PARAMETRIC SPECTRAL ANALYSIS OF MULTIPLE NON-LINEAR CHIRPS USING EVOLUTIONARY ALGORITHMS

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ABSTRACT

This paper describes a new parametric method of spectral analysis of complex signals which may contain multiple, overlapping, non-linear and linear chirps. The method parameterizes the time variation of the chirp frequencies and also provides an estimate of the phase and relative amplitudes of each chirp. The method exploits time windowing of the received signal and uses an Evolutionary Algorithm to optimize the estimated parameters. The new method works well in high levels of noise corresponding to SNRs of -7dB.

1. INTRODUCTION

Spectrum analysis of complex signals and parametric estimation of their component waveforms is immensely important in applications such as the detection and classification of signals, speech analysis and communication over time-varying multipath channels. Many complex signals comprise of a combination of non-linear frequency chirps, linear frequency chirps and pure sinusoids. 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 [1]. However, these distributions only obtain a time-frequency plot of the signal and, in themselves, do not parameterize the signal directly.

In order to parameterize the time-frequency distribution, image-processing methods such as the Hough-Radon transform (HRT) must be used in conjunction with the time-frequency distribution [2]. If it is known *a priori* that the chirps are linear or have a non-linearity that can be described by relatively few parameters (such as a hyperbolic function), these methods can be very effective. However, for non-linear chirps where the degree of non-linearity is not known or where it is defined by a larger number of parameters (such as a general parabolic function), such methods become very computationally intensive. 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 HRT. Furthermore, these methods do not directly provide any estimate of the phase or amplitude of these chirps, which may be of importance in applications such as interference cancellation.

This paper describes a new method that can be used to analyze the spectrum of complex signals. It analyzes the entire window of data without performing either a traditional short-term spectral analysis or obtaining a time-frequency distribution. The method detects the presence of any non-linear or linear chirps as well as pure sinusoids and it parameterizes their change of frequency with time. The multiple chirps may overlap in frequency and they may have different amplitudes. Each chirp is described using a non-linear function of frequency and time, where the variables are the start and stop frequencies and the coefficient(s) of non-linearity. In addition to these parameters, the output of the algorithm includes an estimate of the phase and normalized amplitude for each chirp. The accuracy in the estimation of the chirp frequencies is not limited by peak broadening or the presence of sidelobes due to time windowing.

The method is based on matching the spectrum of a locally generated chirp signal to the time-windowed spectrum of the received signal. Possible algorithms that achieve this include MMSE and ML methods. However, when the signal of interest is not known *a priori*, a maximum likelihood method would require a very large number of templates for the signal to be checked against. In addition, when the solution to the problem is multimodal, as here, the key requirement is for an effective optimization algorithm that has a high probability of converging to the global optimum. Consequently, in this paper we propose a method that is based on Evolutionary Algorithms. These algorithms are particularly useful in this problem because they initially have a very wide search space, but they quickly converge to pockets of potential solutions distributed about the search space. As a result of this initial global search, the Evolutionary Algorithm is far less likely to be trapped in a local minimum.

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2. EVOLUTIONARY ALGORITHMS

Evolutionary Algorithms are optimization procedures which operate over a number of cycles (generations) and are designed to mimic the natural selection process through evolution and survival of the fittest [3]. 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 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) [4] 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 the optimization problem.

2.1. Differential Evolution

Differential Evolution [4] 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. 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:

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

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:

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

In general, the scaling parameter F and the crossover parameter C lie in the range $[0.5, 1]$. We have found F=0.9 and C=0.9 to be most suitable. 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 non-linear chirp detection, each possible chirp is characterized by parameters represented by a start frequency, a stop frequency, its phase and the coefficient of non-linearity. These correspond to a set of four *genes* for each chirp. A number of such sets of genes would comprise a chromosome. Figure 1 shows a conceptual structure of a chromosome. The number of genes in the chromosome is related to the number of chirps required to be detected. Thus for detection of a single chirp, each chromosome would consist of just four genes, whereas for detection of three chirps, the number of genes in a chromosome would increase to twelve. By simply increasing the number of genes that describe each chirp it would be possible to analyze non-linear chirps whose time-frequency variations are described by higher order polynomials.

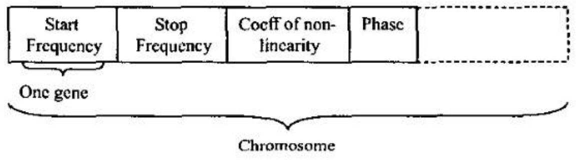

Figure 1: Conceptual structure of a chromosome

An *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 comparing the FFT obtained by the combined spectrum of all its chirps with the FFT of the actual signal from which the chirps need to be parameterized. 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 matched. Thus, the objective function is not only based on matching just the peaks but the position of nulls and peaks are equally important in achieving the best possible match.

3. ALGORITHM STRUCTURE FOR PARAMETRIC ESTIMATION OF MULTIPLE CHIRPS

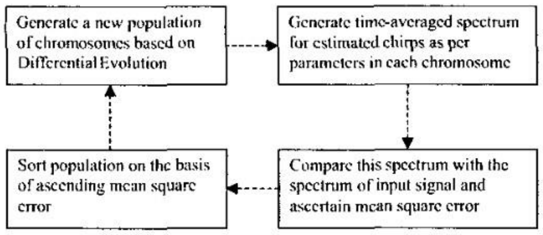

Figure 2: Algorithm for chirp parameter estimation

Figure 2 shows the schematic representation of the algorithm for chirp parameter estimation using DE. The DE algorithm begins by generating an initial population of 350 chromosomes at random with $F = 0.9$, $C = 0.9$ and it is then run for 150 generations. For each generation, the DE algorithm evaluates each chromosome to find the best fit using a least mean square error approach. This is done by generating the spectrum for each chirp from the parameters stored in the chromosome. The spectra of the chirps in each chromosome are then summed and a least squares amplitude fit performed on both the real and imaginary components of the spectrum. 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. For assessing the mean square error, both the real and imaginary values of the spectrum are used to obtain an accurate phase estimate for each chirp.

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.

4. RESULTS

In order to demonstrate the effectiveness of the new method, an arbitrary multiple-chirped test waveform was generated. This comprised two non-linear chirps: one swept up in frequency and the other swept down in frequency with a common frequency at some point in time. The normalized amplitudes of the two chirps were 0.8 for the up-chirp and 1.0 for the down chirp. The variation of frequency with time, $f_c(t)$, for the non-linear chirp is described by the following parabolic equation:

$$f_c(t) = at^2 + bt + c \tag{3}$$

where $a = f_2 - f_1 - s$, $b = s$, $c = f_1$, and f_1 and f_2 are the start and stop frequencies respectively and s describes the non-linear time variation of the chirp. Both the sinusoid and the linear chirp are special cases of (3) and in contrast, a hyperbolic chirp function (4) has just two coefficients, a and b:

$$f_c(t) = b\sqrt{\left(\frac{t^2}{a^2} - 1\right)} \tag{4}$$

Table 1 provides the main parameters of the test waveform. In the following sets of results, the effect of SNR on the performance of the algorithm is demonstrated.

Table 1: CHIRP PARAMETERS

	Chirp 1	Chirp 2
Normalized Amplitude	0.8	1.0
Time duration for chirp	0.9s	0.9s
Start frequency, f_1	240Hz	260Hz
Stop frequency, f_2	285Hz	210Hz
Coefficient of non-linearity, s	15	45

Figure 3 shows the frequency spectrum of a 0.9 second block of the received signal at an SNR of 10dB evaluated using a 1024 point FFT. The effect of the two chirps is to smear out the spectrum, as would be expected. Figure 4 shows a plot of the time variation of the frequency of each chirp obtained from the new algorithm. The solid line shows the time frequency plot of the original waveform whereas the dashed line shows the mean of the estimated time variation of the two chirps using the new algorithm. It is clear that the new method is able to track the frequency changes of the two chirps with great accuracy.

The error bars on this plot have been obtained by performing 50 runs under identical conditions and setting the length of each error bar to ±1 standard deviation of the frequency error about the mean. The mean of the estimated amplitudes using this method was 0.81 for chirp 1 (cf. an actual amplitude of 0.8) and 0.98 for chirp 2 (cf. an actual amplitude of 1.0).

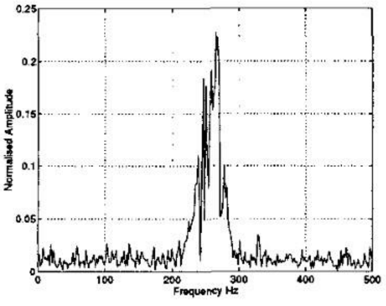

Figure 3: Spectrum of the received signal at SNR=10dB

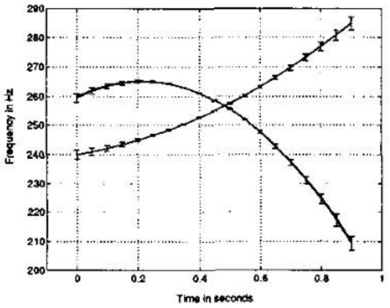

Figure 4: Actual (solid) and estimated (dashed) time-frequency variation of two non-linear chirps at SNR=10dB

Figure 5 shows the spectrum of a similar signal but at an extremely poor SNR of -7dB. Again, the spectrum is evaluated using a 1024 point FFT. Despite the extremely high noise level, figure 6 shows that the new algorithm is still able to differentiate and extract the time-frequency variations of the two chirps. There is close agreement between the mean of the estimated time variation of the two chirps (dashed line) and the original chirp waveforms (solid line), but the standard deviation is larger. The mean of the estimated amplitudes using this method was 0.75 for chirp 1 and 0.94 for chirp 2.

5. CONCLUSIONS

The results show that the method provides high accuracy in estimating non-linear chirps in high levels of noise. It does not suffer from the limitations of peak broadening of the main spectral lobe due to windowing. Considering the high number of possible solutions that the multiple non-linear chirp waveform could have taken, the evolutionary algorithm has been found to be highly effective in providing an initial global search that is subsequently focussed on a few potential candidate solutions.

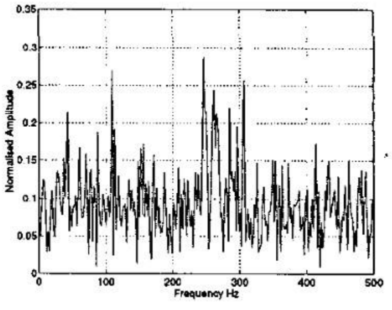

Figure 5: Spectrum of the received signal at SNR=-7dB

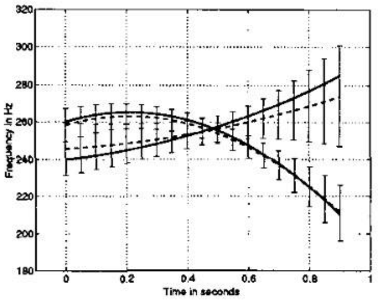

Figure 6: Actual (solid) and estimated (dashed) time-frequency variation of two non-linear chirps at SNR=-7dB

While the results show the performance of this method in analyzing parabolic non-linear chirps, it is possible to analyze chirps with higher degrees of non-linearity by increasing the number of genes describing each chirp.

6. REFERENCES

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