

# Image-Based Gating of Intravascular Ultrasound Pullback Sequences

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**Abstract**—Intravascularultrasound (IVUS) sequences recorded *in vivo* are subject to a wide array of motion artifacts as the majority of these studies are performed within the coronary arteries of a beating heart. To eliminate these artifacts, an electrocardiogram (ECG) signal is typically used to gate (collect) those frames recorded at the points in time associated with a particular fraction of the cardiac cycle. However, this technique may be suboptimal for a number of reasons, among which is the difficulty of determining the optimal fraction at which to gate. This value is generally nonobvious. To circumvent this problem, we introduce a frame-gating method for IVUS pullbacks that mimics ECG (i.e., in the sense that it selects only one frame per cardiac cycle), but will automatically choose the fraction of the cycle that renders the most stable gated frame set. Stability here is gauged by measuring inter-frame similarity. Our method operates exclusively on the imagery data and does not require ECG or any form of image segmentation or other high-level image analysis. To validate our algorithm, we compare its behavior versus true ECG gating.

**Index Terms**—Cardiac cycle, electrocardiogram, frame gating, heart rate, intravascular ultrasound (IVUS).

## I. INTRODUCTION

**I**NTRAVASCULAR ultrasound (IVUS) is an invasive, catheter-based imaging modality that provides cross-sectional images of the interior of a blood vessel in real time and at video framerates. For studies of vessel morphology, plaque characterization, and other purposes requiring 3-D imagery, the transducer-bearing catheter can be gradually withdrawn through the vessel during recording. The resulting frame sequence is referred to as a *pullback* and allows the extent of the vessel swept by the sensor to be digitally reconstructed in the form of a volumetric image. However, motion artifacts relating to the beating heart may render these types of sequences difficult to analyze without subsequent gating. A simple and generally effective way to account for these motions is to gate the sequences according to an electrocardiogram (ECG) signal. By choosing an appropriate fraction of the interval between adjacent R-waves and only retaining the frame captured nearest in time to this

Manuscript received March 12, 2007; revised October 27, 2007. This work was supported in part by the National Science Foundation (NSF) under Grant IIS-0431144 and in part by the NSF Graduate Research Fellowship (SMO).

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Digital Object Identifier 10.1109/TITB.2008.921014

fraction during every heartbeat, the heart and imaging sensor are generally always oriented similarly during frame capture. In this way, the electrical behavior of the heart is used as an indicator of its physical pose. While ECG-based gating methods are simple to implement and have a long track record of use, they are potentially suboptimal for image stabilization purposes. For obvious reasons, ECG-based gating also cannot be applied to sequences for which associated ECG signals are not available.

We introduce a gating method for IVUS pullback sequences. This method emulates ECG by selecting one imaging frame per cardiac cycle, where each frame is taken at roughly the same point in the cycle. The algorithm we present is driven by the imaging data alone and does not employ ECG. This being the case, it cannot report the true fraction at which it is gating; however, the fraction it chooses is selected based on interframe stability criteria that help guarantee an optimally-stabilized gated set. As standard ECG gating is performed blindly with respect to the imaging data, it cannot provide such guarantees. In addition, as robust fully automated algorithms for IVUS segmentation do not currently exist, our method was developed so as to not require prior segmentation of the IVUS frames, feature tracking, or other advanced image analysis. Instead, we rely on pairwise frame comparisons that may be performed using common registration metrics. As a result, our method is computationally inexpensive and its most time-consuming portion is easily parallelized. Depending on the IVUS system employed, in most cases, we also do not require video preprocessing (e.g., noise reduction, artifact suppression, or masking of the nonimaged portions of the frame such as the catheter artifact).

This paper is organized as follows.<sup>1</sup> In Section II, we discuss prior research in the field, and in Section III, we introduce our gating method. In Section IV, we validate our pullback gating method by comparing it to the performance obtained by standard gating with synchronously-recorded ECG. We offer our conclusions in Section V.

## II. PREVIOUS WORK

The use of ECG signals in medical imaging is ubiquitous as a means of stabilizing image sequences that suffer from cardiac motion artifacts. As the features exhibited by this time-domain signal correspond closely to cardiac activity, ECG may be used as a noninvasive indicator of cardiac pose. The most apparent feature in this signal is the R-wave: due to its prominence, points in time during the cardiac cycle are typically referred to as a fraction of the interval between adjacent R-waves. Of importance is the fact that, in principle, the heart should be in

<sup>1</sup>Portions of this work have appeared in [1].

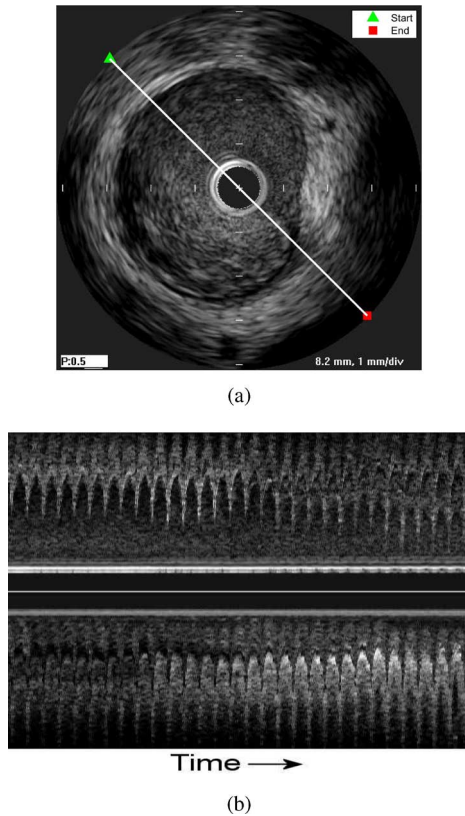


Fig. 1. (a) First frame of a pullback sequence. (b) Longitudinal slice through the stacked pullback volume. The “start” and “end” points of the line in (a) correspond to the top and bottom of the slice, respectively.

roughly the same pose at each point in time corresponding to the same R–R fraction.

Gating methods based on ECG are effective for two reasons: if data are always collected when the heart is in a similar pose, they will be more consistent. In addition, if the data are collected at a point in time when the heart is relatively motionless, motion-blur artifacts should be reduced. In IVUS, gating is used to reduce motion artifacts otherwise visible in the volumetric vessel images reconstructed from pullback recordings [1]–[4]. Without gating, the long (time) axis of these volumes presents sawtooth-like artifacts that confound their analysis. This is illustrated in Fig. 1.

The first question that arises in the context of gating is whether the ECG signal should be used at all. One practical difficulty with ECG is that of acquiring the signal and guaranteeing synchronization with the captured images. A more difficult conceptual problem is that of choosing the most effective R–R fraction at which to gate in order to obtain maximal interframe stability: this point is usually nonobvious. In modalities other than IVUS, the selection of the appropriate fraction may involve a function of 1) the site being imaged (i.e., which artery); 2) the heart rate of the subject; and 3) which modality is being employed [5], [6]. There is little reason to believe similar principles do not apply to IVUS. Regardless, for most studies in this field, the 0% point (i.e., the R-wave itself) is usually chosen. While this point is not necessarily optimal, selecting a fraction other than this can be subject to decreased performance in the presence of

certain heart rate variations, as interpolation from the R-wave landmarks is needed [7].

To circumvent some of these ECG-related problems and allow gating to be performed on image sequences for which ECG signals are not available, methods have been developed that aim to derive ECG-like signals from the sequences themselves. These methods rely on the ability to generate some derivative signal from the imagery that has the cardiac signal we are interested in embedded within it [8], [9]. The gating task then becomes one of developing a filter to reliably locate suitable landmarks in this signal. However, depending on how the signal is produced, it may gate at an essentially random fraction of the R–R interval. Due to frequency estimation issues, these methods may also not be robust with respect to variations in the heart rate of the subject during recording.

Given a high-level segmentation of each IVUS frame, it is possible to develop image-based gating algorithms that are capable of more intelligent behavior [10]. Unfortunately, reliable fully automated IVUS segmentation tools do not currently exist, limiting the applicability of these types of methods. Feature-tracking approaches relax the requirement of a complete segmentation, though they may remain computationally expensive. Such methods have been proposed for cardiac cycle estimation, both in IVUS [11] and 4-D ultrasound [12].

An image-based gating system has been presented for IVUS that claims to locate the frames captured nearest in time to the R-waves, but few details are provided about its operation [13]. For stationary-catheter IVUS sequences (i.e., those in which the catheter is not intentionally moved during recording), a method has been proposed by our group [14].

### III. MATERIALS AND METHODS

#### A. IVUS Sequences

Pullback sequences were obtained *in vivo* in the coronary arteries of normal swine using a 40-MHz IVUS system. The mechanically controlled pullback rate was 0.5 mm/s. The IVUS frame rate was 30 frames/s. Each recorded sequence contains  $\sim 2000$  frames, providing images from vessel segments  $\sim 30$  mm in length.

#### B. Dissimilarity Matrix Construction

The algorithm we describe operates on a dissimilarity matrix constructed from pairwise comparisons of the frames in an IVUS pullback sequence. Specifically, given an  $n$ -frame sequence  $F_{1..n}$ , a symmetric,  $n \times n$  proximity matrix  $\mathbf{D}$  is constructed where each entry  $d_{i,j}$  represents the dissimilarity between frames  $F_i$  and  $F_j$ . In principle, almost any registration metric may be used to accomplish this; here, we use normalized cross-correlation (NCC). For a pair of frames  $F_i(\cdot, \cdot)$  and  $F_j(\cdot, \cdot)$  of dimensions  $p \times q$ , this is given by

$$\text{NCC}(F_i, F_j) = \frac{\sum_{k=1}^p \sum_{l=1}^q [F_i(k, l) - \mu_i][F_j(k, l) - \mu_j]}{\sqrt{\sum_{k=1}^p \sum_{l=1}^q [F_i(k, l) - \mu_i]^2 \sum_{k=1}^p \sum_{l=1}^q [F_j(k, l) - \mu_j]^2}} \quad (1)$$

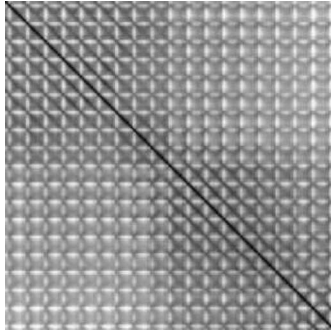


Fig. 2. Visualization of the dissimilarity matrix from the first 300 frames of a pullback sequence.

where  $\mu_i$  and  $\mu_j$  are the grey-level means of each image. As NCC normally returns values on the interval  $[-1, +1]$ , we let our dissimilarity function be as follows:

$$d_{i,j} = 1 - \text{clamp}[\text{NCC}(F_i, F_j)] \quad (2)$$

where  $\text{clamp}(x)$  returns 0 if  $x < 0$  and returns  $x$  otherwise. This results in a matrix with the following properties: 1) the main diagonal is zero; 2) all other entries are nonnegative; and 3) frame pairs that differ more in appearance represent a greater positive value than more similar frames. While an ultrasound-specific metric such as  $\text{CD}_2$  [15] or  $\text{CD}_{2\text{bis}}$  [16] could be employed in lieu of NCC, these three properties must still be enforced (e.g., through a simple linear remapping).

A typical matrix from a pullback sequence is depicted in Fig. 2. This matrix exhibits a periodic structure, as the changes in IVUS image appearance due to the beating heart are far more rapid than any other change that will occur during recording. While the appearance of the matrix is dominated by periodic motion, note also that its features gradually change over time (i.e., from top-left to bottom-right) as the catheter is mechanically withdrawn.

For illustration purposes, the matrices in this paper will be shown in full; however, in Section III-D, we will describe how to avoid the computational cost of constructing the full matrix.

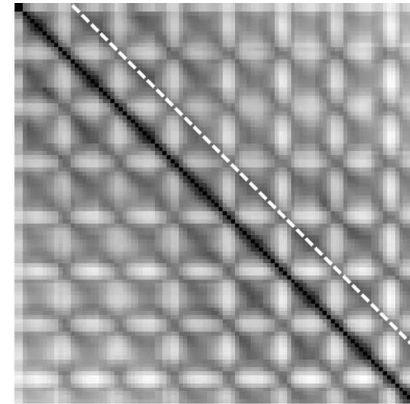
### C. Gating

We seek to extract a set of frames from the pullback sequence from which  $\mathbf{D}$  was derived such that 1) one frame is picked per cardiac cycle; 2) the frames are picked at the point in the cycle when the heart is maximally motionless; and 3) all the frames are at roughly the same fraction of the R–R cycle (i.e., so that in each frame the heart is in a similar pose).

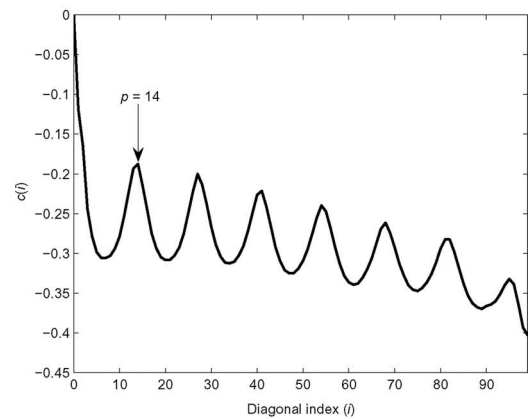
To begin, we obtain an initial estimate of the heart rate over the entire recording with the function

$$c(i) = -\frac{1}{n-i+1} \sum_{j=1}^{n-i+1} d_{i+j-1,j} \quad (3)$$

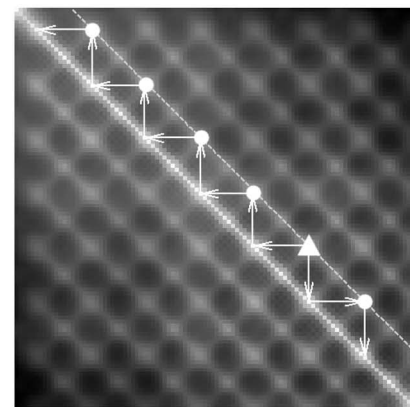
where  $i$  ranges from 1 to  $n$ . We then find the index  $p$  of the first peak from the left in this signal [Fig. 3(b)]. Due to the amount of redundancy present in the matrix, this point is usually unambiguous. The value  $p$  represents the average length, in



(a)



(b)



(c)

Fig. 3. (a) Dissimilarity matrix for the first 100 frames of a typical pullback sequence, along with dynamic-programming path (dotted line). (b)  $c$  function for the same matrix. (c) Matrix  $\tilde{\mathbf{D}}$  [derived from (a)], with the same dynamic-programming path overlaid (dotted), the origin of the stepping process ( $\Delta$ ) along with associated steps ( $\rightarrow$ ), and the final frame pairs representing the gated sequence ( $\Delta, \circ$ ).

frames, of the cardiac cycle over the complete recording. To observe why this is the case, note that if  $p$  is the known length of the cardiac cycle (in frames), then for a given frame  $i$ , there will be a diagonal-parallel valley around entry  $d_{i,i+p}$ , indicating that the heart has achieved the same pose at frame  $i + p$  as at frame  $i$ . The function  $c$  will exhibit peaks at these off-diagonal valleys.

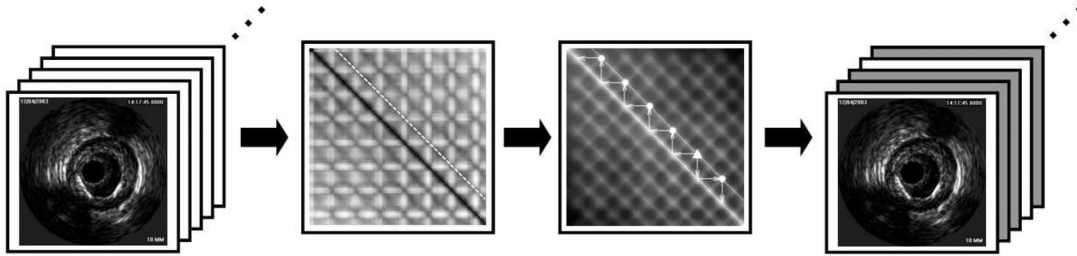


Fig. 4. Flowchart of complete gating process. From left to right: the initial ungated recording, the dissimilarity matrix  $\mathbf{D}$  with traced path, the filtered matrix  $\hat{\mathbf{D}}$  with steps indicating gated frames, and the final gated sequence with unused frames removed.

While at this point we have an estimate of the *overall* heart rate, we do not know, if given a *specific* frame  $i$ , the time offset from  $i$  at which the heart returns to the same pose. If this offset were exactly  $p$  for all frames, then we would expect that  $d_{i,i+p} < d_{i,i+p-1}$  and  $d_{i,i+p} < d_{i,i+p+1}$ . However, we expect perturbations from this due both to changing heart rate and to how the IVUS frame rate imposes a discretization on the re-valued heart rate in every cycle. To find a more accurate offset from each frame, we trace a path  $\mathbf{v}$  along the off-diagonal valley that represents the cardiac cycle length locally at each frame [Fig. 3(a)]. This is accomplished through a dynamic programming step that begins at  $d_{1,p}$  and traces down and to the right. That is, each step may proceed one entry downward, one entry to the right, or one entry down-right diagonally.<sup>2</sup> Tracing terminates when the path  $\mathbf{v}$  exits  $\mathbf{D}$  near its lower-right corner, globally minimizing the sum of all matrix entries through which the path traverses. A second tracing step may also be performed from the end-point toward the upper-left so as to make this procedure invariant to the starting point,  $d_{1,p}$ .

It remains to determine a set of frames, each captured at the same point in the cardiac cycle, which is associated with the point in phase when the heart is maximally motionless. We note that if the path we traced earlier passes through a point  $(i, j)$ , this indicates that the heart obtains the same position in frame  $j$  as it did in frame  $i$ . In addition, if  $i$  and  $j$  are captured when the heart is moving slowly, the valley around  $(i, j)$  will be more pronounced. There will also be low-dissimilarity structures in the matrix that are *perpendicular* to the main diagonal at these points (due to the cyclic nature of the motions of interest). To accentuate both of these features, we construct a filter in the form of an X-shaped, inverted Gaussian kernel

$$G_{\sigma}(x, y) = \begin{cases} -\exp\left(-\frac{x^2 + y^2}{2\sigma^2}\right), & \text{if } |x| = |y| \\ 0, & \text{otherwise} \end{cases} \quad (4)$$

where  $\sigma = \lceil p/3 \rceil$ . This filter is used primarily for localizing X-shaped features and only secondarily for denoising, as  $\mathbf{D}$  tends to be fairly clean for our purposes. We let  $\hat{\mathbf{D}} = \mathbf{D} \otimes G_{\sigma}$ , where  $\otimes$  denotes convolution. The matrix  $\hat{\mathbf{D}}$  exhibits maxima in areas, where a frame pair is associated by both high similarity and low motion.

<sup>2</sup>In practice, this tracing step operates only on a narrow band around the  $p$ th diagonal to prevent it from seeking the main diagonal. This band's width may be set to a fraction of  $p$  so that it adjusts to the heart rate of the subject.

To begin our final step, we find a single phase-associated frame pair that we are also most confident is at the maximally-stable point in the cardiac cycle. We trace through  $\hat{\mathbf{D}}$  along  $\mathbf{v}$  to find a global maximum,  $(s_0, t_0)$ . We use this starting point and  $\mathbf{v}$  to proceed stepwise upward and downward through  $\hat{\mathbf{D}}$ , collecting the frames that will comprise our gated sequence [Fig. 3(c)]. The downward step sequence is as follows.

*Step 1:* Let  $i \leftarrow 0$

*Step 2:* The point on the diagonal below  $(s_i, t_i)$  is  $(t_i, t_i)$ . Locate the column  $j$ , where  $\mathbf{v}$  intersects row  $t_i$ . If this does not exist, then we have reached the end of the sequence and may stop. Otherwise, let  $(s_{i+1}, t_{i+1}) = (t_i, j)$ .

*Step 3:* Following a simple gradient ascent, adjust the position of  $(s_{i+1}, t_{i+1})$  to the local maximum of  $\hat{\mathbf{D}}$ . This again helps account for heart rate/sampling variations.

*Step 4:* Let  $i \leftarrow i + 1$

*Step 5:* Continue to Step 2.

Stepping upward proceeds analogously. Assuming that, after these steps, the series of off-diagonal points that we collected are ordered chronologically (i.e., from top-left to bottom-right) as  $(u_0, v_0), (u_1, v_1), \dots, (u_m, v_m)$ , then the frame numbers in our gated sequence are indicated by  $\{u_0, v_0, u_1, v_1, \dots, u_m, v_m\}$ .

The complete process is illustrated in Fig. 4.

#### D. Computational Considerations

The primary source of complexity in the algorithm described here is the construction of the dissimilarity matrix  $\mathbf{D}$ ; this is an  $O(n^2)$  operation in the number of frames as  $n(n-1)/2$  pairwise comparisons must be performed. We note though that the algorithm actually only operates on a narrow band of  $\mathbf{D}$ . The width of this band is dependent on the length of the cardiac cycle as well as the IVUS frame rate. It remains to determine a reasonable width that will work in all cases. To begin, we let  $\rho$  be an estimate of the minimum heart rate, in beats/minute, we expect to encounter in any subject. More conservative estimates (i.e., lower values such as 30 beats/min) will result in greater processing time, but have no effect on accuracy. Next, let  $\phi$  be the frame rate of the IVUS system, in frames/second. Now, if during the construction of  $\mathbf{D}$ , we compare each frame to only its  $2^{\lceil \frac{60\phi}{\rho} \rceil}$  successors, we reduce the cost of matrix formation to  $O(n)$ . Note that the multiplication by 2 is only to provide padding in the convolution to find  $\hat{\mathbf{D}}$ . This results in a banded matrix of sufficient width for the algorithm to proceed normally.

TABLE I  
COMPARISON OF FOUR PULLBACK CASES

#	$n$	$\delta$	$n_{ecg}$	$n_{alg}$	$\mu_{phase}$	$\sigma_{phase}$
1	1828	30.5 mm	135	135	54%	8.1%
2	1945	32.4 mm	116	115	47%	4.4%
3	1774	29.6 mm	109	110	47%	12.0%
4	2283	38.0 mm	140	140	53%	7.8%

If a further reduction in processing time is required, the pairwise frame comparisons needed to create  $\mathbf{D}$  may be easily divided among multiple processors, as these comparisons are independent.

#### IV. RESULTS

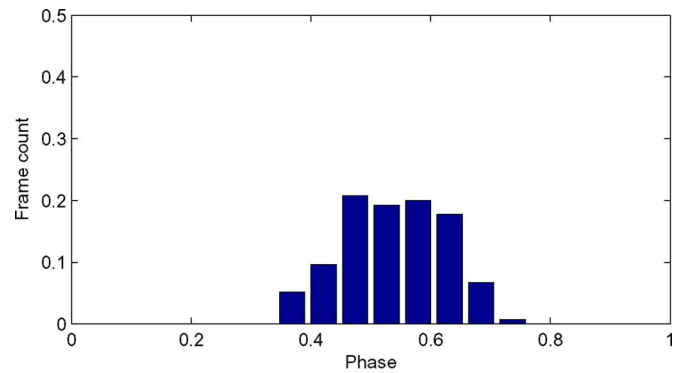
For the purpose of comparing ECG gating with our image-based gating method, four IVUS pullbacks were recorded with ECG *in vivo* in healthy swine. While the IVUS video and ECG were both recorded continuously, they were captured synchronously such that temporal correspondence could be made between each IVUS frame and its associated ECG signal. The mechanical pullback was also continuous at 0.5 mm/s. Properties of the frames picked by our method were then compared against those picked by ECG. These results are summarized in Table I, where  $n$  is the count of frames in each sequence,  $\delta$  is their physical length,  $n_{ecg}$  and  $n_{alg}$  are the counts of frames gated by ECG and by our algorithm, respectively, and  $\mu_{phase}$  and  $\sigma_{phase}$  are, respectively, the mean and standard deviation of the fraction of the R–R cycle of the algorithm-selected frames.

In Fig. 5, the relationship between the algorithm- and ECG-picked frames is illustrated in more detail. These histograms indicate the relative number of frames our algorithm selects, according to their phase with respect to ECG. For instance, if 40% of the frames in a sequence were picked at 50% of phase, the 0.5 bin of the histogram would reach 0.4 on the vertical axis. Case 1, for example, shows that approximately 80% of its frames were picked between 45% and 65% of phase.

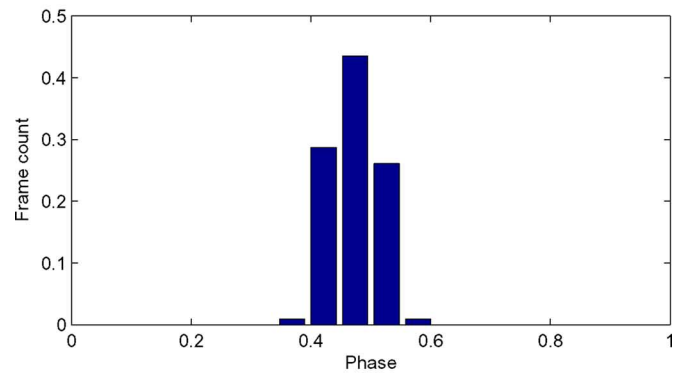
Note that the occasional  $\pm 1$  discrepancy between the number of frames picked by the two methods (Table I) and the isolated histogram outliers (Fig. 5) is due to the boundary conditions of the sequence, and is expected. The “spread” of the histograms is also expected, as the 970-Hz ECG signals must be resampled onto the 30-Hz frame sequences, leading to quantization effects. In general, though, lower  $\sigma_{phase}$  values indicate closer reproduction of ECG behavior. The significance of the  $\mu_{phase}$  values and other issues will be discussed further in Section V.

As our ultimate goal is the reconstruction of motion artifact-free pullback volumes, we visually compare these gating methods in Fig. 6 for our first two cases (the remaining cases are similar). Differences in appearance between the algorithm- and ECG-gated images for the same case are primarily due to their being captured at different fractions of cardiac phase. These differences can be dramatic, as IVUS image appearance can change significantly over the cardiac cycle.

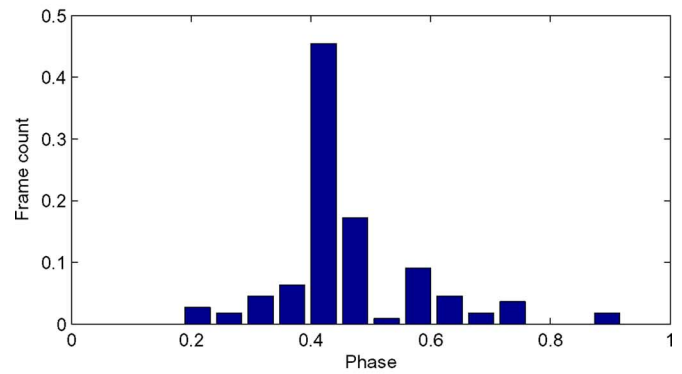
If we gauge the “stability” of a gated set according to how similar (i.e., well-correlated) each gated frame is with its gated successor, then we can derive statistics indicative of the success



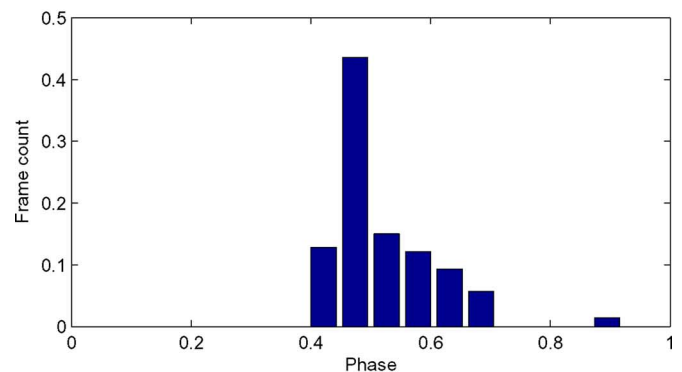
(a)



(b)



(c)



(d)

Fig. 5. Phase histograms for each of four cases. The  $y$ -axes are normalized for comparability.

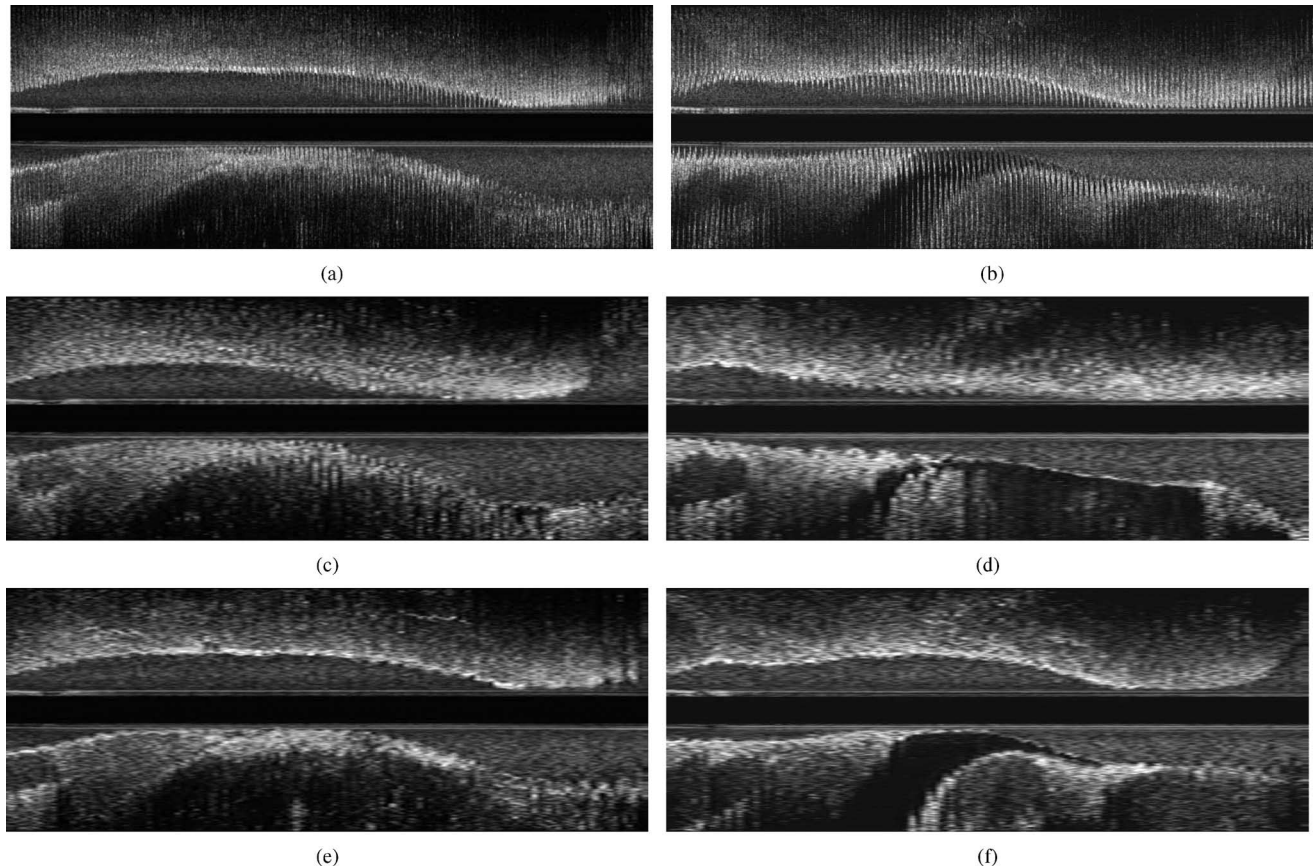


Fig. 6. (a) Ungated, (c) ECG-gated, and (e) algorithm-gated time-axis views of IVUS pullback volumes for case 1. (b), (d), and (f) Same for case 2. As in Fig. 1(b), the time of recording proceeds from left to right (i.e., from distal to proximal). Note that due to gating, there is an apparent loss of resolution on the horizontal axis between (a) and (b) and the remaining images; this is a known tradeoff of the gating process. This also leads to the impression that the ultrasound speckle has been “stretched” horizontally.

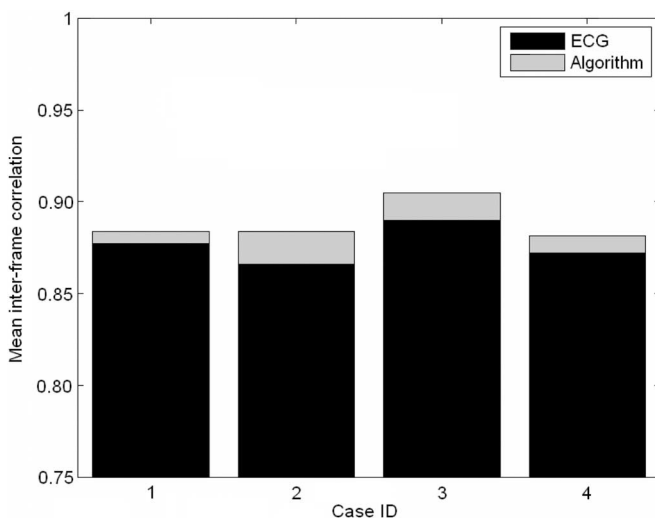


Fig. 7. Mean interframe correlation over all adjacent gated frames in the ECG- and algorithm-gated frame sets for the four cases.

of a particular gating method. We do this for our four cases in Fig. 7. Higher correlation indicates a more stable frame set. Here, we observe that the 0% gating point usually chosen with ECG may not be appropriate, and in spite of our algorithm lacking the support of ECG, it has provided a more stable frame set in all cases. However, it should be noted that interframe corre-

lation is only one possible metric of stability, and others could be devised based on the minimization of error for a particular diagnostic study.

## V. CONCLUSION

We have described an image-based frame-gating method for IVUS pullback sequences. This method relies on the analysis of dissimilarity matrices derived from pairwise frame comparisons. We note that the algorithm’s R–R fraction selection varies slightly by subject, as we would expect from prior research (Sec. II). Such variability could not be obtained by blind ECG triggering based on a fixed R–R fraction. It is interesting to note that a previous study performed in humans [17] has indicated that a gating fraction of 80–90% is more effective than 0%. This suggests the possibility that we would obtain systematically different results with our algorithm if we were to apply it to human subjects (i.e., as opposed to swine).

While we have chosen to select the most visually-stable points in the sequence as our gating points, these tend to be at roughly the same R–R fraction ( $\sim 50\%$ ). This being the case, truer ECG emulation could be accomplished by temporally shifting the algorithm-selected frames appropriately. However, as previous studies have hinted and our results show empirically (Fig. 7), ECG may not be a reliable standard to aspire to.

As our method relies on the visible manifestation of heart motion in the sequence, portions of a pullback, where no such motion is apparent, are incapable of being analyzed. Fortunately, this is a rare occurrence: the only situation we have noted where this occurs consistently is when the pullback approaches the ostium, where only blood (which is featureless) is in the field of view of the transducer. This exception may be easily accounted for by truncating the sequence at the point when it ceases to record useful data. We have also not encountered any confounding effects due to, e.g., respiratory motion, as the magnitude and frequency of cardiac motion far outweigh any other factors.

We have not tested our method on pathological cases (e.g., subjects with irregular heartbeat) and so have not modeled how these would affect performance and the regularity of the dissimilarity matrix. Future work will involve further validation and refinement to account for such special cases. It will also be of interest to determine if using ECG in conjunction with an algorithm similar to our own could provide better results than either method individually.

A more complete discussion of the topics presented in this paper may be found in [18].

#### ACKNOWLEDGMENT

We would like to thank M. Vavuranakis, T. Papaioannou, C. Stefanadis, A. Tellez, and all the members of the Ultimate IVUS team for their valuable assistance. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the NSF.

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