Research interface on a programmable ultrasound scanner

Vijay Shamdasani a, Unmin Bae b, Siddhartha Sikdar a, Yang Mo Yoo a, Kerem Karadayi b, Ravi Managuli a, Yongmin Kim a,b,*

a Department of Bioengineering, University of Washington, Seattle, WA 98195-5061, USA
b Department of Electrical Engineering, University of Washington, Seattle, WA 98195-2500, USA

Received 8 August 2007; received in revised form 1 November 2007; accepted 24 November 2007
Available online 23 December 2007

Abstract

Motivation: Commercial ultrasound machines in the past did not provide the ultrasound researchers access to raw ultrasound data. Lack of this ability has impeded evaluation and clinical testing of novel ultrasound algorithms and applications.

Objectives: Recently, we developed a flexible ultrasound back-end where all the processing for the conventional ultrasound modes, such as B, M, color flow and spectral Doppler, was performed in software. The back-end has been incorporated into a commercial ultrasound machine, the Hitachi HiVision 5500. The goal of this work is to develop an ultrasound research interface on the back-end for acquiring raw ultrasound data from the machine.

Methods: The research interface has been designed as a software module on the ultrasound back-end. To increase the amount of raw ultrasound data that can be spooled in the limited memory available on the back-end, we have developed a method that can losslessly compress the ultrasound data in real time.

Results and discussion: The raw ultrasound data could be obtained in any conventional ultrasound mode, including duplex and triplex modes. Furthermore, use of the research interface does not decrease the frame rate or otherwise affect the clinical usability of the machine. The lossless compression of the ultrasound data in real time can increase the amount of data spooled by ~2.3 times, thus allowing more than 6 s of raw ultrasound data to be acquired in all the modes. The interface has been used not only for testing of new ideas with in vitro data from phantoms, but also for acquiring in vivo data for fine-tuning ultrasound applications and conducting clinical studies. We present several examples of how newer ultrasound applications, such as elastography, vibration imaging and 3D imaging, have benefited from this research interface. Since the research interface is entirely implemented in software, it can be deployed on existing HiVision 5500 ultrasound machines and may be easily upgraded in the future.

Conclusions: The developed research interface can aid researchers in the rapid testing and clinical evaluation of new ultrasound algorithms and applications. Additionally, we believe that our approach would be applicable to designing research interfaces on other ultrasound machines.

© 2007 Elsevier B.V. All rights reserved.

Keywords: Ultrasound research interface; Complex baseband ultrasound data; Real-time lossless compression; Translational research

1. Introduction

Most clinical ultrasound machines do not allow the researchers working in ultrasound imaging to have access to the raw ultrasound data [1]. Inability to access the raw ultrasound data in the laboratory and clinic has not only limited the basic research, but also hindered the clinical testing of novel ultrasound applications. In order to access the raw ultrasound data in the laboratory, researchers have worked with the ultrasound manufacturer to make custom hardware modifications to the ultrasound machine [2–10] or have resorted to building custom ultrasound systems [11]. Several of these raw data interfaces have involved...
the use of external digitizers and computers [3–6,9,10], which makes it cumbersome to acquire data in the clinic. The problems faced by ultrasound researchers and their potential solutions were discussed by representatives from the industry, academia and government at a workshop in 1999 organized by the US Public Health Service’s Office on Women’s Health (OWH) and the National Cancer Institute (NCI) [1]. The specifications for basic and advanced research interfaces that could allow researchers to control the machine and acquire raw ultrasound data were established at the workshop, and Siemens Medical Systems was subsequently awarded a contract to develop such an interface on their machine [12,13]. As a result, the Axius Direct Ultrasound Research Interface has been commercially available on the Siemens high-end Antares ultrasound platform, which allows the researchers to acquire around 200 Mbytes of beamformed radio-frequency (RF) ultrasound data sampled at 40 MHz [14]. Users can control beamforming parameters, such as receive aperture, color Doppler ensemble size and vector interleave, and can create macros to automate commonly-used key sequences. More recently, Ultrasonix Medical Corporation (Vancouver, BC, Canada) introduced the ES500 ultrasound machine. Beamforming on the machine is performed on field programmable gate arrays (FPGA), while the software performing the back-end processing runs on the personal computer (PC) platform. Using the research package, RF data sampled at 40 MHz can be acquired. However, the raw ultrasound data can be acquired at only one-third the frame rate supported during routine clinical imaging [15,16]. Furthermore, the data acquisition is restricted to a user-selectable 8-cm region of tissue in the depth direction.

To aid in the quick testing and evaluation of new applications, we have developed a research interface on an ultrasound back-end of a clinical ultrasound machine (HiVision 5500, Hitachi Medical Systems America, Twinsburg, OH) [17,18]. We describe how the acquisition of raw baseband (IQ) ultrasound data are enabled in the laboratory and the clinic without compromising the clinical features and frame rates available on the machine. We also present several examples of how the ultrasound research interface has helped the clinical evaluation of new algorithms and applications.

2. Methods

2.1. The ultrasound machine

Fig. 1 shows the block diagram of the HiVision 5500 ultrasound machine, where the front-end activates the array transducer to transmit the ultrasound beam and digitizes the received ultrasound echoes. The beamformer shifts and combines the ultrasound signals from individual elements of the transducer to create a RF ultrasound vector, which is demodulated to obtain the in-phase (I) and quadrature (Q) data. The IQ data are then transferred to the four media accelerated processors (MAP) in the back-end for regular clinical mode processing. In the back-end, the IQ data may be processed differently depending on the ultrasound mode. The processed ultrasound data are transferred to the host processor of the PC for display. The user interface is also handled by the host.

2.2. The research interface

For the research interface, the IQ data are sampled at 16 MHz and may be decimated before being transferred to the ultrasound research interface (URI) module in the back-end. We have set the decimation factor such that a fixed number of samples along each vector are sent to the URI module. For example, in B and M modes, the decimation factor is selected such that only 512 samples along each vector are sent to the back-end. There is no decimation when the imaging depth is less than 2.5 cm, while the decimation factor is set to 2 when the imaging depth is between 2.5 cm and 5 cm. Larger decimation factors are used when imaging deeper tissues. The data in the color Doppler mode are decimated such that only 256 samples for each vector are sent to the URI module while only

![Fig. 1. Block diagram of the HiVision 5500 ultrasound machine showing the location of the research interface. The conventional mode processing has not been changed and the machine retains all the clinical features and frame rates in the research mode.](image-url)
128 samples from the Doppler range gate are sent in the spectral Doppler mode. Each complex baseband sample is represented in 32 bits (i.e., 16 bits for each of I and Q components).

As shown with the dotted lines in Fig. 1, the URI module spools the baseband data to a dedicated buffer in the main memory of the MAP processor. The MAP processor is an embedded media processor that has four execution units, on-chip data and instruction cache, a direct memory access engine, and on-chip controllers for interfacing to external memory and data buses [19]. The URI module allows acquisition of the raw ultrasound data in all the conventional ultrasound modes, including B, color Doppler, spectral Doppler and M. The raw data are continuously spooled to memory while imaging in any of the modes, and the spooling operation does not affect the frame rates and clinical features of the machine. By pressing a special sequence of keys on the keyboard of the ultrasound machine, the user can transfer the ultrasound data from the MAP memory to the hard disk on the ultrasound machine. Multiple sets of ultrasound data can be acquired during a patient study, and the data files can be offloaded from the ultrasound machine by connecting it to the network at the conclusion of the study. Since each MAP processor can have only 128 Mbytes of main memory shared between the processing modules and the research interface buffer, 32–48 Mbytes of memory are allocated for spooling the raw data. Multiple MAP (up to 4) processors could be used to increase the total URI buffer size up to 192 Mbytes and quadruple the amount of data that can be acquired.

To further increase this capacity, the ultrasound data could be losslessly compressed. However, the compression method must not only offer good compression ratios (e.g., >2), but also be computationally efficient such that it can compress the ultrasound data in real time using the available hardware resources (i.e., <10% of MAP computing cycles). We have developed such a method for losslessly compressing the complex baseband data on the HiVision 5500 in real time.

2.3. Lossless compression of complex baseband ultrasound data

Several researchers have focused on lossless compression of B-mode ultrasound images [20,21], but very few researchers have worked on compressing RF or IQ ultrasound data. Pesavento et al. [22] developed a method to compress RF ultrasound data before time-gain compensation (TGC), by using linear prediction followed by adaptive word-length coding. They obtained a compression ratio of 1.81–3.33, where the compression ratio (CR) is defined as

\[
CR = \frac{\text{Size of an uncompressed frame (bytes)}}{\text{Size of a compressed frame (bytes)}}
\]  

Although the method worked fairly well for pre-TGC RF data, the HiVision 5500 provides complex baseband data, which have already been time-gain compensated and hence have a larger dynamic range. Furthermore, the method by Pesavento et al. [22] is computationally quite expensive as it uses the Burg’s algorithm for every vector to determine the optimal coefficients for linear prediction.

Although the complex baseband data from the HiVision 5500 have a large dynamic range, most of the ultrasound data still do not occupy the entire 32 bits, thus the research interface can take advantage of this. The lossless ultrasound compression (LUC) method that we have developed uses linear prediction followed by entropy coding. Since ultrasound imaging is a real-time modality, consecutive frames (over time) are often correlated, and the ultrasound data from the same location in the previous frame can be used to predict values in the current frame. An improvement in the compression ratio can be obtained by entropy encoding the errors between the ultrasound data and their predicted values instead of encoding the ultrasound data. The errors are entropy-encoded using Rice–Golomb coding [23,24], which is equivalent to Huffman coding with a fixed codebook and can efficiently compress the ultrasound data in a single pass. The LUC module was developed to run on the MAP processor using C language with intrinsics [17].

The same LUC module was also implemented on the PC platform using generic C language and used to compress baseband ultrasound data sets acquired during B-mode scanning of the heart, liver, carotid artery and tissue-mimicking agar phantoms. Since the compression ratios that can be expected with the LUC method depend on the echogenicity of the tissues and the amount of motion between consecutive frames, the three anatomical locations (i.e., heart, carotid artery and liver) were selected because they differ widely in echogenicity of tissues and amount of motion between frames. Furthermore, these scans are representative of types of examinations frequently performed with ultrasound. The transducer was held steady for the heart, liver and carotid artery data acquisitions, while the agar phantom underwent freehand physical deformation during data acquisition. The imaging parameters, such as depth, time-gain control and gain, were set to typical values used clinically. The in vivo protocols on four human subjects were approved by the Institutional Review Board. For each of the four subjects, two independent data sets from each of the three anatomical locations, each consisting of 1 s of ultrasound data (30–72 fps), were combined to yield three datasets with 60–144 frames each. Similarly, a 2-s dataset consisting of 90 frames was acquired from the agar phantom. The compression time and CR achieved with the LUC module on a PC with an Advanced Micro Devices Sempron 3200+ processor (at 1.8 GHz) running Linux (Fedora Core 5) were compared to that with commonly-used compression programs, such as gzip [25] and bzip2 [26].

2.4. Off-line tools to extract the ultrasound data

Each acquired data set is stored to the hard disk of the ultrasound machine. We have developed a stand-alone exe-
cutable that runs on a PC and can decompress and extract the ultrasound frames from the archived data. The I and Q components for each frame are extracted to a separate file. For example, extracting the frames from a data set containing 6 s of B-mode ultrasound data acquired at 54 fps results in 648 files, and a typical clinical study involves the acquisition of 8–20 data sets. The baseband ultrasound data are now available for in-depth analysis and processing. The extraction executable also creates a text file containing information about the scan geometry, which can be used to perform scan conversion on the processed images before they are displayed [27].

3. Results

3.1. Comparing the LUC method with other lossless compression programs

Fig. 2 shows the distribution of compression ratios (CR) with the LUC method for each of the three datasets acquired from a volunteer and that from the phantom. The CR distribution for the heart and liver data has a smaller spread around the mean, with a higher mean CR of 2.43 being obtained for the heart data. For the heart data, even though the motion between consecutive frames is large, there are many areas with low echogenicity, thus resulting in a higher mean CR. For the liver data, the echogenicity is high, and the motion due to breathing and heart movements between frames is also large, resulting in a lower mean CR of 2.07. The carotid data have a wider spread with more frames having a higher CR due to the low echogenicity within the artery and less motion between frames, resulting in a high mean CR of 2.34. For the phantom data, the large motion between frames due to physical deformation and high echogenicity cause more frames to have a lower CR for a low mean CR of 1.81. The overall mean CR with LUC is 2.23 when all the frames are pooled together as shown in Table 1. The results from other three volunteers were consistent with Table 1. Thus, lossless compression of the baseband ultrasound data with the LUC method can more than double the amount of data that can be spooled in the available amount of memory.

Table 1 also lists the time required to compress an ultrasound frame with the LUC, gzip and bzip2 compression algorithms on the PC as well as the CR with gzip and bzip2. For the heart data, the CR of 2.43 obtained with LUC is 34% higher than 1.81 obtained with the best compression setting of gzip and 8% higher than 2.25 obtained with bzip2. Similar results were obtained for the liver dataset. The increase in CR with LUC was much higher for the carotid data, where the CR with LUC is 54% and 28% higher than that obtained with gzip and bzip2, respectively. For the phantom data, the CR of 1.81 with LUC was much better than 1.49 and 1.48 with the best and fastest setting of gzip, but only marginally better than 1.80 and 1.77 obtained with bzip2. For all the four data sets, the time to compress a frame with the LUC method was lower than gzip and bzip2. The fastest setting of gzip was 15% slower than the LUC method. At the same time, the overall CR with LUC was higher by 29%. The best setting of bzip2 yielded a 14% lower CR than that with LUC, but the time to compress a frame was more than four times of that with the LUC method. Of all the compression methods tested, the LUC method yielded the best CR for lossless compression of baseband ultrasound data and was also the fastest.

3.2. Performance of the LUC module on the MAP processor

Table 2 shows the time required to compress each frame of baseband ultrasound data for the heart, liver, carotid and agar phantom data sets on a single MAP processor running at 400 MHz. Each ultrasound frame from the heart, liver, carotid and phantom data sets consists of 122, 266, 298 and 358 vectors, respectively, while the number of samples per B-mode vector is fixed at 512. Acquiring a frame of baseband ultrasound data from the heart takes 13.9 ms, while the mean time to compress the frame on the MAP processor is 2.33 ms. As seen from the minimum and maximum compression time of 2.30 ms and 2.35 ms, the time to compress a frame is nearly constant. Similarly, the time to compress a frame from the liver, carotid and phantom datasets are nearly constant and much lower than the acquisition time. The ratio of compression vs. acquisition time depends on the imaging depth, and it ranges from 0.15 for the liver data to 0.29 for the carotid and phantom data.

It is desirable to have a lower ratio of compression vs. acquisition time because less computational resources would be required to compress the ultrasound data in real time. For example, a ratio of 0.29 means that 29% of the
computing cycles available on a MAP processor would be needed to compress the ultrasound data at the acquisition frame rate. When multiple processors are used to spool the ultrasound data, an even smaller fraction would be required for compression. For example, when the ultrasound data are being spooled across four MAP processors, every fourth ultrasound frame is compressed on the same MAP processor and only 7.3% of the computing cycles on each MAP are used for compressing the carotid and phantom data. Most of the processor’s cycles can thus be used on carrying out compute-expensive operations in back-end ultrasound processing.

3.3. Examples of preclinical studies conducted with the ultrasound research interface

We have extensively used the developed ultrasound research interface to acquire in vivo data from patients in the clinic as well as phantom and in vitro ultrasound data in the lab. Three examples that have benefited from the ultrasound research interface are presented. All the protocols for acquiring data from human volunteers and patients were approved by the Institutional Review Board, and a written informed consent was obtained from all subjects.

### 3.3.1. Noninvasive ultrasound elastography

Finger palpation, feeling the organs or tissues underneath, has been one of primary tools for detecting pathological tissues in the human body, e.g., thyroid and breast nodules. Over the last two decades, various ultrasound-based techniques have been developed to noninvasively obtain tissue stiffness information [28–31]. A main approach in ultrasound elasticity imaging is elastography, where tissue deformation or strain caused by compression is estimated using pre- and post-compression ultrasound signals. To evaluate the potential of ultrasound elastography for differential diagnosis of thyroid nodules, we recruited patients who were scheduled to undergo a thyroid biopsy at the University of Washington Medical Center (UWMC). Using the natural pulsation of the carotid artery as the compression source, we used the URI to acquire baseband ultrasound data from the thyroid and the surrounding tissues just prior to the biopsy. This ultrasound data acquisition for elastography took 5 min. Fifty-five patients participated in the study over 6 months. On offline processing of the ultrasound data, we found that the nodules with papillary carcinoma, the most common kind of thyroid cancer, are stiffer than other types of thyroid nodules ($p < 0.05$) [32]. The results indicate that ultrasound elastography could be a valuable tool for noninvasive differential diagnosis and management of thyroid nodules.

![In vivo B-mode and strain images of a papillary carcinoma](image)

Table 1

<table>
<thead>
<tr>
<th></th>
<th>Mean compression ratio</th>
<th>Mean compression time per frame (ms)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>LUC</td>
<td>gzip</td>
</tr>
<tr>
<td>Heart</td>
<td>2.43</td>
<td>1.81</td>
</tr>
<tr>
<td>Liver</td>
<td>2.07</td>
<td>1.61</td>
</tr>
<tr>
<td>Carotid</td>
<td>2.34</td>
<td>1.52</td>
</tr>
<tr>
<td>Phantom</td>
<td>1.81</td>
<td>1.49</td>
</tr>
<tr>
<td>Overall</td>
<td>2.23</td>
<td>1.61</td>
</tr>
</tbody>
</table>

Table 2

<table>
<thead>
<tr>
<th>Imaging depth (mm)</th>
<th>Frame size (samples)</th>
<th>Frame rate (fps)</th>
<th>Time of acquire a frame, $t_d$ (ms)</th>
<th>Time to compress a frame (ms)</th>
<th>$t_c/t_d$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heart</td>
<td>140</td>
<td>$122 \times 512$</td>
<td>72</td>
<td>13.9</td>
<td>2.30</td>
</tr>
<tr>
<td>Liver</td>
<td>170</td>
<td>$266 \times 512$</td>
<td>30</td>
<td>33.3</td>
<td>4.93</td>
</tr>
<tr>
<td>Carotid</td>
<td>50</td>
<td>$298 \times 512$</td>
<td>54</td>
<td>18.5</td>
<td>5.28</td>
</tr>
<tr>
<td>Overall</td>
<td>50</td>
<td>$358 \times 512$</td>
<td>45</td>
<td>22.2</td>
<td>6.31</td>
</tr>
</tbody>
</table>

### 3.3.2. Doppler vibrometry

The stethoscope is a venerable clinical instrument for the diagnosis of cardiovascular disease by hearing abnormal sounds from the human body, e.g., characteristic high-pitched diastolic heart murmurs in patients with atherosclerotic coronary artery stenosis [35,36]. However, its utility is limited when the abnormal sounds do not have sufficient...
intensity to reach the skin surface. We have developed a new method, called Doppler vibrometry, to detect and measure the coherent audio-frequency vibrations of the blood vessel wall and surrounding tissue associated with these flow murmurs in deep tissue [37,38]. To evaluate the Doppler vibrometry for noninvasively detecting coronary artery stenosis, we used the URI to acquire baseband ultrasound data from 49 patients who were suspected to have coronary artery disease and admitted to the UWMC for coronary angiography. We found that patients with angiographically minor stenosis (<50%) had a lower vibration energy than patients with moderate or severe stenosis (>50%) [39]. Fig. 4A shows the angiogram from a patient with severe luminal narrowing in the proximal segment of the left anterior descending artery. In Fig. 4B, high-amplitude vibrations can be seen in the tissues close to the stenosed region of artery while a diastolic murmur in the 300–1000 Hz range can be seen in Fig. 4C.

To perform vibrometry, the ultrasound data have to be acquired in the color Doppler and pulsed Doppler modes prior to any conventional processing steps. Since the vibrations can be transient and often occur only during certain phases of the cardiac cycle, the raw ultrasound data have to be acquired at high frame rates and should preferably span multiple cardiac cycles. During data acquisition, the ability to adjust the imaging parameters, such as color Doppler ROI, ensemble size, beam density, pulse repetition frequency and spectral Doppler range gate, is essential. Furthermore, the patients participating in the vibrometry study were symptomatic for heart disease, and the ultrasound data had to be acquired quickly without affecting their clinical care. The developed URI provided all these features, and the raw ultrasound data acquired by URI enabled the quantitative characterization of the vibration parameters, which was not possible using conventional Doppler processing.

3.3.3. Adaptive clutter rejection for 3D color Doppler imaging

Three-dimensional ultrasound color Doppler imaging (i.e., 3D CDI), in which 3D anatomical structure from B-mode imaging and blood flow information from Doppler imaging are integrated, is emerging as a useful tool for noninvasively evaluating complex vascular morphology with respect to surrounding tissues (e.g., tumors and transplanted organs) [40–43]. However, 3D CDI suffers from low image quality due to excessive flash artifacts caused by the remaining clutter originating from surrounding tissues and slowly-moving vessel walls [44–47], which negatively impacts clinical productivity [42]. Since conventional static clutter rejection methods, such as down-mixing (DM), have difficulty in adequately removing clutter, we have developed an adaptive clutter rejection (ACR) method that uses the underlying clutter characteristics to dynamically select an optimum filter at each location [48,49]. Using the URI we had developed, 3D in vivo kid-

![Fig. 3. (a) B-mode and (b) strain images for a thyroid nodule (indicated by arrows). The thyroid nodule appears stiffer than its surroundings. The lesion was diagnosed as a papillary carcinoma.](image)

![Fig. 4. (A) X-ray angiogram of a patient with coronary artery disease showing a severe narrowing in the proximal left coronary artery, (B) ultrasound color Doppler vibration imaging of the patient shows vibrations in the anterior myocardial tissues near the severe narrowing, and (C) Doppler vibrometry by placing the range gate in the region showing vibrations in (B) shows a diastolic murmur in the 300–1000 Hz range.](image)
ney data with color Doppler frames were acquired from 39 renal transplant patients. Fig. 5 shows the vasculature structures of a transplant kidney patient, where the residual clutter with the DM method in Fig. 5a significantly lowers the quality of 3D vasculature visualization for the transplanted kidney. As shown in Fig. 5b, the ACR method successfully removes the residual clutter while visualizing all the vascular structures, which was also confirmed quantitatively [49].

To fine-tune and evaluate the ACR method for 3D CDI, access to the unprocessed 3D color Doppler data were required. Since clutter often results from tissue motion that has a cardiac and/or respiratory origin, it was desirable to acquire raw ultrasound data spanning several, if not tens of, seconds. Furthermore, ultrasound data need to be acquired at a full clinical frame rate to evaluate the efficacy of the ACR method in suppressing flash artifacts in clinical settings. Furthermore, since 3D CDI detects weak echoes from the blood and is sensitive to noise in the ultrasound signal, it may not be desirable to use externally digitized RF signals from an ultrasound machine [3–6,9,10] for evaluating improvements in 3D CDI processing methods. In vivo evaluation of ACR for 3D CDI could not have been possible without access to the extended sequences of baseband ultrasound data in the color Doppler mode, enabled by URI.

4. Discussion

The OWH/NCI-sponsored workshop on infrastructure for improving ultrasound imaging methods identified the desirable specifications for basic and advanced ultrasound research interfaces. One characteristic required by both interfaces is the ability to acquire digital RF or complex baseband ultrasound signals. When the user enters the research mode on the Siemens Antares ultrasound machine, a special URI menu appears on the screen, which allows the user to acquire 16-bit digital RF data sampled at 40 MHz for a maximum of 200 Mbytes of data per acquisition [14]. RF data can be acquired in the B, M, color and spectral Doppler modes. The URI menu also allows the user to modify some imaging parameters, such as aperture size, focus depth, color ensemble size and color interleave. When operating at the highest frame rates and storing the RF data for the entire frame, only a few seconds of RF data can exceed 200 Mbytes. Thus, the user can window the data in the axial (i.e., depth) direction to decrease the RF data stored per frame, thus increasing the amount of time over which the data are acquired. Each data acquisition results in a data file that contains the RF data and a descriptive header that includes acquisition parameters, such as transmit frequency, time-gain control setting and beam geometry. An open-source MATLAB-based toolbox can then be used for postprocessing the RF data from the files [14]. On the Ultrasonix ES500, an FPGA-based ultrasound module performs the signal amplification, beam-forming and signal preprocessing, after which the ultrasound data are transferred to a PC running the Microsoft XP operating system. In the non-research mode, the examination software running on the PC provides the regular clinical user interface. However, when the research package on the machine is enabled, the examination software runs as an independent application in its own window. Moving the mouse to the edge of the examination software window frame causes “mouseover windows” to appear, which allows the user to modify transmit and receive parameters and acquire RF ultrasound data. The research package on the Ultrasonix ES500 allows the acquisition of 14-bit digital RF data sampled at 40 MHz. A limitation of this package is that the RF data acquired from every vector in the frame are restricted to an 8-cm range. Additionally, the frame rates in RF data acquisition mode are 66.7% lower than that achieved during routine clinical imaging without data acquisition. The length of time over which the RF data can be acquired is limited by the amount of PC memory available on the system. Additionally, the research package on the ES500 includes a software development kit, which allows researchers to develop custom applications that run on the PC and can receive raw ultrasound data from the ultrasound module.

Fig. 5. Rendered 3D color Doppler images from a kidney transplant patient by using (a) the conventional DM clutter rejection method and (b) the ACR method. The ACR method removes the flash artifact that is seen in (a) while retaining the vascular structures in the kidney.
In this mode, the examination software does not need to be run.

The research package that we have developed on the HiVision 5500 allows the acquisition of 32-bit digital baseband ultrasound data (i.e., 16 bits each of I and Q components) at the sampling frequency up to 16 MHz. The raw ultrasound data along the entire vector can be acquired at clinical frame rates, and the size of each data set can range from 128 Mbytes to 192 Mbytes, depending on the ultrasound mode. Using the real-time compression method that we developed, more than 6 s of ultrasound data (i.e., multiple cardiac cycles and at least one respiratory cycle) can be acquired in all the ultrasound modes. The ability to acquire raw ultrasound data over several seconds is desirable for applications that can benefit from averaging multiple cardiac cycles and at least one respiratory cycle) can be acquired in all ultrasound modes. The ability to acquire raw ultrasound data over several seconds is desirable for applications that can benefit from averaging multiple cardiac cycles, such as thyroid elastography using Doppler imaging, where a single volume takes several seconds to acquire without using a 2D array transducer.

Several research interfaces developed in the past involved the use of additional computers and specialized high-end digitizers attached to the ultrasound machine [3–6,9,10]. Although these systems are useful for in vitro experiments in the lab, their use in the clinic tends to be limited due to the difficulty in transporting the system and using them in the confined clinical exam rooms. Furthermore, an additional person is needed to operate the PC, and the data acquisition procedure can be cumbersome, thus elongating the duration of the study. In contrast, the HiVision 5500 is a compact cart-based machine, and the research interface involves only a software upgrade. We have been able to wheel a single machine between our research laboratory and the Radiology, Cardiology and Surgery departments at the University of Washington Medical Center. The research interface is simple to operate and can even be managed by the clinician scanning the patient.

Even though the URI on the HiVision 5500 has been useful in conducting research on diverse ultrasound applications, the interface has a few limitations that may make it unsuitable for some research. The raw ultrasound data acquired by URI only contain the ultrasound signal received at the fundamental carrier frequency. Currently, the higher harmonics of the ultrasound carrier frequency cannot be acquired with URI. Thus, it may not be used for research on tissue/microbubble harmonics. Furthermore, since URI was primarily developed as a tool to acquire the raw ultrasound data, researchers cannot modify the transmit/receive beamforming parameters. However, commonly-used imaging parameters, such as the center frequency, pulse repetition frequency, ensemble size, number of focal regions and imaging depth, can be easily adjusted through the regular clinical menus on the machine.

An advantage of the URI developed on the HiVision 5500 is that the interface is entirely developed in software using C language, with intrinsics only used for the core part of the LUC module. This URI could be made available to many researchers and clinicians who are currently using the HiVision 5500 machine via a software upgrade. URI can also be extended to incorporate application-specific data acquisition strategies. For example, for elastography using carotid artery pulsation, the strain signal-to-noise ratio may be the highest for ultrasound frames that are acquired in a certain phase of the cardiac cycle, such as systole. URI can be modified to only grab frames during systole, such that a single data set can now include ultrasound data acquired during systole over 30–40 consecutive cardiac cycles. Lossy compression techniques may also be considered for further increasing the duration over which the ultrasound data are acquired. For example, by encoding only the most significant 12 bits (of 16 bits) for each I and Q component, we could increase the compression ratio for the in vivo liver ultrasound data from 2.07 to 3.72. Similar increases in the compression ratio were obtained for the carotid, heart and agar phantom data.

Another example of the flexibility of the URI is the tagging of each raw ultrasound data frame with the spatial location/orientation of an ultrasound transducer, as determined by the Flock of Birds (Ascension Technology, Milton, VT) position sensor. The receiver is attached to the ultrasound transducer, and the Bird is connected to the RS-232 port of the host computer in Fig. 1. The 3D location and orientation of the transducer is captured by a small application running on the host computer and transferred to the MAP processor for tagging each raw ultrasound frame. This feature was particularly useful for freehand 3D ultrasound imaging, as demonstrated by the 3D CDI study.

The LUC method that we developed for losslessly compressing the baseband ultrasound data in real time has allowed us to more than double the amount of baseband ultrasound data that can be acquired. Not only is the compression ratio obtained with the LUC method better than commonly-used compression algorithms, the LUC method is fairly simple to implement and parallelize on modern programmable processors using single-instruction multiple-data extensions, such as MMX, SSE and 3DNow!. Furthermore, its computing time is deterministic and changes by less than 5% with varying statistics in the input data.

Although we have used LUC for complex baseband data, the technique can also be used for compressing RF data. To test this, we obtained several frames of RF ultrasound data by simulating the ultrasound signal from homogeneous phantoms [50] that were similar to the agar phantoms used for in vitro experiments. The RF data were demodulated and decimated to obtain the complex baseband data. With the simulated baseband ultrasound data, the mean compression ratio of 1.69 was obtained with LUC. The compression ratio for the corresponding RF data was 1.64, indicating that the LUC method could be used for compressing the RF data. Compression of RF ultrasound data on ultrasound machines, such as the Sie-
mens Antares and Ultrasonix ES500, could increase the amount of RF data that can be spooled in the available memory and potentially overcome the 8-cm range limitation on the Ultrasonix research package. Furthermore, compressing the RF/baseband data before transferring it from the front-end to the back-end can decrease the data bandwidth requirement on the internal bus.

In addition to aiding research in ultrasound imaging, the URI on the HiVision 5500 may also be used to refine newer applications before they are implemented on the programmable back-end for real-time performance. An example is the vibration imaging, where URI was used to acquire baseband ultrasound data from volunteers and patients with coronary artery disease. The data were processed off-line using different signal processing algorithms to evaluate their efficacy in identifying tissue vibrations in the presence of clutter and blood flow signal [38]. By considering the various trade-offs between their relative efficacy and computational requirement, we selected the algorithms that were then implemented for real-time vibration imaging on the HiVision 5500 ultrasound machine.

5. Conclusion

We have developed a research interface on the HiVision 5500 ultrasound machine by incorporating a new software module on the programmable back-end of the machine without affecting the clinical processing paths. Via our lossless compression technique running in real time, the research interface can acquire up to 6 s of raw complex baseband ultrasound data in all the ultrasound modes, including duplex and triplex modes. The clinical usability of the machine, including the frame rate, is unaffected by activating the research interface. All ultrasound imaging parameters, such as depth and width of imaging, pulse repetition frequency, focus, Doppler range gate, gain and time gain compensation, can be adjusted through the clinical menus on the machine. The research interface has been extensively tested and used for in vitro, in vivo animal and in vivo human studies. The interface has also helped us refine the processing algorithms for new and/or promising applications, such as vibrometry and elastography, before they could be implemented on the programmable back-end for real-time performance. The interface is written in C language, thus making it straightforward to customize and improve in the future. We believe that the research interfaces can contribute to accelerated advancements in ultrasound imaging by allowing more ultrasound researchers to test and clinically evaluate promising new applications.

References