# Genetic algorithm for rigid body reconstruction after micro-Doppler removal in the radar imaging analysis

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ABSTRACT

Recently, an L-statistics based method for the micro-Doppler effects removal has been proposed by the authors. Order statistics is performed on the spectrogram, while the rigid body signal synthesis is done by using the remaining STFT samples, after micro-Doppler removal. By the proposed method, the Fourier transform is recovered with a concentration close to the original one. However, during the procedure of the micro-Doppler removal, the STFT samples that correspond to the rigid body are retracted, as well. Consequently, in the reconstructed Fourier transform of the rigid body, we get one very highly concentrated pulse, as in the original Fourier transform, and a number of low-concentrated components, being spread around the peak. These low concentrated components are summed up by different random phases. In this paper, we propose a genetic algorithm for the estimation of the removed STFT samples corresponding to the rigid body. Each individual in the genetic algorithm contains possible estimation of the phases of the missing STFT samples, whereas fitness function forces individuals (combination of phases) for which a minimal energy of the side lobs is obtained. The individual with the highest fitness is considered as the final phases' estimation of the missing STFT values, and then used for the reconstruction of the original Fourier transform. The amplitude of a STFT sample is estimated as median of the amplitudes of the remaining samples at the same frequency. Performance of the proposed genetic algorithm is illustrated by examples.

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## 1. Introduction

Micro-Doppler (m-D) effect appears in the inverse synthetic aperture radar (ISAR) imaging when a target has one or more fast moving parts [1–7]. Similar effect appears in the synthetic aperture radar (SAR) imaging as well [8]. This effect may decrease readability of radar images by covering the rigid body and making it difficult to detect. Thus, the extraction of the m-D effect from the radar images has attracted significant research attention [9–14]. Recently, an effective and simple method for the m-D removal has been proposed in [15]. It is based on the L-statistics. In order to remove the m-D effect, the short time Fourier transform (STFT) is calculated within the coherent integration time (CIT). Then, the fact that a rigid body and fast rotating points behave differently in the time frequency (TF) plane is used for the m-D removal. Namely, the frequency content of an m-D signal is time variant and it covers a wide range of frequencies, but only for short time intervals. On the other hand, the frequency content of a rigid body return is almost constant in time. Consequently, in the STFT sorted along the time axis the m-D part of the signal has non-zero values over a wide frequency range, but only for a few samples in the sorted

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plane. Thus, it is easily removed by omitting, for each frequency, a fixed number of the highest STFT samples, as it is proposed in [15]. By summing the rest of the STFT values, over time, the FT of the rigid body is obtained. This approach is very simple to use and produces better results than the other approaches [9–14]. However, since the same number of the highest STFT samples is removed for each frequency, some of the STFT samples that correspond to the rigid body are removed by this procedure, as well. Influence of the missing STFT values to the concentration of the reconstructed rigid body is analysed analytically and by simulations in [15]. It has been shown that, after summing the remaining STFT values over time, there will be a highly concentrated component corresponding to the original Fourier transform (FT) (that would be obtained by summing all the STFT samples), surrounded by low-concentrated values (corresponding to the omitted STFT samples). Number of omitted rigid body samples in the STFT, that cause residual spreading in the reconstructed FT, is high. Therefore, classical optimization approaches cannot be used in their reconstruction due to the high computational load. In this paper, we propose a genetic algorithm for the estimation and recovering of the missing STFT samples that correspond to the rigid body.

Genetic algorithms are widely used as stochastic optimization methods [16–18]. They start with an initial population composed of a number of possible solutions (individuals represented by chromosomes). Then, by emulation of the evolutionary process in the nature, i.e. by crossover of individuals, where the best adopted individuals (those with the highest fitness) have the highest chance to survive and to be recombined with the others, and mutation, different populations of fixed size are generated. After a couple of generations, the average fitness of the new populations increases, meaning that they consist of the best adopted individuals from each generation and their recombinations. In our application, as the final solution we use the best adopted individual of the last generation, i.e. the one with the highest fitness.

Chromosomes of each individual consist of potential phase values of the missing STFT samples that correspond to the rigid body. The number and positions of these samples in the TF plane can be easily determined. We know that Hann(ing) window is used for the STFT calculation and zero-padded in order to produce the same number of samples as in the FT [15]. Therefore, we know the width (the number of columns) of the STFT that corresponds to the rigid body. The position of the rigid body is obtained from the position of the peak in the FT reconstructed by summing the STFT samples remaining after the m-D removal. On the other hand, for each time instant (row), the STFT samples of the rigid body are equal to the low concentrated FT of the used window, shifted to the frequency of the rigid body. Then, for each frequency (column), the STFT samples of the rigid body are with equal amplitudes, but with different phases, except at the position of the rigid body, where they are in phase [15]. Therefore, the amplitudes of the missing STFT values at the same frequency (column) can be set to the median of the amplitudes of the remaining STFT values at that

frequency. We only need to estimate their phases. The initial population is formed by randomly choosing values of the phases within $[0, 2\pi)$ for each individual. Possible solutions are then binary coded, and they form chromosomes of an individual. In each generation, the new individuals are generated by uniform cross-over, after selecting two individuals which will exchange their genetic material, [18]. The individuals that are better adopted (with higher fitness) will be selected with higher probability. In [15], it has been shown that after summation of the STFT samples over time, the obtained FT of the rigid body is the same as its FT directly calculated with a window close to the rectangular one (with a small transition at the ending points) or even with the rectangular window. Thus, the FT of the rigid body component reconstructed by summing over time the STFT samples filled with the recovered values should have only one non-zero value, at the frequency that corresponds to its position. Consequently, for the fitness calculation of an individual, the sum of the absolute squared values of the corresponding reconstructed FT, except the maximal one, is calculated for the frequencies covered by the STFT of the rigid body. The individual with the smallest sum (i.e. the smallest residual spreading) has the highest fitness, and represents the best phases estimation of the missing STFT samples.

The paper is organized in five sections. In Section 2, the radar signal model and the procedure for the rigid body separation, based on the L-statistics, are presented. The genetic algorithm for the reconstruction of the missing STFT samples is proposed in Section 3. Calculation complexity of the proposed algorithm is also discussed in this section. Performance of the proposed method is illustrated through simulations in Section 4, while the conclusion is given in Section 5.

## 2. Rigid body separation based on the L-statistics

Consider a continuous wave (CW) radar that transmits signal in a form of coherent series of $M$ chirps [19]. The received signal, reflected from a target, is delayed with respect to the transmitted signal for $t_d = 2d(t)/c$, where $d(t)$ is the target distance from the radar and $c$ is the speed of light. This signal is demodulated to the baseband, with possible distance compensation and other preprocessing operations (such as pulse compression) [19,20]. In order to analyze the influence of cross-range non-stationarities in the radar imaging, we will consider only the Doppler part in the received signal of a point target, in the continuous dwell time, as it is usually done in the radar literature [19]:

$$s(t) = \sigma e^{j2d(t)\omega_0/c}, \tag{1}$$

where $\sigma$ is the reflection coefficient of the target, while $\omega_0$ is the radar operating frequency. The repetition time of a single chirp will be denoted by $T_r$, while the number of samples within each chirp is $N$. The CIT is $T_c = MT_r$.

The Doppler part of the received radar signal that corresponds to a rigid body point can be modelled as a complex sinusoid, while the Doppler part that corresponds to a rotating reflector is sinusoidally frequency