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DETERMINATION OF TARGET LOCATION FOR BISTATIC SYNTHETIC APERTURE RADAR BY GENETIC ALGORITHM

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ABSTRACT

In this work, the problem of determining the target locations with minimum error is studied by means of the genetic optimization method for synthetic aperture radars. The measurements at each antenna location along the synthetic aperture are being used in the genetic algorithm for error minimization. To increase the amount of data, a second receiver positioned at a different location is used and bistatic synthetic aperture is formed. The additional phase information increases the error minimization rate in the optimization algorithm. It is observed that the results are better in mobile antenna case with respect to the stationary antenna case for the bistatic radars.

Keywords: *Synthetic Aperture Radar, Genetic Algorithm, Bistatic Radar, High Resolution Imaging*

I. INTRODUCTION

High-resolution target imaging studies by means of synthetic aperture radars (SAR) have become most popular in recent years [1-2]. The studies to increase the target resolution in lack of information are being utilized more [3-4]. In this work, the problem of target location estimation from the information obtained by the synthetic aperture radar by means of the genetic algorithm is investigated.

The difference between the received signal values calculated by the estimated target locations, and the actual measurements, is minimized by the optimization algorithm. The number of linear independent measurements must be kept large to reach the real minimum. In a single antenna system, when the sampling number on the antenna location is kept high, a similar increase will not be observed on the linear independent measurement vectors. To increase the information rate, bistatic synthetic aperture is formed by using a second receiver antenna at a different location. Therefore the additional phase difference information between the measurement data taken from the two antennas enhances the error minimization and the location information becomes more precise.

In this study, the results are compared when the second antenna moves on a platform with the other antenna or is placed independent of the first

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antenna location. It is observed that, in the case where the second antenna is in motion, the results are better. Also the variation in the results with respect to the motion model of the second antenna, are studied and the error minimization – system parameters relationships have been determined.

2. FORMULATION OF THE PROBLEM

As shown in Figure 1, the object is illuminated in (X_1,Y_1+u) and (X_2,Y_2+u) for the synthetic aperture synthesized on the (x,y) plane, and in the aperture $u \in [-L,+L]$. Receiver antennas record the signal reflected from the object at the coordinates (X_1,Y_1+u) and (X_2,Y_2+u).
Here, (X_1,Y_1) and (X_2,Y_2) are the known constants. On the (x,y) plane the phase delay of the signal for each receiver can be stated as $k\sqrt{(X_1-x)^2+(Y_1+u-y)^2}$, $k\sqrt{(X_2-x)^2+(Y_2+u-y)^2}$ where k is the wave number of the free-space. In the radar receivers reflected signals, $S_1(u,\omega)$ and $S_2(u,\omega)$, which are recorded as functions of location and angular frequency ω, are given as

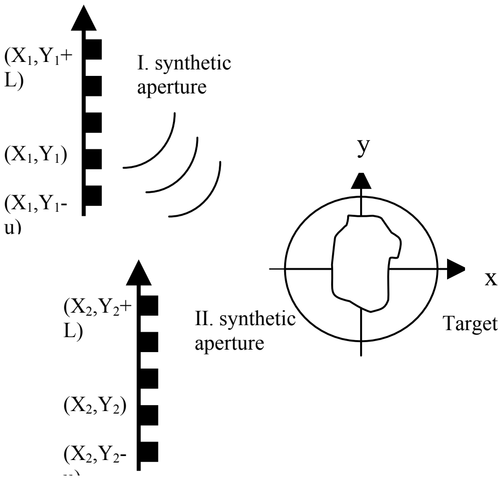

Figure 1. Geometry of a Bistatic SAR Imaging System

$$S_1(u,\omega)=\iint dxdyf(x,y).\exp(jk\sqrt{(X_1-x)^2+(Y_1+u-y)^2})$$

$$S_2(u,\omega)=\iint dxdyf(x,y).\exp(jk\sqrt{(X_2-x)^2+(Y_2+u-y)^2}) \quad (1)$$

in terms of target reflection function f(x,y). The two spherical wave functions seen on the right side of Equation (1) can be expressed with the Fourier expressions in (2)

$$\exp(jk\sqrt{(X_i-x)^2+(Y_i+u-y)^2})= \int dk_u \exp(\sqrt{k^2-k_u^2}(X_i-x)+jk_u(Y_i+u-y)) \quad (2)$$

Equation (3) is obtained by using (2) in (1), [5]

$$S_i(u,\omega)=\int dk_u \exp(j(\sqrt{4k^2-k_u^2}X_i+k_uY_i)). \quad (3)$$

The spatial Fourier transform of $S_i(u,\omega)$ with respect to u is denoted by $S_i(k_u,\omega)$, where k_u is the spatial frequency domain for u, $k_u \in (-2k,2k)$. Taking spatial Fourier transform of (3) we have obtained Equation (4) as follows,

$$F_i(\sqrt{4k^2-k_u^2},k_u)= \exp(-j(\sqrt{4k^2-k_u^2}X_i+k_uY_i))S_i(k_u,\omega) \quad (4)$$

$$k_x=\sqrt{4k^2-k_u^2} \qquad k_y=k_u$$

The transformation expressed by Equation (4) gives the samples of $F(k_x,k_y)$ without requiring the Fresnel approach used in stripmap mode SAR's along the synthetic aperture. The bistatic SAR signal is as a bandpass signal. The algorithm transforms the bandpass to lowpass the target reflection function in the spatial domain and/or frequency domain.

In the algorithm, for each frequency of the radar signal $S_i(k_u,\omega)$, $F_i(k_x, k_y)$ terms are calculated. After repeating the steps for the present frequencies of the radar signals, the data obtained is placed on a rectangular grid by interpolation. In this filled two-dimensional space, the two dimensional inverse Fourier transform is taken and the amplitude of the result is obtained and imaged.

With the classical SAR algorithm, the error diverges when the number of samples and the viewing angles are limited. In the cross range and range resolution, the pulse duration, operation frequency and the synthetic aperture lengths are important. For the target distribution selected in this study, the genetic algorithm [6] is applied to the imaging algorithm and the target locations are determined with minimal error. The additional information for error minimization is obtained by the bistatic receiver. In the cases where the second antenna moves in accordance and independent of the first antenna, the comparison of the results are implemented with respect to the parameters of the genetic algorithm.

When the genetic algorithm is applied for the SAR imaging algorithm, the range and angles of the point targets are taken as the decision variables. The image is also enhanced by varying parameters of the genetic algorithm such as the iteration number, bit number, chrosome number and the synthetic aperture sampling number.

3. APPLICATIONS AND RESULTS

As shown in Figure 1, the radar moves from start position (X_1, Y_1) and transmits - receives the signals of (nn) samples along $u \in [0, L]$. The target consists of point scatterers and it is assumed to be the same plane with the radar. The first radar transmits the signal at the (X_1, Y_1+u) coordinates on the (x,y) plane and $u \in [0, L]$ synthesized aperture and receives at the same coordinate. The second antenna moves from the (X_2, Y_2) coordinates and receives the signal along the synthetic aperture $u \in [Y_2, Y_2 + L]$.

Considering the object reflection function f(x,y) is known at the first step at the simulation, the total reflected signal information $s_i^m(u,\omega)$ is calculated in terms of polar coordinates via $X_1 - x = R\cos\phi,\quad Y_1 - y = R\sin\phi$. Then

$$s_i^m(u,\omega) = \sum_{i=1(u=0)}^{nn(L)} f(x,y).$$

e: ◊ Real Location of Point Targets
o Simulation Results

(5)

In the second step, the total reflected signal information obtained in the first step $s_i^m(u,w)$ and the phase delay of the reflected signals are used to estimate the object reflection function f(x,y) by means of the genetic algorithm. By using this estimated f(x,y) value the total reflected signal information $s_i^c(u,w)$ is obtained as

$$s_i^c(u,w) = \sum_{i=1(u=0)}^{nn(L)} f(x,y)$$

$$\exp\left[j2k\sqrt{(R_i^c \cos\theta_i^c)^2 + (R_i^c \sin\theta_i^c + u)^2} \right] \tag{6}$$

The range and angle values depicting the location of the object are chosen as the variable parameters of the optimization algorithms, and the error function is defined by using the measured and calculated reflected signals (measured at the receiver) as:

$$e = \sum_{j=1}^{nn} \left\{ \mathrm{Re}\left[s_i^m(u,\omega)\right] - \mathrm{Re}\left[s_i^c(u,\omega)\right] \right\}^2 + \\ + \sum_{j=1}^{nn} \left\{ \mathrm{Im}\left[s_i^m(u,\omega)\right] - \mathrm{Im}\left[s_i^c(u,\omega)\right] \right\}^2 \tag{7}$$

In the application, the target estimation is fulfilled by the minimization of this error. The error calculations are implemented for monostatic, bistatic (moving or stationary) second antenna cases. The obtained results are given in Figures 2, 3 and 4, respectively. The results are obtained for 10 samples in the synthetic aperture.

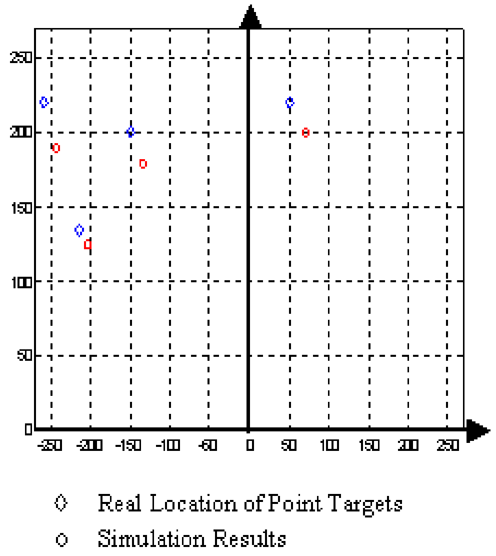

Figure 2. Bistatic SAR, moving receiver

For the genetic algorithm, total number of chromosomes is selected as 100, and each chromosome is formed by 7 bits/parameter. Mutation process has been applied for 1% of the chromosomes at each iteration.

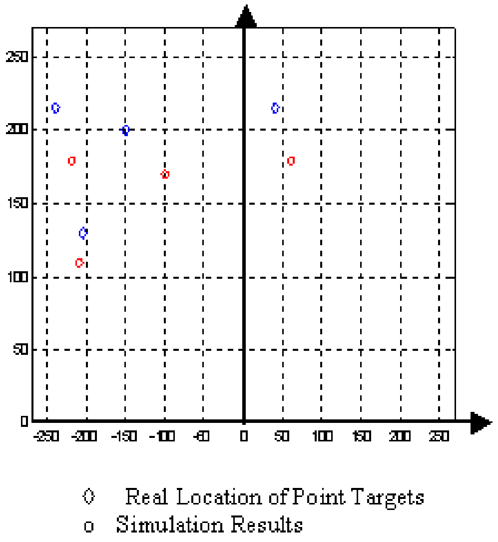

Figure 3. Bistatic SAR, stationary receiver

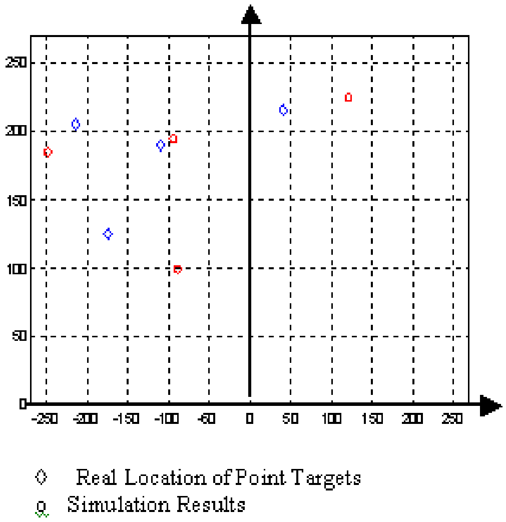

Figure 4. Monostatic SAR

4. CONCLUSIONS

It is seen that the results are enhanced as expected, because the error function is defined by using the monostatic and bistatic antenna arrays for the target distribution and the solution space shrinks for the optimum solution that will be obtained by the error function minimization.

For the bistatic structure, the additional phase information changes when the secondary antenna is stationary or moves with the first antenna and so does the result obtained. It was seen that, the results are better when the second antenna is moving.

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