Position Estimation by Improved Genetic Algorithm for Hyperbolic Location

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***Abstract*—An effective technique in locating a source based on intersections of hyperbolic curves defined by the time differences of arrival of a signal received at a number of sensors is proposed. By making use of the knowledge of the cell's ID, the approach uses coverage shrinkable improved genetic algorithm to search the position coordinates. It is an approximation of the maximum-likelihood estimator and is shown to attain the Cramer-Rao lower bound. Comparisons of performance with the fixed coverage genetic algorithm and the Chan's method are made. The proposed method has higher accuracy than the fixed coverage algorithm and follows closely to the Cramer-Rao bound even at high noise level.**

***Index Terms*—Hyperbolic location, TDOA, genetic algorithm, coverage shrinkable, un-uniform mutation**

I. INTRODUCTION

THE TDOA (Time Difference of Arrival) technique has been found suitable for CDMA wireless cell location system. This technique is based on estimating the difference in the arrival times of the signal from the source at multiple receivers. This is usually accomplished by taking a snapshot of the signal at a synchronized time period at multiple receivers. The cross-correlation of the two versions of the signal at pairs of receivers is done and the peak of the cross-correlation output gives the time difference for the signal arrival at those two base stations. A particular value of the time difference estimate defines a hyperbola between the two receivers on which the mobile may exist, assuming that the source and the receivers are coplanar. If this procedure is done again with another receiver in combination with any of the previously used receivers, another hyperbola is defined and the intersection of the two hyperbolas results in the position location estimate of the source. This method is also sometimes called a hyperbolic position location method.

Once the TDOA estimates have been obtained, they are converted into range difference measurements and these measurements can be converted into nonlinear hyperbolic equations. As these equations are non-linear, solving them is not a trivial operation. Several algorithms have been proposed for this purpose having different complexities and accuracies. Fang [1] gave an exact solution when the number of TDOA measurements is equal to the number of unknowns (coordinates of transmitter). This solution, however, cannot make use of extra measurements, available when there are extra sensors, to improve position accuracy. The more general situation with extra measurements was considered by Friedlander [2], Schau and Robinson [3], and Smith and Abel [4]-[5]. Although closed-form solutions have been developed, the estimators are not optimum. The divide and conquer (DAC) method [6] from Abel can achieve optimum performance, but it requires that the Fisher information is sufficiently large. To obtain a precise position estimate at reasonable noise levels, the Taylor-series method [7]-[8] is commonly employed. It is an iterative method: it starts with an initial guess and improves the estimate at each step by determing the local linear least-squares (LS) solution. An initial guess close to the true solution is needed to avoid local minima. Selection of such a starting point is not simple in practice. Chan [9] proposed a kind of two-step LS algorithm. The solution is in closed-form and is an approximation of the maximum-likelihood (ML) estimator when the TDOA estimation errors are small. Chan's method performs significantly better than spherical interpolation and has a higher noise threshold than DAC before performance breaks away from the Cramer-Rao bound. But if the estimation errors are higher than the threshold, the performance of this algorithm is not optimum too.

This paper gives a new algorithm for hyperbolic position fix. The solution is based on improved genetic algorithm (GA). By making use of the knowledge of the cell's ID, the algorithm searches the optimum solutions directly. Section II considers a 2-D localization problem with an arbitrary array manifold. Section III gives the algorithm. Section IV compares the estimator's localization accuracy with the CRLB and Chan's method. Conclusions are drawn in section V.

II. MATHEMATIC MODEL OF THE HYPERBOLIC POSITIONING

Assume that there are M sensors distributed arbitrarily in a 2-D plane as shown in Fig.1. Let r_i be the measured distance between the mobile and the receiver i. Let $\Delta\vec{r} = [r_{2,1}, r_{3,1}, \dots r_{M,1}]$ be the estimated TDOA vector, where

$$r_{i,1} = r_i - r_1, \quad i = 2,3,\dots,M \qquad (1)$$

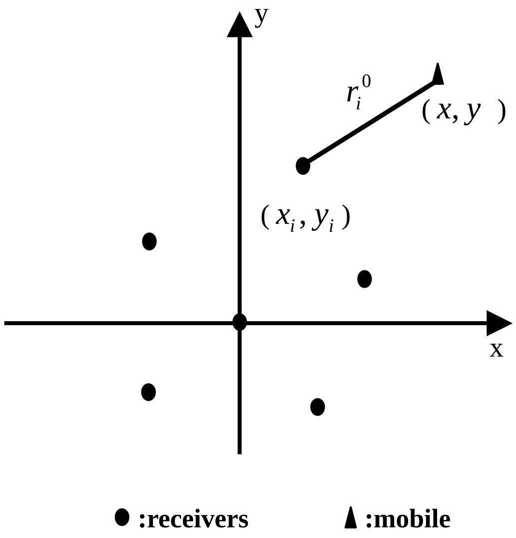

Fig.1 Localization in a 2-D plane

Denote the noise free value of $\{*\}$ as $\{*\}^0$. TDOA $r_{i,1}$ will then be

$$\begin{aligned} r_{i,1} &= r_{i,1}^0 + cn_{i,1} \\ &= r_i^0 - r_1^0 + cn_i - cn_1 \end{aligned} \quad , i = 2,3,\dots,M \qquad (2)$$

with $n_{i,1} = n_i - n_1$ representing the noise (delay estimation error) component. c is the light speed. Define the noise vector as $\vec{n} = [n_{2,1}, n_{3,1}, \dots n_{M,1}]$. cn_i, $i = 1,2,\dots M$ are assumed to be independent, zero mean, white Gaussian noise with the variance σ^2. Then the covariance matrix of $c\vec{n}$ is

$$\begin{aligned} R &= \begin{bmatrix} 2\sigma^2 & \sigma^2 & \dots & \sigma^2 \\ \sigma^2 & 2\sigma^2 & \dots & \sigma^2 \\ \vdots & \vdots & \ddots & \vdots \\ \sigma^2 & \sigma^2 & \dots & 2\sigma^2 \end{bmatrix} \\ &= \sigma^2 \begin{bmatrix} 2 & 1 & \dots & 1 \\ 1 & 2 & \dots & 1 \\ \vdots & \vdots & \ddots & \vdots \\ 1 & 1 & \dots & 2 \end{bmatrix} \overset{\Delta}{=} \sigma^2 \Omega \end{aligned} \qquad (3)$$

Let (x, y) be the coordinates of the mobile and (x_i, y_i), $i = 1,2,\dots M$ be the coordinates of the receiver i, then

$$\begin{aligned} \vec{r}^{\,0} &= \left[r_2^0, r_3^0, \dots r_M^0 \right]^T \\ &= \begin{bmatrix} \sqrt{(x_2 - x)^2 + (y_2 - y)^2} \\ \vdots \\ \sqrt{(x_M - x)^2 + (y_M - y)^2} \end{bmatrix}_{(M-1)\times 1} , \\ \vec{r}_1^{\,0} &= \left[r_1^0, r_1^0 \dots r_1^0 \right]^T \\ &= \begin{bmatrix} \sqrt{(x_1 - x)^2 + (y_1 - y)^2} \\ \vdots \\ \sqrt{(x_1 - x)^2 + (y_1 - y)^2} \end{bmatrix}_{(M-1)\times 1} \end{aligned} \qquad (4)$$

$\Delta\vec{r}$ can be written as

$$\begin{aligned} \Delta\vec{r} &= \vec{r}^{\,0} - \vec{r}_1^{\,0} + c\vec{n} \\ &= \begin{bmatrix} \sqrt{(x_2 - x)^2 + (y_2 - y)^2} \\ \vdots \\ \sqrt{(x_M - x)^2 + (y_M - y)^2} \end{bmatrix} - \begin{bmatrix} \sqrt{(x_1 - x)^2 + (y_1 - y)^2} \\ \vdots \\ \sqrt{(x_1 - x)^2 + (y_1 - y)^2} \end{bmatrix} + c\vec{n} \end{aligned} \qquad (5)$$

The likelihood function of $\Delta\vec{r}$ that depends on the parameter vector $\theta = [x, y]^T$ is

$$\begin{aligned} & p(r_{2,1}, r_{3,1}, \dots r_{M,1} | \theta) = \\ & \left\{ (2\pi)^{\frac{M-1}{2}} |R|^{\frac{1}{2}} \right\}^{-1} \exp\left\{ -\frac{1}{2} (\Delta\vec{r} - \vec{\mu})^T R^{-1} (\Delta\vec{r} - \vec{\mu}) \right\} \end{aligned} \qquad (6)$$

where $\vec{\mu} \overset{\Delta}{=} [r_{2,1}^0, r_{3,1}^0, \ldots\ r_{M,1}^0]^T$.

III. Improved Genetic Algorithm For The Hyperbolic Positioning

According to (6), the maximum-likelihood estimate of the unknown coordinates will be

$$\begin{aligned}\theta &= [x, y]^T \\ &= \arg\left\{\max\left[\exp\left(-\frac{1}{2}(\Delta\vec{r}-\vec{\mu})^T R^{-1}(\Delta\vec{r}-\vec{\mu})\right)\right]\right\}\end{aligned} \quad (7)$$

Substituting (3) to (7), and omitting the scale σ^2 , we can get

$$[x, y]^T = \arg\left\{\min\left[(\Delta\vec{r}-\vec{\mu})^T \Omega^{-1}(\Delta\vec{r}-\vec{\mu})\right]\right\} \quad (8)$$

Solving the nonlinear equations in (8) is difficult. We propose improved genetic algorithm to search the coordinates. With GA we look for the best solution among a number of possible solutions in the search space. In the process of using GA, the process of finding solutions generates other points as evolution proceeds. This is very useful in finding the global optimum solution.

First, get the cell's ID by protocol analyzing. The ID gives the area in which the mobile may exist. Thus the solution space can be determined. Let chromosomes represent the unknown coordinates. The fitness is defined as $1/[(\Delta\vec{r}-\vec{\mu})^T \Omega^{-1}(\Delta\vec{r}-\vec{\mu})]$. The chromosomes are value encoded. Un-uniform mutation[10] is used to improve the accuracy. The mutation operator is defined as

$$\vec{z}^{t+1} = \begin{cases}\vec{z}^t + N_{K\times K}(UB-\vec{z}^t)(1-t/T_0)^b & \text{Random number is 0} \\ \vec{z}^t - N_{K\times K}(\vec{z}^t - LB)(1-t/T_0)^b & \text{Random number is 1}\end{cases} \quad (9)$$

where $\vec{z}$ is the chromosome vector. t is the iterative number. T_0 is the maximum iterative number. $N_{K\times K}$ is a diagonal matrix and the diagonal elements are random numbers in [0,1]. K is the dimension of the chromosome vector. *UB* is the upper bound of the chromosome vector and *LB* is the lower bound of the chromosome vector. Here, the values of *UB* and *LB* depend on the cell's ID. And b is a parameter that determines to what degree the system depends on the iterative number. Usually it is between 4-6[10]. In (11), the item $N_{K\times K}\, y(1-t/T_0)^b$ (y is $(UB-\vec{z}^t)$ or $(\vec{z}^t - LB)$) returns the value between [0, y]. When the iterative number increases, the item will return the value near zero in high probability. At the beginning, the GA searches in the whole space. And when the iterative number increases, the probability that the new offspring are around the parents will increase. By this way, the search in the local space is strengthened, which will help to increase the accuracy.

Based on the un-uniform mutation operator, we propose range shrinkable improved genetic algorithm. When the iteration comes to some extent, the chromosomes will concentrate into a smaller space that the global solutions exist in. And then the new upper bound UB' and lower bound LB' can be decided based on those chromosomes. In the following iteration, the new bounds will work. In this way, the new offspring generated by the mutation will be in the local space. The density of the new offspring in the local space will increase, which helps to strengthen the search and increase the accuracy.

In hyperbolic positioning, supposing the size of the population is $popsize$ and the chromosomes of the t th iteration are $(\vec{z}_1^{\,t}, \vec{z}_2^{\,t} \ldots \vec{z}_{popsize}^{\,t})$, when $t > t_0$, define

$$\begin{aligned} x_{UB'} &= \max[\vec{z}_i^{\,t}(1,1)] + \alpha\,, \\ y_{UB'} &= \max[\vec{z}_i^{\,t}(2,1)] + \alpha\,, \\ x_{LB'} &= \min[\vec{z}_i^{\,t}(1,1)] - \alpha\,, \\ y_{LB'} &= \min[\vec{z}_i^{\,t}(2,1)] - \alpha\,, i = 1,2\ldots popsize \end{aligned} \quad (10)$$

where α is a parameter decided by the cell's radius and $\alpha > 0$. Then, $[x_{LB'}, x_{UB'}]$ and $[y_{LB'}, y_{UB'}]$ outline a rectangular area in which the mobile exist. As shown in Fig.2, the search coverage shrinks.

Supposing the maximum iteration is T_0, the crossover probability is p_c, the mutation probability is p_m, the algorithm is as follows:

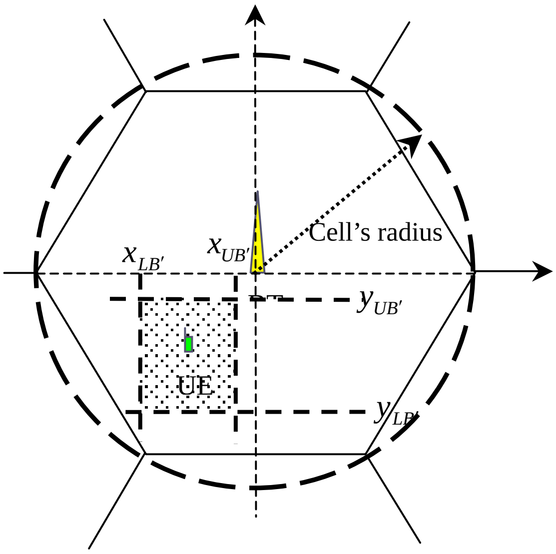

Fig.2 Search coverage

```
$t \leftarrow 0$
initialize the chromosomes;
$flag = 0$ ;
while $t < T_0$
calculate the fitness for each chromosome vector;
roulette wheel selection;
evenly crossbreed according to $p_c$ ;
if $t < t_0$
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```
        if   $randomnumber < p_m$
            un-uniformly mutate based on the cell's size;
        end
    elseif   $t > t_0$ & $flag == 0$
        outline the new search coverage;
        $flag = 1$;
    end
    if   $t > t_0$
        if   $randomnumber < p_m$
            un-uniform mutation based on the new search coverage;
        end
    end
    record the chromosome vector that has the best fitness in this iteration;
    $t = t + 1$;
end
$[x, y]^T$ is the chromosome vector that is finally recorded;
```

In the algorithm, the selection of t_0 is important. If t_0 is small, the algorithm may encounter the problem of prematurity. However, if t_0 is too large, there will be little improvement as the iteration based on the new bounds will not be enough. According to computer simulation, when t_0 is between $0.6T_0 \sim 0.7T_0$, the accuracy of the range shrinkable algorithm is better than the fixed range algorithm with the same population size.

IV. SIMULATION RESULTS

Two kinds of simulations are performed. One is to compare the accuracy of the range shrinkable algorithm and the fixed range algorithm. The other is to compare the location performance of the improved genetic algorithm and Chan's two-step LS algorithm. As Fig.3 shown, there are five receivers distributed arbitrarily in a 2-D plane. The sensor positions are: $(x_1 = 0, y_1 = 0)$, $(x_2 = 500, y_2 = 500)$, $(x_3 = -500, y_3 = 500)$, $(x_4 = -500, y_4 = -500)$, $(x_5 = 500, y_5 = -500)$. The source is at $(x_0 = 100, y_0 = 230)$.

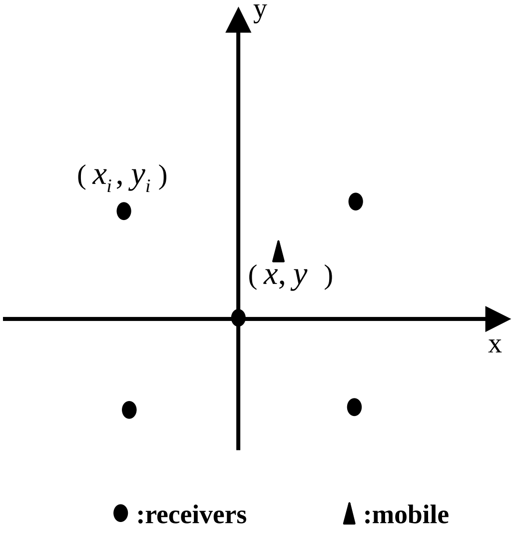

Fig.3 Localization in a 2-D plane

The parameters of the genetic algorithm are as follows: $popsize = 50$, $T_0 = 80$, $t_0 = 0.7T_0$, $p_c = 0.15$, $p_m = 0.25$, $b = 5$.

First, the accuracy of the proposed genetic algorithm and the fixed coverage genetic algorithm is compared. The MSE=$E[(x - x_0)^2 + (y - y_0)^2]$ are obtained from the average of 1,000 independent runs. The results are shown in Fig.4.

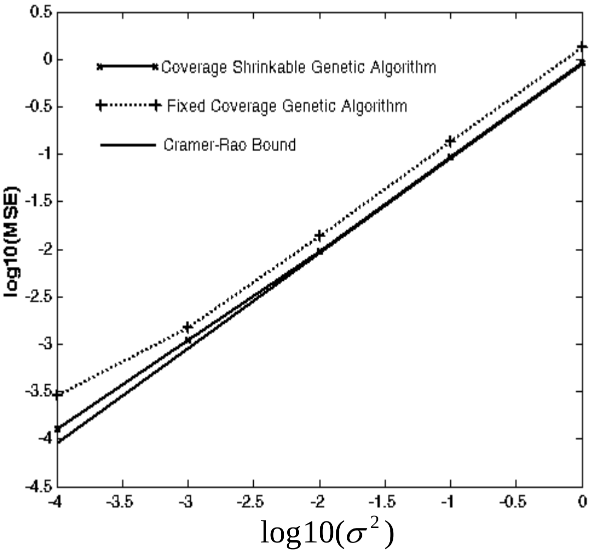

Fig.4 Comparison of MSE for the proposed genetic algorithm and the fixed coverage genetic algorithm

In Fig.4, the MSE of the proposed algorithm and the fixed coverage algorithm are compared with the Cramer-Rao bound (CRLB). Both of these genetic algorithms follow closely with the Cramer-Rao bound. And the accuracy of the coverage shrinkable improved genetic algorithm is better than that of the fixed one.

To give a performance comparison of the proposed method and Chan's two-step LS algorithm, the MSE is studied by varying the TDOA noise power. The condition and parameters are the same as the former simulations. The results are shown in Fig5.

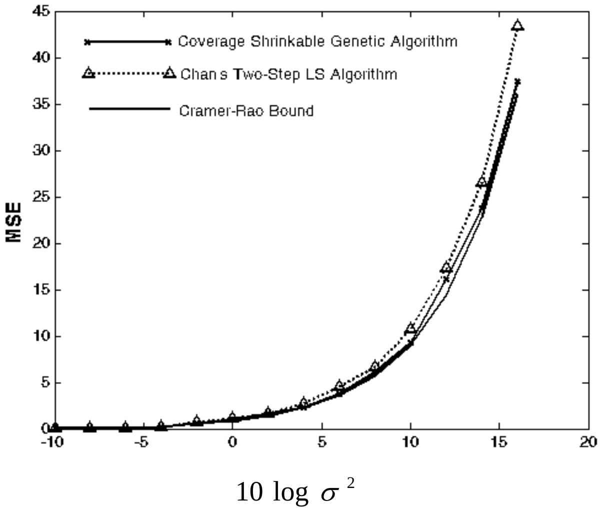

Fig. 5 Comparison of MSE for the proposed method and Chan's method

It can be seen in Fig.5 that the proposed genetic algorithm follows the CRLB more closely than Chan's method. Especially, when the noise power becomes large, the MSE of Chan's method jumps to a large value. The reason is that Chan's method ignores the square noise item. When the noise is small, this kind of approximation is justified. However, when the noise level is high, the approximation is no longer justified. The coverage shrinkable improved genetic algorithm searches the ML solutions directly and the MSE can follow the CRLB closely even at the high noise level.

V. CONCLUSION

A new approach for localizing a source from a set of hyperbolic curves defined by TDOA measurements is proposed. By making use of the knowledge of the cell's ID, a coverage shrinkable improved genetic algorithm can find the position coordinates directly. Simulation results show that this kind of method follows the CRLB closely even at high noise level. No initial guess near to the true solution is needed.

The complexity of the algorithm is larger than other methods. But with the improvement of the CPU, this kind of complexity is acceptable. And in this paper, we have only considered TDOA error. In practical localization system, sensor position uncertainty is often encountered [11]. If the variances of the uncertainties of individual sensors are known, it will not be difficult to incorporate the reciprocal of the variances as weights in equation (10) to give an ML estimator.

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