Accurate Doppler Velocity Estimation using a Non-linear Frequency-Modulated Acoustic Pulse

J. S. Dhanoa Member IEEE, R. F. Ormondroyd Member IEEE, E. J. Hughes Member IEEE

Department of Aerospace, Power and Sensors,
Cranfield University, Royal Military College of Science,
Shrivenham, SN6 8LA, United Kingdom
j.s.dhanoa@cranfield.ac.uk, r.f.ormondroyd@cranfield.ac.uk, e.j.hughes@cranfield.ac.uk

Abstract- **This paper presents a novel method for estimating the Doppler velocity using complex broadband waveforms such as non-linearly chirped waveforms in SONAR systems. For such waveforms, even when the Doppler velocity is constant, the Doppler shift on these waveforms varies across the bandwidth, resulting in a frequency spread, and traditional Doppler velocity estimators based on estimating a single frequency shift do not perform well. The new method uses Evolutionary Algorithms to relate the spread in the spectrum of most complex wide bandwidth signals to the Doppler velocity that caused it. Furthermore, if the signal return is affected by multiple targets, each with Different velocities, the method will resolve each Doppler velocity. The use of this method as a novel means of mitigating range-Doppler coupling is also presented.**

I. INTRODUCTION

Simple SONAR systems use narrowband pulses for range estimation. By measuring the frequency shift in these pulses, it is possible to obtain a coarse Doppler velocity estimate. These methods of Doppler velocity estimation have often been based on fast Fourier transforms (FFT). Recently, Susaki [1] has proposed a method for the improved estimation of Doppler velocity using a narrowband SONAR signal. The method estimates the Doppler shift on a pulse-to-pulse basis using an FFT. The errors from the single pulse estimates are reduced by averaging the Doppler estimate over a number of pulses. However, the Doppler-induced shift in frequency is estimated using peak detection and, therefore, the accuracy of the measurement of Doppler shift is limited by peak broadening as a result of windowing due to the finite length of the acoustic pulses over which the FFT is obtained.

More complex SONAR systems use wideband signals to obtain accurate long-range estimates of targets using pulse compression techniques [2]. Recently, Kay and Thanos [3] have proposed the use of complex waveforms as a means of improving the target detection in the presence of high levels of reverberation. However, these wideband waveforms, which may have non-linear time-frequency variations, do not readily lend themselves for Doppler velocity estimation using the current methods. In fact, the changes that occur in these waveforms due to the effect of an unknown Doppler velocity can severely degrade their performance as a result of imperfect pulse compression. This results in a decrease in the correlator output [2].

To overcome this particular limitation, the use of Doppler tolerant waveforms has been proposed by Doisy *et al* [4] Being Doppler tolerant however, it is difficult to accurately estimate the target Doppler velocity from them! In addition, it is also difficult to design waveforms that are Doppler tolerant over a wide range of Doppler velocities. It is desirable, therefore, to have a method that can estimate the Doppler velocity from complex wideband waveforms and then use this Doppler estimate in subsequent processing to compensate for the performance degradation.

The estimation of Doppler velocity using a wideband signal can be considered as a problem of spectral estimation of the Doppler *spread* in the frequency of this signal. Recent methods based on time-frequency distributions in conjunction with Hough or Radon transforms, have been used to detect and estimate chirped waveforms as a two-part process. When the signal is a non-linear chirp however, such methods are computationally intensive. Furthermore, the impact of the Doppler spread on non-linear chirps is to distort the shape of the chirp in the time-frequency distribution and this can make reliable extraction of the Doppler parameters very difficult.

In some circumstances, it is possible for the SONAR return to comprise multiple overlapping pulses, each with a different Doppler spread. An example of this is when there are multiple targets, each with a different velocity. Under these conditions, it is difficult to estimate accurately and simultaneously the Doppler velocity components from the composite signal using traditional methods. This problem is compounded by the fact that in general there is no *a priori* knowledge of the exact number of overlapping SONAR returns.

This paper has three aims. First, it introduces a new method based on Evolutionary Algorithms for Doppler velocity estimation on a pulse-to-pulse basis using frequency-modulated acoustic pulses in SONAR systems. Second, it demonstrates that the proposed method can estimate *multiple* Doppler velocities that may exist in a SONAR return consisting of multiple overlapping frequency-modulated pulses due to the different velocities of the multiple targets. Finally, the problem of range-Doppler coupling of these frequency-modulated pulses is considered and results are presented whereby range-Doppler coupling is mitigated using the Doppler velocity estimates, thereby providing a more accurate range estimate. The key feature of this method is that it relates the Doppler-induced frequency spread of the wide-band signal spectrum directly to the Doppler velocity that caused the spread.

Whereas traditional FFT-based methods suffer from the problem of windowing, the proposed method exploits the presence of the sidelobes due to the finite length window and, as a result, the method is effective at signal to noise ratios (SNR) as low as -15dB. In addition to estimating the Doppler velocity, the proposed method also estimates the amplitude and phase of the received pulse(s).

II. EVOLUTIONARY ALGORITHMS

Evolutionary Algorithms are optimization procedures that operate over a number of cycles (generations) and are designed to mimic the natural selection process through evolution and survival of the fittest [5].

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A *population* of P independent individuals is maintained by the algorithm, each individual representing a potential solution to the problem. Each individual has one *chromosome*. This is the genetic description of the solution and may be broken into m sections called *genes* that represent a single parameter in the problem. Therefore, a problem that has eight unknowns would be described by a chromosome with eight genes.

The three simple operations found in nature, natural selection, mating and mutation are used to generate new chromosomes and therefore new potential solutions. Each chromosome is tested at every generation using an *objective function* that is able to distinguish good solutions from bad ones and score their performance. Based on this test, a new population of chromosomes is generated in which the highest scoring chromosomes of the previous generation are retained and new ones created using mutation, selection and crossover. To maintain the population size, the lowest scoring chromosomes are discarded to make room for the new improved offspring.

Evolutionary Algorithms achieve excellent results, yet are simple to code, require no directional or derivative information from the objective function and can handle a large number of parameters simultaneously.

Although there are various optimization techniques available within Evolutionary Algorithms, we have found that Differential Evolution (DE) [6] is most suitable for this application because initially it carries out a random search of the entire solution space that is subsequently focussed on a few potential candidate solutions. This is important given the multimodal nature of this optimization problem. considered here.

A. Differential Evolution

Differential Evolution [6] is an evolutionary technique in which the generation of new chromosomes is related to the current spatial distribution of the population. The algorithm generates new chromosomes by adding the weighted difference between two chromosomes to a third chromosome. At each generation, for each member of the parent population, a new chromosome is generated. Elements of this new chromosome are then crossed with the parent chromosome to generate the child chromosome. The child chromosome is evaluated and if it has a better objective value than the parent, the child chromosome replaces the parent. In this way, no separate probability distribution has to be used for mutation. This makes the scheme completely self-organizing. A feature of this algorithm is that the populations of the chromosomes form clusters around the possible solutions so that a number of possible solutions are investigated simultaneously in a bid to ascertain the global optimum solution.

The trial chromosome, $\vec{P}_t$, may be described as:

$$\vec{P}_t = F\left(\vec{P}_a - \vec{P}_b\right) + \vec{P}_c \qquad (1)$$

where chromosomes $\vec{P}_a$, $\vec{P}_b$ and $\vec{P}_c$ are chosen from the population without replacement and F is a scaling factor.

The crossover process is controlled by a crossover parameter C. The crossover region begins at a randomly chosen parameter in the chromosome, and then a segment of length L genes is copied from $\vec{P}_t$ to the parent chromosome to create the child chromosome. If the segment is longer than the remaining length of the chromosome, the segment is wrapped to the beginning of the chromosome. The length L is chosen probabilistically and is given by:

$$P\left(L \ge v\right) = \left(C\right)^{v-1},\ v > 0 \qquad (2)$$

In general, the scaling parameter F and the crossover parameter C lie in the range [0.5,1]. We have found from extensive tests that $F = 0.9$ and $C = 0.9$ to be most suitable for this particular application. Within the population, each individual chromosome represents a possible solution to the estimation and the gene values within the chromosome are the Doppler parameters themselves.

B. Chromosome Structure

For the purpose of Doppler velocity estimation when the signal is wideband with a non-linear chirp waveform, the required solution is parameterized by: (a) the Doppler velocity and (b) the phase. These correspond to a *pair* of genes for *each* Doppler spread SONAR return. For example, in a multi-target environment where up to six moving targets are expected, the chromosome would comprise a total of twelve genes. The number of expected target returns, M, is a required parameter for the algorithm since this specifies the length of each chromosome. However, as will be described below, if fewer targets actually exist than specified, the impact of over-specifying the number of the targets on the Doppler velocity estimates of the actual targets is negligible. This can be contrasted with other methods, such as MUSIC, where the order of the model has an important bearing on the final estimate. Consequently, the algorithm simply requires the maximum number of targets to be specified. Fig. 1 shows the conceptual structure of a chromosome.

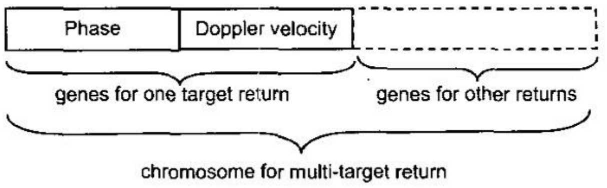

Fig. 1. Conceptual structure of a chromosome

A third parameter, the amplitude of the target return, could also have been specified as a gene, and the DE algorithm used to provide an estimate of this parameter. However, this significantly broadens the search space to three dimensions per target; requiring a larger initial population and probably many more generations for the population to converge to the global optimum solution. However, a better method of estimating the amplitude of each target return exists and a constrained least-squares amplitude fit is carried out here for each target return. The objective function is then used to quantify the best match from within the population of chromosomes on the basis of mean square error.

C. Objective function

At the outset, it is assumed that the SONAR receiver has knowledge of the non-linear chirp function used to generate the transmitted signal. In the receiver, a locally generated sampled version of this waveform is distorted using the Doppler velocity and starting phase parameters stored as the i^{th} pair of genes representing the i^{th} target return. This distorted, regenerated signal is represented as a sequence of samples, $s_i[n]$. This is carried out for all the gene pairs in the chromosome. The weighted spectra of the regenerated waveforms for each pair of genes are then summed to form the spectrum of the regenerated waveform of the SONAR return:

$$S[k] = \sum_{i=1}^{M} W_i S_i[k] \tag{3}$$

where $S_i[k]$ is the discrete complex spectrum of the sample sequence $s_i[n]$, $S[k]$ is the discrete complex spectrum of the composite regenerated signal, W_i is the weight for the i^{th} component which is obtained using a constrained least squares amplitude fit.

The objective function given in (4) is the mean square error, E, between the amplitude scaled spectrum, $S[k]$ and the discrete spectrum of the received signal, $R[k]$. Note that this objective function matches not only the spectral peaks but ALL spectral components thus providing an accurate estimate of the Doppler-induced spread over this wideband signal.

$$E = \frac{\sum_{k=1}^{N} (R[k] - S[k])^2}{N} \tag{4}$$

where N is the number of discrete frequency components in the spectrum.

III. ALGORITHM STRUCTURE FOR SONAR TARGET VELOCITY ESTIMATION

Fig. 2 shows the schematic representation of the algorithm for Doppler estimation using DE. The DE algorithm begins by generating an initial population of 75 chromosomes at random with F=0.9, C=0.9 and it is then run for 45 generations. For each generation, the DE algorithm evaluates each chromosome to find the best fit using a least mean square error approach as described in Section II C. The chromosome giving the least mean square error is selected as the best fit and the others are ranked on the basis of ascending mean square error. Thereafter a new set of chromosomes is generated using crossover and mutation. Of these new chromosomes, those providing a better fit are included in the population while the less fit individuals are removed. In this manner, the fitness of the population is improved with each successive generation, while retaining the original population size.

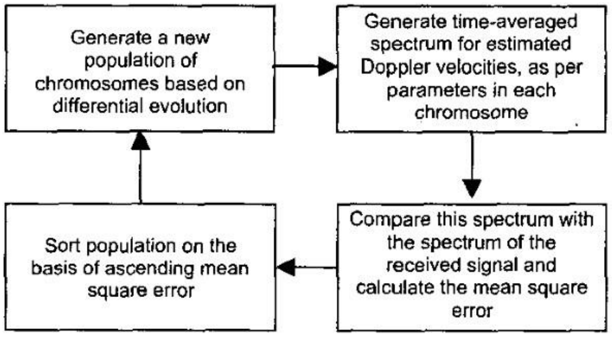

Fig. 2. Algorithm for chirp parameter estimation

The algorithm can be tasked to find a larger number of chirps than are actually present. In this case, the least squares estimate of the amplitude of each chirp will null-out non-existent chirps. Thus, this method does not rely on prior knowledge of the correct order of the model.

IV. RESULTS

The main parameters of the non-linearly chirped SONAR signal used to test the new algorithm are given in Table I.

TABLE I

SONAR SIGNAL PARAMETERS

Transmitted frequency, f_c	10kHz
Pulse duration	0.1s
Chirp bandwidth	600Hz
SNR of received pulse	-15dB to 0dB
IF before estimator	5kHz
Range of expected Doppler velocities	±20m/s

The algorithm requires an upper and lower bound on the Doppler velocity search space which has been set, in this instance, to ±20m/s. Equation (5) defines the non-linear chirp used for the results presented in this paper.

$$y(t) = A\sin(2\pi f_t t + \phi) \tag{5}$$

where ϕ is the random phase and the (arbitrary) non-linear chirp function used in the tests is:

$$f_t = f_c + A\tanh(x) \quad \text{for } -2 < x < 2 \tag{6}$$

where A is a bandwidth scaling parameter that is adjusted to provide the bandwidth of the signal. Fig. 3 shows the spectrum of the transmitted non-linear chirp.

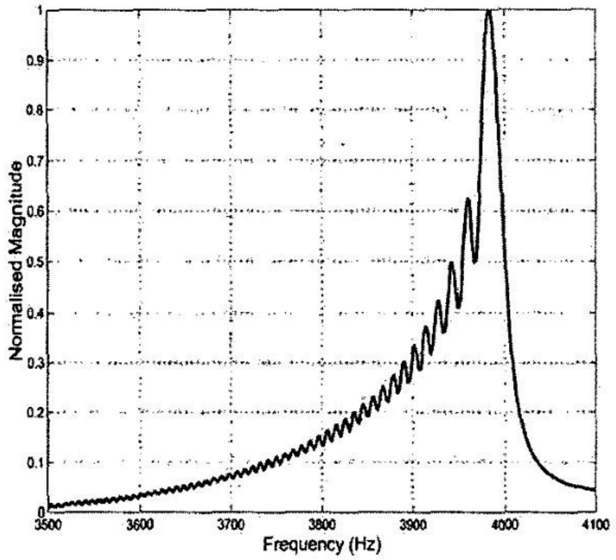

Fig. 3. Spectrum of the transmitted chirp

However, due to the effect of the Doppler, this spectrum is modified and each spectral component f is altered to $f_d = f(1+v/c)$ where v is the relative velocity between the two platforms and c is the velocity of the acoustic waves in the medium. Using normal spectral estimation techniques, this spectral broadening of the broadband signal would make accurate parameterisation of the Doppler velocity that causes the spread difficult. Furthermore, since we wish to estimate the Doppler velocity on a pulse-to-pulse basis, the effect of time-windowing due to the finite number of samples taken would generally limit the spectral resolution of conventional FFT-based spectral estimators, and more sophisticated spectral estimators such as parametric autoregressive methods or non-parametric sub-space methods generally require knowledge of the model order for the methods to be accurate. In the new method, it is assumed at the outset that the signal has a finite duration and the spectrum of the regenerated signal uses this fact.

It is assumed that the received acoustic pulse is filtered and down converted into In-phase and Quadrature components before being passed onto the EA-based Doppler estimator.

The results in the following subsections show the representative performance of the new method for SNRs in the range 0dB to -15dB. The performance of the new method as a means of mitigating range-Doppler coupling is shown in Section IV D.

A. SNR 0dB

Fig. 4 shows a spectrum 'snapshot' of a typical Doppler spread received pulse at an SNR of 0dB. It is clear from the figure that the spectral peak is not clearly defined in comparison with the transmitted signal of Fig. 3 and for each pulse, noise causes a spurious peak in the spectrum. Because of this, a simple spectral peak detector is likely to be in Doppler velocity errors on a pulse-to-pulse basis.

In comparison, Fig. 5 shows a histogram of the errors in the Doppler velocity estimate using the new method over 100 pulses. The mean of the errors is only 0.0055m/s and the standard deviation is 0.0371m/s.

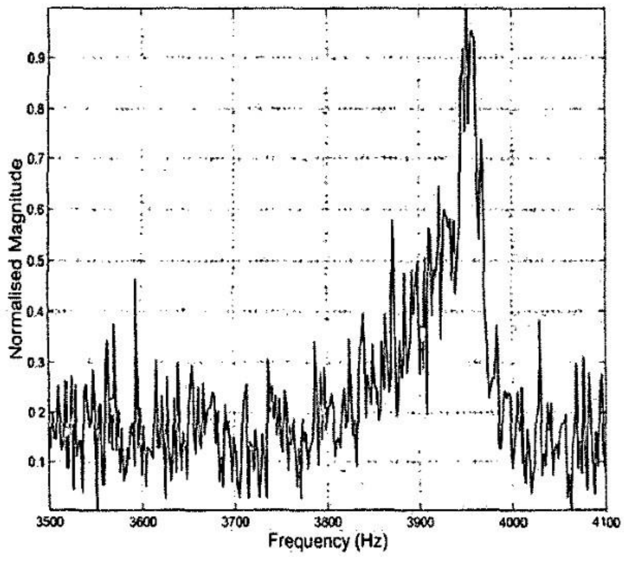

Fig. 4. Spectrum of the received pulse at an SNR of 0dB

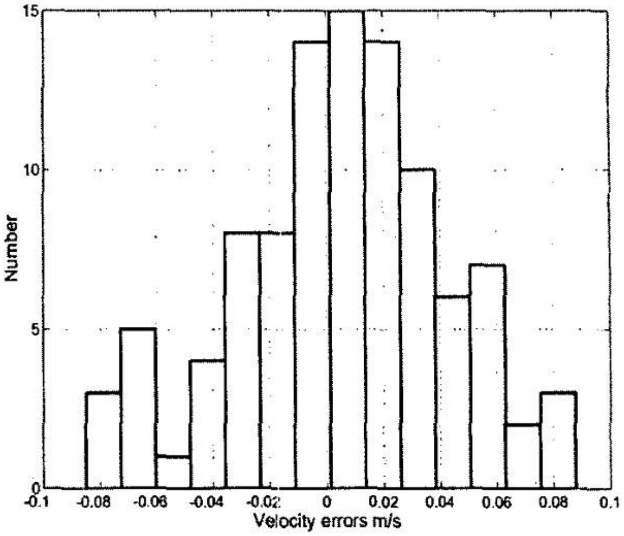

Fig. 5. Histogram of errors in the velocity estimate at an SNR of 0dB using the new method

In contrast, a simple spectral peak detector would need to estimate the Doppler shift of the peak to within ±0.3Hz to get similar accuracies, which from Fig. 3 is clearly unrealistic because of the wide spread in the spurious peaks.

B. SNR -15dB

Figure 6 shows a spectrum 'snapshot' of a Doppler shifted received pulse at an SNR of -15dB. It is clear that at this SNR there is no obvious spectral peak and if conventional FFT-based spectrum estimation techniques are used, it would be extremely difficult to ascertain an accurate shift in frequency that occurs due to the effect of Doppler. In comparison. Fig. 7 shows a histogram of the errors in the Doppler estimate using the new method. Again, this histogram is obtained over 100 pulses. In this case, the mean of the errors is 0.0261m/s and the standard deviation is 0.2291m/s.

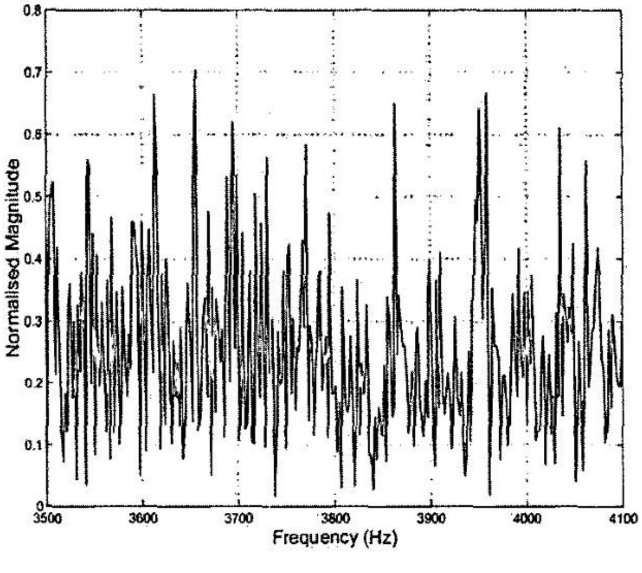

Fig. 6. Spectrum of the received pulse at an SNR of -15dB

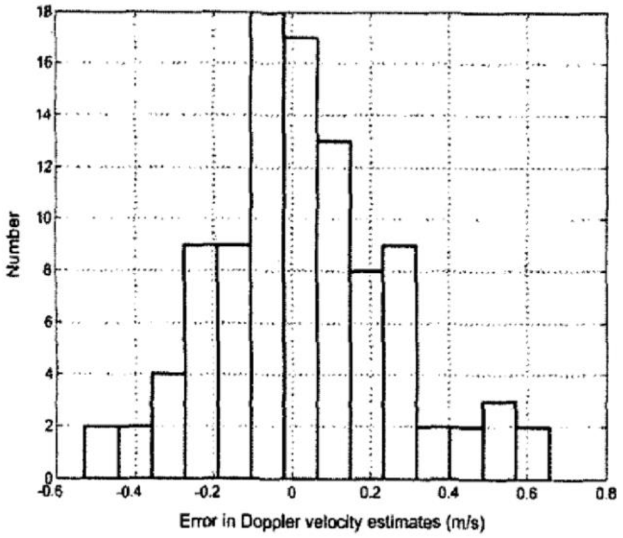

Fig. 7. Histogram of errors in velocity estimate at an SNR of -15dB

It can be seen that despite a 15dB decrease in SNR, the accuracy of the Doppler velocity estimate is exceptionally good.

C. Performance as a multi-target tracker

To test the ability of the new method to resolve multiple targets, a scenario was created with two targets that fell in the same range gate, had similar return amplitudes and whose Doppler velocities differed by just 3.0m/s. Fig. 8 shows the histogram of the estimates of Doppler velocities of the two targets over 100 runs at an SNR of 0dB. It can be seen that although there is a larger error in estimating each Doppler velocity, than for the previous case (shown in Fig. 5), the new method is clearly able to isolate the two target returns. In this case, mean errors in Doppler velocity are still only ±0.25m/s.

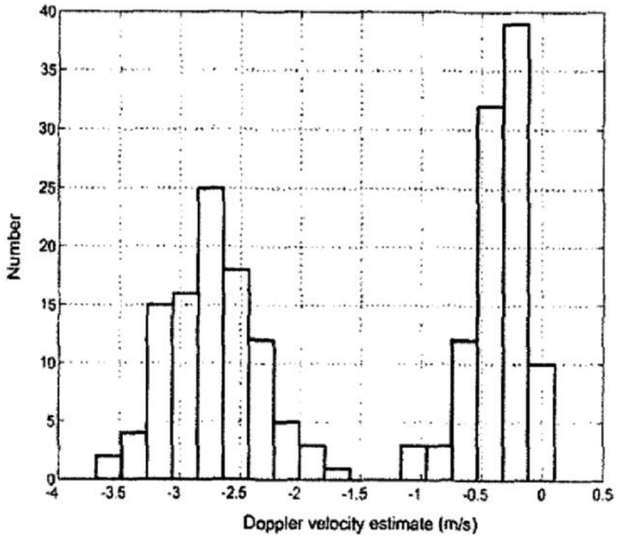

Fig. 8. Histogram of velocity estimates of closely spaced targets at an SNR of 0dB

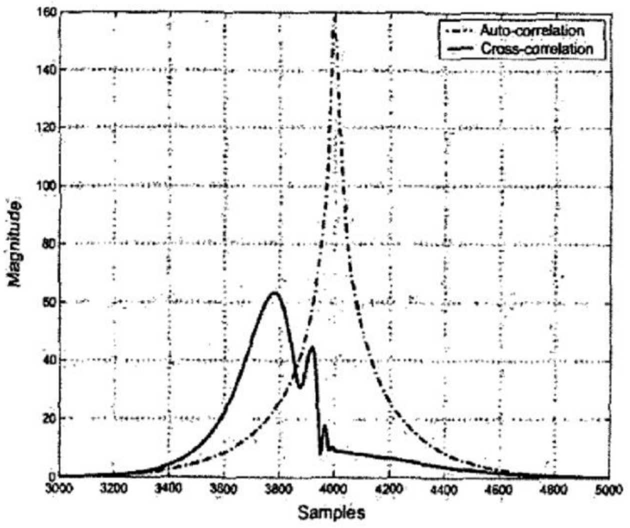

Fig. 9. Correlation properties of the signal with no noise

D. Mitigation of range-Doppler coupling

Fig. 9 shows the correlation properties of the test waveform and it's sensitivity to Doppler when no noise is present. In this figure, the dotted line is the autocorrelation function of the transmitted signal and the solid line is the cross-correlation function of the transmitted waveform with the received Doppler-spread waveform. It is clear from this figure that the effect of the Doppler is to: (i) reduce the amplitude of the correlation function and (ii) distort and shift the peak of the correlation function. In this case the Doppler velocity is 5m/s. The shift in the peak of the cross-correlation function results in a range error (range-Doppler coupling) and the reduction in peak amplitude significantly reduces the dynamic range of the SONAR target detection. When noise is now added (-15dB SNR), it is clear from Fig. 10 that when both Doppler and noise are present, the correlator output is severely degraded.

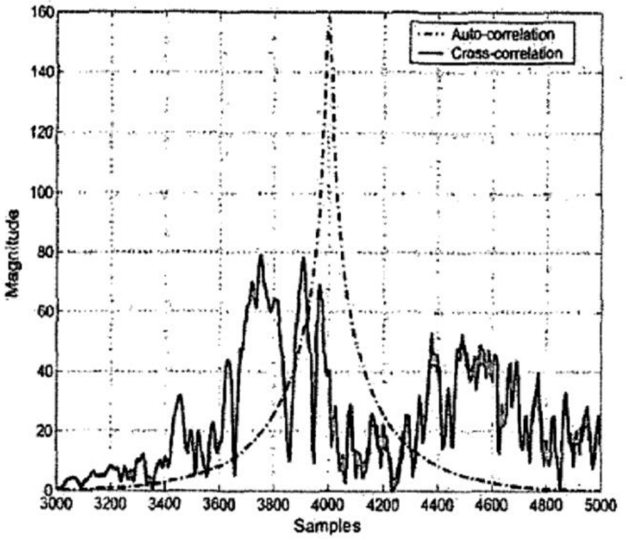

Fig. 10. Correlation properties of the signal return at a noise level corresponding to an SNR of -15 dB

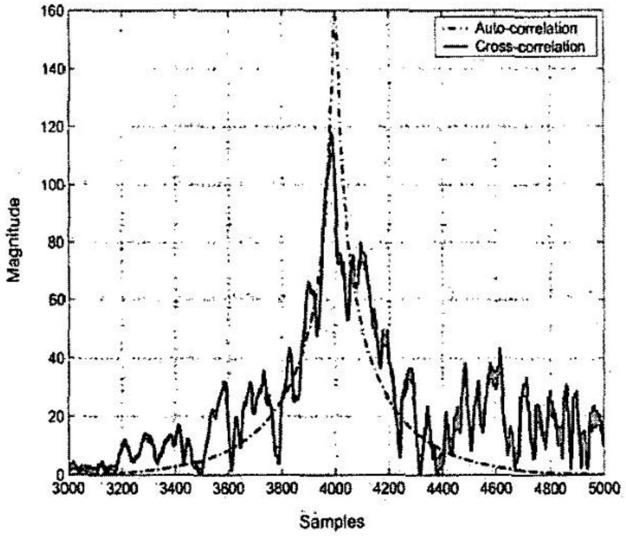

Fig. 11. Correlation properties of the signal return at a noise level corresponding to an SNR of -15 dB using the new system

There are now multiple peaks and, depending on the type of detector used, this will result in range errors and also the indication of multiple targets.

The new method has been applied to this particular problem. In this case, the transmitted signal is not correlated directly with the received signal. First, an accurate Doppler velocity estimate is estimated using the techniques described earlier and this is used to distort the transmitted waveform prior to correlation. The solid line in Fig. 11 shows the cross correlation of the received signal with the distorted replica of the transmitted waveform for the case where there is a single target return. The dashed line represents the ideal auto-correlation of the transmitted waveform. It is clear from the figure that by using the new method, there is: (i) a significant reduction in the distortion of the cross-correlation function which improves the dynamic range of SONAR target detection, (ii) there is a significant reduction in the effects of range-Doppler coupling even for waveforms that may not be Doppler tolerant and (iii) there is only one main peak, which reduces the likelihood of false target detection.

V. CONCLUSIONS

The paper has introduced a new method that is able to provide an accurate Doppler velocity estimate for non-linearly chirped SONAR pulses on a pulse-by-pulse basis. The results have shown that the resolution of the new method is not limited by the effect of time-windowing due to the finite duration of the pulses. Furthermore, the new method is able to provide accurate Doppler velocity estimates at SNRs as low as -15dB. In addition, the paper has demonstrated that the new method will detect multiple targets within the same range gate, where each target has a different Doppler velocity. Finally, the paper has demonstrated the effectiveness of this method for mitigating range-Doppler coupling at very poor SNRs.

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