

Combined Ultrasound Speckle Pattern Similarity Measures

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Abstract. We present an enhanced block matching approach to improve displacement accuracy in ultrasound sequences using a combination of matching measures. The first measure uses the normalised cross correlation for regions of strong signal and the second measure CD_2 , specifically for regions of speckle determined by the speckle signal to noise ratio. We also show displacement field results for simulated speckle and *in vitro* data.

1 Introduction

With modern ultrasound machines providing realtime sequence digitisation, motion estimation research in this area for noise filtering, tracking and registration has increased. In this paper we investigate a novel practical alternative to elastography using speckle tracking to infer tissue motion. Our contribution includes applying two speckle pattern similarity measures, adapting to regions of varying signal and noise within a multiresolution framework with displacement processing. We focus on synthetic and *in vitro* interframe and trajectory displacement accuracy.

Scatter occurs when small imperfections (scatterers) cause seemingly random reflections and refractions of the sound wave. Scatterers account for a decrease in image quality, causing blurring and decreased intensity at impedance boundaries, while within the medium they create speckle. The statistics of the signal depends on the density of scatterers, with a large number of randomly located scatterers following a Rayleigh distribution (fully developed speckle). These conditions are seldom met, resulting in different statistical speckle models being used.

Using B-mode images 2D tissue motion can be measured by tracking the movement of the speckle produced by the back scattering of the ultrasound itself. To date, the most popular approaches to speckle tracking use 2D region-based matching that assumes the optical flow is constant over a defined region, for example [1], favouring normalised cross correlation (NCC) compared to other matching criteria, and optical flow to estimate tissue motion. Cohen and Dinstein [2] and Boukerroui et al. [3] use an alternative speckle matching measure (CD_2), that assumes the speckle patterns in ultrasound images can be represented by a multiplicative Rayleigh distributed noise.

In our recent work [4] accurate interframe displacements and motion trajectories of individually tracked blocks were reported, using hierarchical blocks and a multiple scale NCC similarity measure. Focusing on musculoskeletal ultrasound, in deeper body regions a general reduction in correlation as a result of increased speckle noise was observed, affecting the correlation measure. Here, by combining two matching measures, we aim to maintain accuracy in strong signal regions using the first measure NCC, with low correlation and a low speckle signal to noise ratio (SNR) indicating necessary re-tracking using the second measure CD_2 .

In this work, we favour displacement estimation with displacement post-processing, rather than speckle filter pre-processing and then displacement estimation. Although much research has been aimed at removing speckle to enhance ultrasound image understanding, many schemes produce increasingly homogeneous regions. This is due to features that are the same scale as the speckle being eliminated [5] impeding local motion estimation. Filter performance tends to be measured by quantifying edges and boundaries, with speckle preservation and fluctuation reduction measured using the co-occurrence matrix and localised mean and standard deviation (speckle SNR). In our situation all echo information is maintained, justifying a region-based motion estimation approach that has some inherent robustness to speckle incoherence and machine noise for speckle tracking.

Although substantial research exists using low frequencies at 3 – 7 MHz (abdominal [2], cardiac and breast [3]), we focus on higher frequencies 8 – 16 MHz for musculoskeletal diagnosis, capturing higher resolution images at a reduced penetration depth. This is due to attenuation where the signal is reduced by approximately 1 dB/cm/MHz [6]. We used three different probes (with bandwidths 5 – 10, 8 – 16 and 10 – 22 MHz), to capture perfect conditions of an *in vitro* tendon section in a still water bath with clamped probe, and normal conditions of an *in vivo* freehand scanning of muscle. Sequences captured with perfect conditions were temporally stable resulting in high tracking

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accuracy using a single NCC tracking scheme. Sequences captured with normal conditions highlighted a reduction in correlation in areas of speckle, tending to occur in the lower regions, Fig. 1.

In the next section we concisely describe our datasets of simulated ultrasound speckle and *in vitro* tendons. Section 3 explains the combined matching measure approach, also defining displacement post-processing and interframe error measurement. Section 4 demonstrates and discusses sample interframe and trajectory results.

2 Ultrasound Datasets

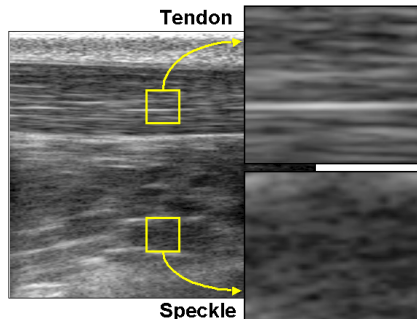
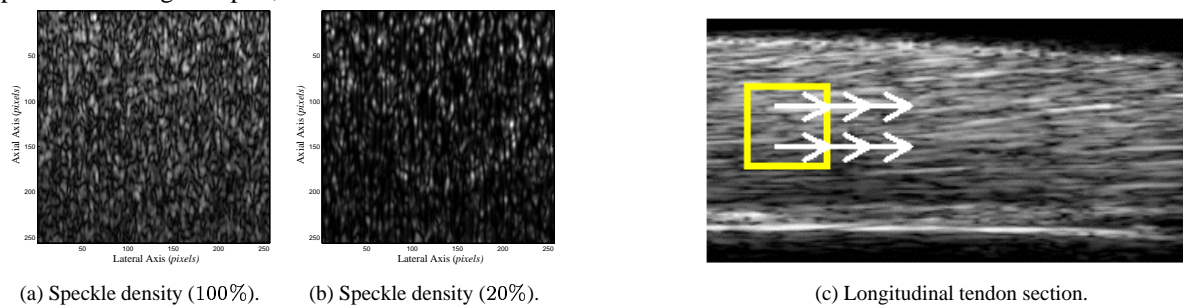


Figure 1. Achilles tendon with enlarged images of tendon and speckle.

To evaluate the advantages of the proposed method we generated spatially uniform and temporally stable speckle textures simulating an echographic speckle sequence [7], illustrated in Figs. 2(a)-2(b). The point spread function (PSF) $H(x, y)$ is assumed to be a Gabor function and the scattering function $T(x, y)$ a normally distributed random field that represents the population of scatterers being imaged. Convolution with the PSF yields the resulting RF echo data $I(x, y) = H(x, y) \otimes T(x, y)$, with envelope detection producing the desired image of echo magnitude. Speckle density is varied generating sequences of high (100%) and low (20%) speckle and varying speckle (containing half of each of these). To measure robustness against speckle reduced temporal coherence, we corrupt $I(x, y)$ with multiplicative Rayleigh distributed noise $\hat{I}(x, y) = \eta_m I(x, y)$ where $\eta_m \sim R(I) = \frac{I}{\sigma^2} \exp(-I^2/2\sigma^2)$ with a non-zero mean specified by the single distribution parameter σ .

Several *in vitro* sequences were captured using an equine tendon that was pulled 3, 6 and 10 mm at known rates and loads whilst continuously scanning using an 8 – 16 MHz clamped probe, Fig. 2(c). All sequences consist of 30 frames (the default acquisition length) captured at ≈ 10 Hz and quantised into 8 bits. All cycles included a positive and negative pull, similar to *in vivo* extension to flexion motions.



(a) Speckle density (100%).

(b) Speckle density (20%).

(c) Longitudinal tendon section.

Figure 2. Sample images of (a) high (100%), (b) low (20%) density speckle and (c) an *in vitro* frame.

Typically, all ultrasound sequences will contain varying amounts of speckle and regions of underlying signal in different quantities. Therefore, we first analyse *in vitro* tendon sequences to demonstrate the good tracking results from using the NCC measure. Second, we analyse simulated speckle sequences to demonstrate the improvement of our proposed method where the speckle density varies across an image. Further information, including *in vivo* experiments using data as shown in Fig. 1, is available online*.

3 Proposed Method

The first measure NCC, applied in [4], assumes an increased SNR from high frequencies and sparse scatterers as shown in the tendon region in Fig. 1. Although we have found the correlation typically high, as described above, speckle noise reduces matching, highlighting the necessity of a suitable second measure. It must also be stated that other causes of correlation reduction are a lack of signal (probe de-coupling or curvilinear tendons), or signal saturation (incorrect gain controls or bone), or minimal features, causing problems for any similarity measure.

To combat reduced NCC accuracy in regions of increased speckle noise, we propose the use of a secondary measure instead of the NCC, namely the CD_2 measure, introduced by Cohen and Dinstein [2]. Recently, Boukerroui et al. [3] showed that in regions of fully developed speckle CD_2 is a more precise measure than for example, NCC or mean square error (MSE). CD_2 assumes (to be matched) blocks x and y from frames f_t and f_{t+1} are corrupted by independent multiplicative Raleigh distributed noise, representing uniform dense speckle. Log-compression

transforms the multiplicative noise to additive, denoted $\tilde{I}' = \ln(I')$ and $\tilde{I} = \ln(I)$. Following [3], we maximise the CD_2 objective function, where i and j are block and pixel indexes in $M \times N$ blocks, defined as:

$$CD_2 = \sum_{j=1}^{MN} \{(\tilde{I}'_{i,j} - \tilde{I}_{i,j}) - \ln(\exp(2(\tilde{I}'_{i,j} - \tilde{I}_{i,j})) + 1)\} \quad (1)$$

We use the two measures with multiple block scales, applying the NCC as the primary matching measure due to its high accuracy in low speckle density regions. However, we require an appropriate means of determining the amount of local speckle present. For this we use the SNR given by the ratio of the mean I_μ to the standard deviation I_σ of those pixels contained within a local region I , defined as $\lambda = \frac{I_\mu}{I_\sigma}$. In an area of uniform dense speckle, Wagner et al. [8] have determined an expected SNR value of $\lambda = 1.91$. We verified this value with *in vivo* data using multiple scaled regions of a uniform area, located at the focal zone of the ultrasound beam, and computed the mean SNR. Results showed that the mean SNR converged at $\lambda \approx 2$, hence we use a tolerance, empirically derived at 25%, to ensure a reasonable speckle sensitivity for *in vivo* images where speckle is seldom uniform. Only regions of $M \times N$, where $M, N \geq 16$ were able to determine reliably that a region contained uniform speckle. Therefore, we propose to use and apply either the NCC or the CD_2 measures, determined by the SNR, where $\lambda = 1.91$, which implies the speckle density present in a region:

$$\text{measure} = \begin{cases} \text{NCC} & \text{if SNR} > 1.25\lambda \\ \text{CD}_2 & \text{otherwise} \end{cases} \quad (2)$$

The SNR increases with a low amount of speckle (reaching infinity for specular reflection), justifying the NCC measure. However, SNR decreases for high amounts of speckle, indicating that the same block should be re-tracked using the secondary CD_2 measure. This is evaluated using the associated reference and candidate blocks in a full search with the same extents as the primary NCC measure for the larger scales. The speckle SNR is used as an indicator of speckle content (rather than correlation), as typically featureless regions of uniform speckle produce high correlation coefficients with surrounding speckle. Unfortunately the SNR is also sensitive to other image components, for example, feature boundaries resulting in a low local SNR, therefore we also check to ensure the NCC peak correlation coefficient c_{max} is low. This approach of alternating specific speckle and signal similarity measures using SNR allows the proposed method to adapt to image content.

Once the combined matching method is applied we perform displacement post-processing. Spurious velocity vectors are inevitable from any tracking process and are not always obvious. Potential causes are from noise or artifacts where multiple block scales have insufficient encapsulated features. Using a coherence based post-processing algorithm, adaptive weighted vector median filter (WVMF) [9], vector displacements are smoothed if inconsistent with their dominant neighbours whilst preserving motion boundaries. Given n displacements inside a sliding window, the WVMF output is a median displacement vector \mathbf{d}^m that minimises the cumulative weighted p -norm distance between an individual \mathbf{d}_i and neighbouring \mathbf{d}_j displacements. A displacement is substituted with \mathbf{d}^m if the cumulative weighted p -norm distance between \mathbf{d}^m and \mathbf{d}_i is significant, expressed as:

$$\sum_{i=1}^n w_i \|\mathbf{d}^m - \mathbf{d}_i\|_p \leq \sum_{i=1}^n w_i \|\mathbf{d}_j - \mathbf{d}_i\|_p \quad j = 1, 2, \dots, n \quad (3)$$

For combined measures our weighting uses the mean of both the NCC and CD_2 measures, defined $w = 0.5[c_{max} + (1 - \|CD_2\|)]$, ranging between 0 and 1. This technique can be iterative and lends itself to both interframe and trajectory smoothing with low computation.

To quantify displacement accuracy the error between the correct groundtruth displacement $\mathbf{d}_{t,c} = (u_c, v_c)$ and the estimated displacement $\mathbf{d}_{t,e} = (u_e, v_e)$ is measured by the angular error [10] combining errors in magnitude and direction into a single value:

$$\psi = \cos^{-1}(\check{\mathbf{d}}_c \cdot \check{\mathbf{d}}_e) \quad (4)$$

where ψ is the angle between the correct spatiotemporal vector $\check{\mathbf{d}}_c = \frac{(u_c, v_c, 1)^T}{\sqrt{u_c^2 + v_c^2 + 1}}$ and, the estimated spatiotemporal vector $\check{\mathbf{d}}_e = \frac{(u_e, v_e, 1)^T}{\sqrt{u_e^2 + v_e^2 + 1}}$. Further, displacement fields are used for displaced frame differencing, quantifying the root mean square (RMS) error between a backward reconstructed frame and the actual next frame.

4 Displacement Results and Discussion

Trajectories, which quantify continuous temporal displacements in sequences, were estimated for an *in vitro* region of tendon. The absolute errors (AE) between the groundtruth and mean estimated trajectories are summarised in

Table 1. The maximum AE was noticeable near the end of each pull cycle, due to the clamped tendon not returning to its original resting state. The mean AE remained low using NCC and combined measures. The NCC consistently produced high correlations $> 91\%$, producing significantly more accurate displacements compared to the single CD_2 and MSE measures. As mentioned later, due to the lack of speckle, using combined measures proved to be only as good as the single NCC measure. Typically, for *in vivo* data the speckle SNR instigates the usage of the NCC in minimal speckled (tendon) regions and the alternative CD_2 measure in dense speckle areas.

Pull mm	MSE			NCC			CD_2			NCC/ CD_2 Combined		
	Max	Mean	STD Dev	Max	Mean	STD Dev	Max	Mean	STD Dev	Max	Mean	STD Dev
^a 3	4.79	3.60	3.53	2.16	2.69	1.21	5.57	3.88	2.23	2.16	2.71	1.22
^a 6	8.97	3.78	4.46	2.62	2.45	1.39	5.32	4.58	2.13	2.63	2.44	1.37
^a 10	25.74	10.35	7.96	5.54	7.79	3.12	19.30	9.00	4.11	5.55	7.79	3.12

Table 1. Summary of trajectory absolute error for *in vitro* tendon data for 3 pulls.

^aSettings: WVMF iterations = 2 and multiple block scales where $M \times N = \{64, 32, 16, 8\}$.

Sample results in Table 2 quantify a comparative analysis between our proposed NCC/ CD_2 combined approach and CD_2 , NCC, MSE measures. The key improvement from our combined approach is observed in sequences with regions of varying speckle density (from multiple objects for example tendon and tissue), whereby using the appropriate measure allows for local signal variation; this is important for *in vivo* analysis. For regions of homogeneous speckle (high or low), the best accuracy is only as good as the appropriate single measure.

Speckle Pattern Measures	High Density Speckle (100%)			Low Density Speckle (20%)			Varying Density Speckle		
	Mean ^o	STD Dev ^o	RMS	Mean ^o	STD Dev ^o	RMS	Mean ^o	STD Dev ^o	RMS
^b NCC/ CD_2 Combined	7.13	6.46	9.22	13.78	15.85	6.56	9.62	10.62	7.48
^b CD_2	7.13	6.47	9.22	15.95	16.63	7.55	11.46	13.91	9.33
^b NCC	7.39	6.60	9.23	13.72	15.83	6.56	11.66	13.42	8.10
^b MSE	7.58	7.45	13.27	23.74	24.55	14.20	13.48	18.05	10.15

Table 2. Interframe velocity angular error and displaced frame difference RMS error.

^bSettings: Affine deformation (4 pel) sequences without noise using WVMF iterations = 0 and a block scale where $M \times N = \{16\}$.

Consequently, in Table 3 we show further results specifically for varying density speckle. These results illustrate a marked improvement compared to using a single measure. For frame pairs with applied noise, the NCC measure produced increasing errors, resulting from a reduction in correlation ranging between 96.84% – 99.99% to 72.75% – 78.15% between best (no applied noise) and worst $\sigma = 0.8$ cases. WVMF noticeably improved all results from just 2 iterations using an 8 neighbourhood region, maintaining a relatively low velocity angular error, for example 7.06 with and 9.62 without. Similar results were obtained from testing over 100 frame pairs.

Speckle Pattern Measures	<i>Uncorrupted</i>		$\eta_m \sim \sigma = 0.4$		$\eta_m \sim \sigma = 0.8$	
	Mean ^o	STD Dev ^o	Mean ^o	STD Dev ^o	Mean ^o	STD Dev ^o
^c NCC/ CD_2 Combined	7.06	6.09	7.41	7.02	11.10	12.44
^c CD_2	7.54	6.92	9.94	10.34	12.84	15.09
^c NCC	7.64	6.09	8.53	9.12	12.10	13.25
^c MSE	7.30	7.49	20.18	18.81	21.28	20.09

Table 3. Interframe velocity angular error for 3 cases of noise corrupted frames of varying density speckle.

^cSettings: Affine deformation (4 pel) sequences with varying noise using WVMF iterations = 2 and a block scale where $M \times N = \{16\}$.

We have demonstrated that using a combination of speckle pattern similarity measures improved interframe and trajectory performance, validating our approach on synthetic speckle and *in vitro* datasets. The real improvement in displacement accuracy is obvious from analysing frames that contain subregions ranging from dense speckle with noise characteristics that are purely multiplicative Rayleigh, to sparse stable speckle, to minimal speckle mixed with a strong underlying signal, all features typically found in *in vivo* data.

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