_ys) ** 2
41 )
42
43 min_dists = np.min(distances, axis=-1)
44 # convert distances to time of flight
45 tor_shifted = min_dists / __VAC_SPEED * 2
46 delta_t = tor_shifted - tor_right
47
48 return delta_t
49
50
51 def align_skin_on_spatial_shift(
52     fd_emp_ref_right,
53     ant_rad,
54     cs_right_shifted,
55     ini_t,
56     fin_t,
57     n_time_pts,
58     ini_f,
59     fin_f,
60     n_fs,
61     scan_ini_f,
62     scan_fin_f,
63 ):
64     """Performs phase shifting procedure based on the spatial shift
65     of the boundary
66
67     Parameters
68     -----
69     fd_emp_ref_right : array_like

```

```

70         Frequency domain data of the unshifted right breast scan
71         (empty chamber reference)
72     ant_rad : float
73         Radius of antenna AFTER applying the corrections
74     cs_right_shifted : PPoly
75         CubicSpline of the shifted right breast boundary
76     ini_t : float
77         Initial time point for ICZT (s)
78     fin_t : float
79         Finishing time point for ICZT (s)
80     n_time_pts : int
81         Number of time points
82     ini_f : float
83         Initial frequency that retains (Hz)
84     fin_f : float
85         Finishing frequency (Hz)
86     n_fs : int
87         Number of frequencies
88     scan_ini_f : float
89         Initial frequency of the scan (Hz)
90     scan_fin_f : float
91         Finishing frequency of the scan (Hz)
92
93     Returns
94     -----
95     s11_aligned_right : array_like
96         Resulting S11 data after the application of the phase shift
97     """
98
99     # if regular scan (up to 9GHz)
100     if scan_fin_f is None:
101         # the range to retain and the range of the scan end at the same
102         # frequency
103         scan_fin_f = fin_f
104
105     # Number of antenna positions
106     n_ant_pos = np.size(fd_emp_ref_right, axis=1)
107
108     #
109     td, ts, kernel = prepare_fd_data(
110         adi_emp_cropped=fd_emp_ref_right,
111         ini_t=ini_t,
112         fin_t=fin_t,
113         n_time_pts=n_time_pts,
114         ini_f=ini_f,
115         fin_f=fin_f,
116     )

```

```

117
118     # Prepare the data to obtain time-domain scan data, time points and
119     # time aligned kernel for cross-correlation
120     _, tor_right = rho_ToR_from_td(
121         td,
122         ts,
123         kernel,
124         ant_rad=ant_rad,
125         peak_threshold=10,
126         plt_slices=False,
127         out_dir="",
128     )
129
130     # Get frequencies for phase shifting
131     freqs = retain_and_tile_freqs(
132         scan_ini_f=scan_ini_f,
133         scan_fin_f=scan_fin_f,
134         n_fs=n_fs,
135         ini_f=ini_f,
136         n_ant_pos=n_ant_pos,
137     )
138
139     # Find delta_t values that correspond to a spatial shift
140     # of the boundary
141     delta_t = extract_delta_t_from_boundary(
142         tor_right=tor_right, cs_right_shifted=cs_right_shifted, ant_rad=ant_rad
143     )
144
145     # Phase shift
146     s11_aligned_right = phase_shift(
147         fd=fd_emp_ref_right, delta_t=delta_t, freqs=freqs
148     )
149
150     return s11_aligned_right

```

Listing C.2: Alignment implementation based on the geometric shift and rotation of the right breast with respect to the left breast.

C.3 Fourier Window Alignment

```

1 def align_skin_window(
2     fd_emp_ref_right,
3     fd_emp_ref_left,
4     ant_rad=0.0,
5     ini_t=0.5e-9,
6     fin_t=5.5e-9,
7     n_time_pts=700,
8     ini_f=2e9,

```

```

9     fin_f=9e9,
10    peak_threshold=10,
11    scan_ini_f=1e9,
12    scan_fin_f=9e9,
13    n_fs=1001,
14 ):
15     """Shifts the skin response in a thin window defined by the earliest
16     and latest skin signals
17
18     Parameters
19     -----
20
21     fd_emp_ref_left : array_like
22         FD data of the left breast (empty chamber reference)
23     fd_emp_ref_right : array_like
24         FD data of the right breast (empty chamber reference)
25     ant_rad : float
26         Radius of antenna position AFTER all the corrections
27     ini_t : float
28         The starting time-of-response to be used for computing the ICZT,
29         (s)
30     fin_t : float
31         The stopping time-of-response to be used for computing the ICZT,
32         (s)
33     n_time_pts : int
34         The number of points in the time-domain at which the transform
35         will be evaluated
36     ini_f : float
37         The smallest frequency to be retained, (Hz)
38     fin_f : float
39         The largest frequency to be retained, (Hz)
40     peak_threshold : int
41         The maximal allowed index jump in time points array
42         (recommended not to change)
43     scan_ini_f : int
44         The first frequency of the scan (Hz)
45     scan_fin_f : int
46         The last frequency of the scan (Hz)
47     n_fs : int
48         Number of frequency steps
49     """
50
51     # convert FD to TD
52     td_left = iczt(
53         fd_emp_ref_left,
54         ini_t=ini_t,
55         fin_t=fin_t,

```

```

56     n_time_pts=n_time_pts,
57     ini_f=ini_f,
58     fin_f=fin_f,
59 )
60 td_right = iczt(
61     fd_emp_ref_right,
62     ini_t=ini_t,
63     fin_t=fin_t,
64     n_time_pts=n_time_pts,
65     ini_f=ini_f,
66     fin_f=fin_f,
67 )
68
69 # time response data
70 ts = np.linspace(ini_t, fin_t, n_time_pts)
71
72 # find the kernels
73 kernel_left = time_aligned_kernel(td_left)
74 kernel_right = time_aligned_kernel(td_right)
75
76 # find all ToR values on each antenna position
77 _, ToR_left = rho_ToR_from_td(
78     td=td_left,
79     ts=ts,
80     kernel=kernel_left,
81     ant_rad=ant_rad,
82     peak_threshold=peak_threshold,
83     plt_slices=False,
84     out_dir="",
85 )
86 _, ToR_right = rho_ToR_from_td(
87     td=td_right,
88     ts=ts,
89     kernel=kernel_right,
90     ant_rad=ant_rad,
91     peak_threshold=peak_threshold,
92     plt_slices=False,
93     out_dir="",
94 )
95
96 # Find time shifts for the skin
97 delta_t = ToR_left - ToR_right
98
99 # Frequencies used in the scan
100 freqs = np.linspace(scan_ini_f, scan_fin_f, n_fs)
101 freqs = freqs[freqs >= ini_f]
102 df = np.diff(freqs)[0]

```

```

103
104 # find a frequency that is the closest positive to zero
105 # with a step size = df
106 f_0 = freqs[0] - df * (freqs[0] // df)
107
108 # Arrange an array of the size *7000* (a very large array)
109 freqs_to_convolve = np.arange(f_0 - 3500 * df, f_0 + 3500 * df, df)
110
111 # Extract the time point to ensure no loss in data (TD -> FD)
112 ifft_ts = np.fft.fftfreq(n=np.size(freqs_to_convolve), d=df)
113 t_0 = np.min(ifft_ts)
114 t_fin = np.max(ifft_ts)
115
116 new_right_breast_fd = np.empty_like(fd_emp_ref_right, dtype=complex)
117
118 for ii in range(np.size(fd_emp_ref_right, axis=1)): # for each antenna pos
119     # ===== EXTRACTING THE SKIN WINDOW ===== #
120     signal_td = np.abs(td_right[:, ii])
121     # Searching for the peaks of the vertically flipped signal
122     # to capture the whole width of the skin peak
123     peaks, _ = find_peaks(-signal_td)
124     # Maximal peak refers to a primary skin response (it might not be
125     # of maximal intensity
126     max_peak = np.argwhere(ts == ToR_right[ii])[0]
127     # The start and the end of the skin are two closest negative
128     # peaks to the primary skin response on either side
129     peaks_to_decide = peaks - max_peak
130     t_start = ts[max_peak + peaks_to_decide[peaks_to_decide < 0][-1]]
131     t_end = ts[max_peak + peaks_to_decide[peaks_to_decide > 0][0]]
132
133     # ===== PREPARE DATA FOR THE CONVOLUTION ===== #
134     # Zero-pad the signal, so it can be easily extracted from the
135     # result of the convolution
136     original_signal_zero_padded = np.zeros_like(
137         freqs_to_convolve, dtype=complex
138     )
139     # Start at the index that corresponds to frequency ini_f in
140     # a large array of frequencies
141     start_freq_for_padding = int(
142         np.size(freqs_to_convolve) // 2 - 1 + freqs[0] // df
143     )
144     # Assign the signal to this region
145     original_signal_zero_padded[
146         start_freq_for_padding : start_freq_for_padding
147         + np.size(fd_emp_ref_right, axis=0)
148     ] = fd_emp_ref_right[:, ii]
149

```

```

150 # ===== APPLY THE FOURIER TRANSFORM RULES ===== #
151 # S11 * sinc for the pre-skin region
152 pre_skin_sinc_conv = np.convolve(
153     original_signal_zero_padded,
154     (t_start - t_0)
155     * np.sinc(freqs_to_convolve * (t_start - t_0))
156     * np.exp(
157         -2j * np.pi * freqs_to_convolve * (t_0 + (t_start - t_0) / 2)
158     ),
159     mode="same",
160 )
161
162 # S11 times phase shift based on the delta_t value * sinc for
163 # the skin region for a given antenna position
164 skin_sinc_conv = np.convolve(
165     original_signal_zero_padded
166     * np.exp(-2j * np.pi * freqs_to_convolve * delta_t[ii]),
167     (t_end - t_start)
168     * np.sinc(freqs_to_convolve * (t_end - t_start))
169     * np.exp(
170         -2j
171         * np.pi
172         * freqs_to_convolve
173         * (t_start + (t_end - t_start) / 2)
174     ),
175     mode="same",
176 )
177
178 # S11 * sinc for after the skin region
179 post_skin_sinc_conv = np.convolve(
180     original_signal_zero_padded,
181     (t_fin - t_end)
182     * np.sinc(freqs_to_convolve * (t_fin - t_end))
183     * np.exp(
184         -2j * np.pi * freqs_to_convolve * (t_end + (t_fin - t_end) / 2)
185     ),
186     mode="same",
187 )
188
189 # Times df due to a large step size and a discrepancy between a
190 # discrete and continuous convolution
191 signal_composed = (
192     pre_skin_sinc_conv + skin_sinc_conv + post_skin_sinc_conv
193 ) * df
194
195 new_right_breast_fd[:, ii] = signal_composed[
196     start_freq_for_padding + 1 : start_freq_for_padding

```



```
197         + np.size(fd_emp_ref_right, axis=0)
198         + 1
199     ]
200
201     return new_right_breast_fd
```

Listing C.3: Alignment implementation using the windowing approach.

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