SIMULTANEOUS DETECTION AND PARAMETER ESTIMATION OF MULTIPLE LINEAR CHIRPS

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ABSTRACT

This paper describes a new method for the simultaneous detection and parametric estimation of multiple chirped waveforms using a method based on evolutionary algorithms. Unlike traditional time-frequency analyzers, which provide a distribution of the signal spectrum over a period of time but do not inherently provide chirp parameters, this new method detects and provides as an output the start and stop frequencies of each chirp, its starting phase and amplitude. The new method is capable of detecting and characterizing multiple chirps which may be overlapping (in time and frequency) and in the presence of significant noise.

1. INTRODUCTION

Parametric estimation of chirped waveforms is of immense importance in the field of signal processing. This has use in applications such as speech analysis, radar, communication over time-varying multipath channels and in the detection and classification of signals. Consequently this is an area which has received considerable attention. Historically, despite the obvious limitation of windowing, the short-time spectral analysis using the Fourier transform and its variants has been the primary method for time-frequency analysis of signals. More recently, there have been studies into alternative methods derived from the Wigner distribution developed for the study of statistical quantum mechanics [1]. However, these distributions only obtain a time-frequency plot of the signal and, in themselves, to do not characterize the signal parameters directly. In order to parameterize the time-frequency distribution, other methods such as the Hough or Radon transforms must be used in conjunction with the time-frequency distribution to extract the main parameters of the chirp, such as the start frequency and the chirp rate [2][3]. A major drawback of the basic Wigner distribution in the presence of multiple chirps is the generation of cross component spectral lines which are not actually present in the signal. These spurious artifacts in the time-frequency distribution can lead to errors in the parameter estimation using these transforms and it is certainly possible for weaker signals to be masked.

In order to overcome these drawbacks, other variants of the Wigner distribution have been developed, such as that developed by Cho-Williams [1], which perform well in the presence of multiple chirps. In addition, broadening of the main peak in these time-frequency distributions due to the inherent tradeoff between time and frequency resolution limits the accuracy with which the chirp parameters can be estimated using the Hough or Radon transforms. Sun et al [2] state that one way to reduce the minimum detectable frequency slope of the chirped signal would be to use a higher order FFT. However, with a finite set of data and a fixed sampling rate, this would reduce the time resolution.

This paper introduces a new technique for direct detection and parametric classification of multiple overlapping chirps within a window of observation. The detection and parametric estimation of multiple chirps in the received signal is based on matching the spectrum of the received set of chirps with the spectrum of a signal that has been reconstructed from a set of chirps that have been generated using the estimated parameters. The estimation method described in this paper is not limited by the effects of peak broadening and cross-spectral components and it can provide accuracies comparable to methods such as MUSIC that are used to detect pure sinusoids, but without the need for a high order FFT. The optimization of the estimated chirp parameters is done iteratively in a non linear process using the evolutionary algorithm.

2. 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 [4]. A *population* of M 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 n sections called *genes*. Each gene represents a single parameter in the problem, therefore a problem that has eight unknowns, for example, would require a chromosome with eight genes to describe it.

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 evaluated at every generation using an *objective function* that is able to distinguish good solutions from bad ones and score their performance. With each new generation, some of the old individuals are removed to make room for the new improved offspring. Despite being very simple to code, requiring no directional or derivative information from the objective function and being capable of handling large number of parameters simultaneously, evolutionary algorithms can achieve excellent results.

While there are various optimization techniques available within Evolutionary Algorithms, we have found Differential Evolution (DE) [5] to be most suitable for this application.

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2.1. Differential Evolution

Differential Evolution is an evolutionary technique that uses mutations that are 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 which makes the scheme completely self-organizing.

The trial chromosome $\vec{P}_t$ may be described as in (1).

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

Where chromosomes $\vec{P}_a$, $\vec{P}_b$ & $\vec{P}_c$ 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 (2).

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

In general, the scaling parameter F and the crossover parameter C lie in the range $[0.5, 1]$. Within the population, each individual chromosome represents a possible solution to the estimation and the gene values within the chromosome are the chirp parameters themselves.

2.2. Chromosome Structure

For the purpose of chirp detection, each possible chirp is characterized by parameters represented by a starting frequency, its phase and the chirp rate. These correspond to a set of three *genes* for each chirp. A number of such sets of genes comprise a chromosome, where the number of genes in the chromosome is related to the number of chirps required to be detected (i.e. the order of the model). This is shown in Fig. 1. Thus for the detection of a single chirp, each chromosome would consist of just three genes representing start frequency, starting phase and the chirp rate, whereas for the simultaneous detection of three chirped signals, the number of genes in each chromosome would increase to nine.

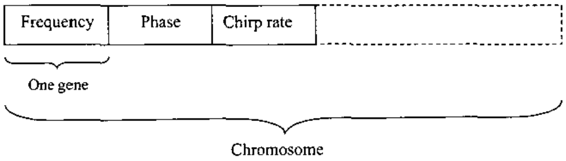

Fig. 1. Simplified block diagram of a chromosome structure

The objective function is used to quantify the best match from within the population of chromosomes on the basis of mean square error.

2.3. Objective function

The fitness of a particular chromosome in the population is based on: (a) regenerating the multiple chirped signal from the genes, (b) obtaining the spectrum of this signal (via the FFT) and (c) comparing this spectrum with the spectrum of the actual signal from which the chirps need to be detected and characterized. The chromosome giving the least mean square error is chosen as the best match. For the purpose of obtaining this error, the entire spectrum of interest is being matched. Thus, the objective function is not only based on matching just the peaks, but the position of the nulls and the peaks are equally important in achieving the best possible match. To make the nulls and low sidelobes equally significant, both the generated and received spectrums are square rooted to reduce the magnitude of the peaks as compared to the sidelobes.

3. ALGORITHM STRUCTURE FOR PARAMETRIC ESTIMATION OF MULTIPLE CHIRPS

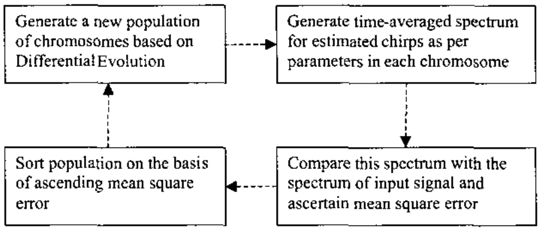

Fig. 2. Schematic block diagram of the algorithm for chirp detection and parameter estimation

Figure 2 shows the schematic representation of the algorithm for chirp detection and parameter estimation using Differential Evolution. The DE algorithm begins by generating an initial population of 350 chromosomes at random with $F = 0.9$, $C = 0.9$, and the algorithm is run to convergence, which is generally less than 100 generations. For each generation, the DE evaluates each chromosome to find the best fit using a least mean square error approach. This is done by regenerating the multiple chirped signal using the parameters for each chirp stored in the chromosome. A least squares amplitude fit is then performed on both the real and imaginary components of the spectrum of the regenerated signal with the received signal. This amplitude-scaled spectrum is then compared with the time-averaged spectrum of the input signal. The chromosome giving the least mean square error is selected as the best fit and the others are arranged on the basis of ascending mean square error.

Since the algorithm uses a least squares fit for the amplitude estimate for each chirp, it can be tasked to find a larger number of chirps than are actually present and the algorithm will null out non-existent chirp estimates. Thus this method does not rely on prior knowledge of the correct order of the model (i.e. the number of chirps present) unlike some other spectral estimators.

4. RESULTS

In order to assess the performance of this method of chirp detection and parameter estimation, we have used linear chirps of constant amplitude and a time duration of 0.9 seconds, which is also the window of observation. The chirped frequencies lie in the range 250Hz to 310Hz. The results shown here have been used to highlight the performance of this method under conditions when multiple chirps are present and where the chirps cause a time-frequency distribution, such as the Wigner distribution, to mask weaker chirps within the crossed spectral components.

4.1. Multiple chirp detection and parameter estimation

4.1.1. Case I: Multiple identifiable chirps

Table 1 shows the chirp parameters used for this test. The Wigner distribution showing the time-frequency spectrum of the three chirps is shown in Fig. 3.

Table 1. CHIRP PARAMETERS FOR CASE I

Number of chirped signals	3
Normalized Amplitudes	1,1,1
Time duration for each chirp	0.9 s
SNR	10dB
Chirp frequency range	259.92 Hz to 264.60 Hz
	264.79 Hz to 278.73 Hz
	273.28 Hz to 306.20 Hz

The grey scale on the right of the graph indicates the magnitude of the distribution and it is clear that for this example the Wigner distribution indicates the presence of the three chirp signals but is not able to automatically parameterize them. The new algorithm, however, estimated the start and stop frequencies of the three chirps as: 259.81 Hz to 264.58 Hz, 264.82 Hz to 278.71 Hz and 273.42 Hz to 306.12 Hz respectively and the normalized amplitudes were estimated as 1.00, 1.00 and 0.97.

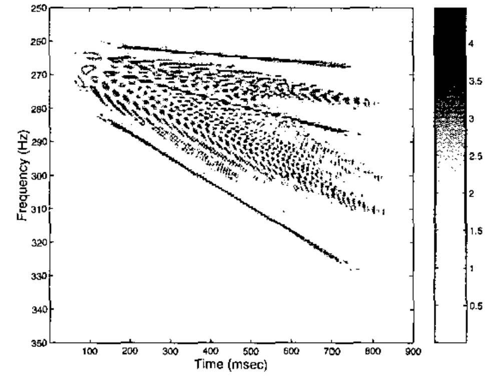

Fig. 3. A section of the Wigner distribution showing the three chirps

Figure 4 shows the estimated chirp frequencies (shown as thick solid lines) superimposed on the time-frequency distribution of Fig 3. The chirp frequencies estimated by the new method have a mean absolute error of about 0.05 Hz. Under similar conditions, if the Hough or Radon transforms had been used in conjunction with the Wigner distribution to detect the chirps, the estimate of the slope of the line would have to be within 0.01° to achieve a similar accuracy. However, with short duration signals such as this, obtaining such fine angular resolution using the Radon transform, for example, would result in the peaks splitting, hence laying a bound to the accuracy with which the chirp parameters can be estimated.

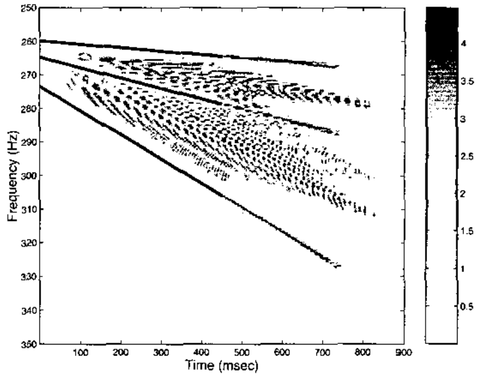

Fig. 4. A section of the Wigner distribution of the actual chirps with the detected chirps superimposed as dotted lines

4.1.2. Case II: Detection of multiple chirps in high noise

While using the same signal parameters as in Table1 ,the noise level was raised to give an SNR of 0dB. Under these conditions, the new algorithm was used to estimate 1000 chirps. Despite the high noise level, the new algorithm had no problem detecting the chirps. For this set of results, the absolute mean in the error of the frequency estimates of the chirps was within 0.3 Hz.

4.1.3. Case III: Detection of 'masked' chirps

One of the characteristics of a Wigner distribution is that when there are a number of signals present, there are spurious intermediate peaks generated which may mask low amplitude chirps. To test the performance of this new algorithm in such a scenario, the same chirp parameters as in Table1 were used, however, the amplitude of the center chirp was reduced to 0.15.

Figure 5 shows the Wigner distribution of the chirps. It can be seen that the high cross component spectral lines have masked the weaker chirp lying between the two dominant ones. If a straight-line detection transform, such as the Hough or Radon transform had been used to extract the chirp parameters from this distribution, only the two dominant chirps would be detected.

However, the new method is able to resolve all the chirps and it estimated the start and stop frequencies as: 259.915 Hz to 264.574 Hz, 263.987 Hz to 278.56 Hz and 273.31 Hz to 306.062 Hz respectively. The errors for the estimation of the start and stop frequency for this demanding chirp signal are approx 0.22 Hz. The normalized amplitudes were estimated as 0.99, 0.151 and 1.0 respectively. Figure 6 shows the estimated chirps (shown as thick solid lines) superimposed on the distribution of Fig 5.

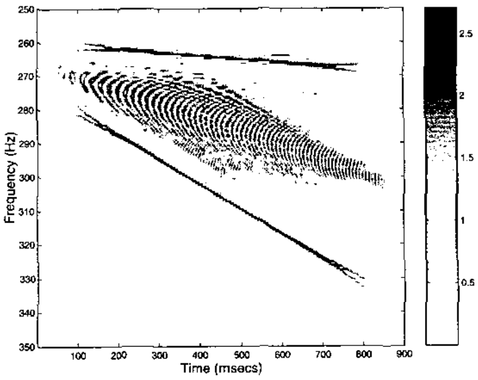

Fig. 5. A section of the Wigner distribution when chirp amplitudes are 1,0.15,1 respectively

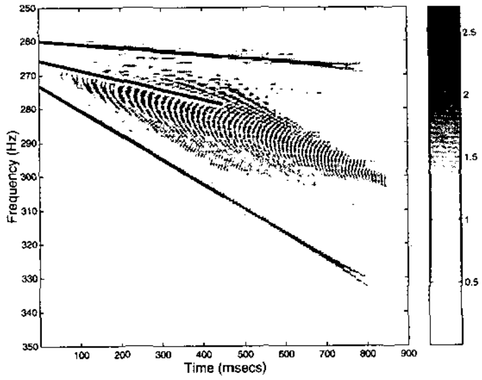

Fig. 6. A section of the Wigner distribution when chirp amplitudes are 1,0.15,1 with the estimated chirps superimposed

4.2. Detection of chirps crossing in the time-frequency domain

The performance of the new method was further validated using positive and negative chirped signal that cross in the time-frequency domain. Table 2 shows the chirp parameters used for this test.

The Wigner distribution for this case is shown in Fig. 7. Also shown as a thick dashed line superimposed on the Wigner distribution are the estimated chirps using the new method. The chirp frequencies were estimated as: 264.62 Hz to 289.79 Hz, 291.30 Hz to 273.35 Hz respectively. The mean of absolute errors in the frequency estimates is approx 0.06 Hz.

5. CONCLUSIONS

The results show that the new method provides high resolution and accurate detection and estimation of linear chirps. The accuracy with which it can estimate multiple chirp parameters simultaneously, does not suffer from the limitations imposed on straight-line transform methods such as Hough or Radon due to spectral broadening of the main lobe and, it performs well even with short duration data. Furthermore, it is not susceptible to the problem of chirp masking due to spurious spectral components which can occur in Wigner based distributions.

Table 2. CHIRP PARAMETERS FOR CHIRPS CROSSING IN THE TIME-FREQUENCY DOMAIN

Number of chirped signals	2
Normalized Amplitudes	1,1
Time duration for each chirp	0.9 s
SNR	10 dB
Chirped frequency range	264.79 Hz to 289.895 Hz 291.24 Hz to 273.28 Hz

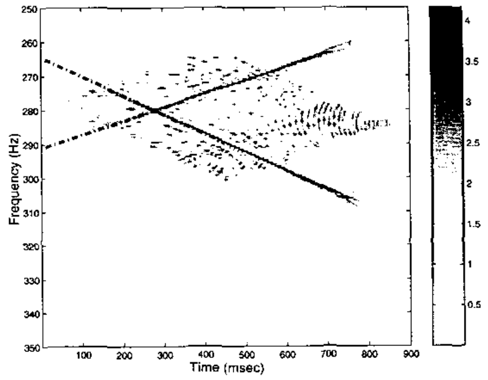

Fig. 7. A section of the Wigner distribution showing the crossing chirps and the detected chirps superimposed

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