An Improved DV-HOP Algorithm for Indoor Positioning Based on Bacterial Foraging Optimization

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Abstract—In order to increase the indoor positioning accuracy and reduce the positioning error in wireless sensor network, the Bacterial Foraging Optimization algorithm is introduced to improve the DV-HOP algorithm. The conventional DV-HOP algorithm is not very accurate in calculating the average distance per-hop, and it greatly affects the positioning accuracy. Hence, a new BFO-DV-HOP (Bacterial Foraging Optimization DV-HOP) algorithm is proposed in this paper. The conventional DV-Hop algorithm calculates the average distance per-hop based on the Euclidean distance and the minimum number of hops directly, and the random distribution of the irregular network topology leads to the low accuracy in average hop distance estimation. In BFO-DV-HOP algorithm, the average distance per-hop is calculated by the Bacterial Foraging Optimization algorithm (BFO) by using the minimum hops of nodes and the position information of anchor nodes. Simulation results show that 30% beacon anchors can effectively reduce the positioning error, and 10% beacon anchors can get a better performance compared with conventional algorithms.

Keywords—DV-HOP algorithm; bacterial foraging optimization model; average distance per-hop

I. INTRODUCTION

With the rapid development of wireless sensors networks (WSN), positioning algorithms attach great importance. Currently, depending on the need to measure the actual distance between nodes, the research about indoor positioning algorithm in WSN is generally divided into two categories: range-based algorithm [1] and range-free algorithm [2]. Owing to the additional range devices, the range-based algorithm consumes more energy and increases the overall cost comparing to the range-free algorithm. Thus the rang-free positioning algorithms which including DV-HOP algorithm [3], Centroid algorithm [4] and many other algorithms have become a hot research field these years.

The DV-HOP algorithm can realize the case where a target node has less anchors at its range, which saves the energy to a great extent. There are a great many of range-free positioning algorithms based on DV-HOP have been proposed. Particularly, since many conventional algorithms fail to reduce the positioning error apparently, some researchers try to focus on swarm intelligence area to tackle this problem. In [9], the authors proposed an ABCDV-HOP algorithm to calculate the optimal average distance per-hop and improved the accuracy.

It reduces the computational complexity, but it does not significantly improve the positioning accuracy.

In this paper, compared with other positioning algorithms, a comprehensive study of DV-HOP was conducted. Also, taking advantages of BFO [5] algorithm, we propose the BFO-DV-HOP algorithm and simulation results show that it can reduce the positioning error and improve positioning accuracy apparently.

The rest of the paper is organized as follows. In Section II, we analyzed the existing positioning methods based on DV-HOP. Then, in Section III, after describing the BFO algorithm, we apply BFO algorithm to DV-HOP and a BFO-DV-HOP algorithm is developed. Simulation results for comparisons between the conventional DV-HOP and BFO-DV-HOP are presented and analyzed in Section IV.

II. RELATED WORK

Comparing with these range-free algorithms, we can conclude that although Centroid algorithm is easy to be implemented, it requires a target node to have three neighbor anchors at least. In addition, other algorithms may accumulate positioning error that would lead to low positioning accuracy. The DV-HOP can solve the problem[6] where a target node has less anchors at its range.

In the DV-HOP algorithm, it disseminates the position information of the anchors in the network so that all the target nodes can obtain their minimum hops to the anchors. Secondly, anchors use the distance between each other to calculate and broadcast its average distance per hop as an adjusted value. After receiving the adjusted value, the target node will express the distances to the anchors as the product of the adjusted value and the minimum hop counts to the anchors. And finally, the target node uses the static parameter estimation which includes the maximum likelihood estimation [7], unbiased estimation [9] to work out their own coordinates according to the distance to each anchors recorded before.

In [10], a Selective 3-Anchor DV-HOP positioning algorithm is proposed, in which any three anchors can form a 3-anchor group. In [11], the DV-HOP uses a new average distance per hop based on the differential error of the distance between any two anchors; [12] presents a DV-HOP algorithm using a new method to assign the weights for average distance per hop. In [13], the authors proposed a method to apply the

BFO in the DV-HOP algorithm, but their work cannot show us the best scheme includes the proportion of anchors and the number of nodes because they fail to find the rational characteristic function. Hence, all of them fail to get the higher positioning accuracy and lead to high positioning error.

III. BFO BASED DV-HOP ALGORITHM

A. Bacterial Foraging Optimization (BFO)

The BFO algorithm, which imitates Escherichia coli phagocytosis of food behavior in the human gut, is a bionics algorithm. It is based on the swarm intelligence by Escherichia coli which has its own special behavior of chemo taxis, reproduction and migration. This algorithm has robustness and adaptability which can reach the optimal solution quickly.

In this algorithm, to keep the survival of the population, Escherichia coli records the rational division of labor, cooperation and mutual transfer of information. In the whole process, there are mainly two parts: attraction and rejection agent. The higher attraction, the more nutrients there are. Meanwhile, the rejection agent has a repulsive effect. Also, the scope of the attraction is far greater than the rejection agent. Through the perception and recognition of different environments, the Escherichia coli guides the movement trend. They are able to move in areas of high nutrient concentrations, while far away from the low nutrient concentrations and with a toxin. Therefore, most of the Escherichia coli can survive through the chemo taxis, reproduction and migration, even if some bacteria will die.

As we mentioned above, chemo taxis, reproduction and migration process are the core of the algorithm. In the procedure of chemo taxis, the Escherichia coli, through the process of continuous turnover and forward movement, and gradually to the nutrient intensive areas of chemo taxis and aggregation Then, the bacteria that keep healthy in the last process, are splitting and evolution. In order to avoid the aggregation of bacteria so that the local density is too high, the bacteria try to find a better environment by migration. And it can also find a better foraging area.

At the initial time, the Escherichia coli is on the initial location, and there are many routes to choose. During the process of chemo taxis, reproduction and migration, the Escherichia coli can find the best solution according to the level of nutritional value in the region.
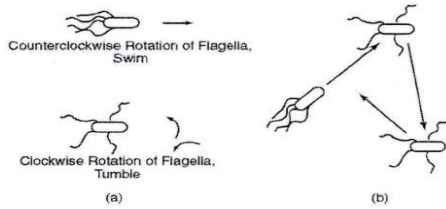

Fig. 1. The process of BFO

B. BFO Algorithm optimized the Average Distance Per-Hop in DV-HOP algorithm

We apply BFO to calculate the optimal average distance per-hop, and reduce the error of the positioning by improving the accuracy of the estimated average distance.

Firstly, we let M represents the number of the anchors in the network, and h_{ij} represents the number of hops from i to j. Also, in the Cartesian coordinate system, we have:

$$d_{ij} = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2} \qquad (1)$$

Here, d_{ij} is the distance from i to j. And Ad_{ij} denotes the average distance per hop. We apply the relation below to estimate the average distance per hop:

$$Ad_{ij} = \frac{\sum_{i \neq j} d_{ij}}{\sum_{i \neq j} h_{ij}} \qquad (2)$$

And we define the error *Error* between the actual distance and the estimated distance from i to j. To attain the most accurate position, we should try to minimize *Error*. We introduce the minimum mean square error to describe this relationship. Hence, we denote $\theta(Ad_{ij})$ as the function of the sum of mean square error, and we select the minimum function value as Eq.3.

$$\theta(Ad_{ij}) = \min \sum_{i \neq j} (d_{ij} - Ad_{ij} \times h_{ij})^2 \qquad (3)$$

To apply BFO to optimize the solution, we present the relationship between the initial solution and the improved solution, and the corresponding relations between the relevant parameters are listed in TABLE I.

TABLE I.　　PARAMETER CONTROL TABLE BETWEEN BFO AND BFO-DV-HOP TABLE STYLES

BFO	BFO-DV-HOP
Initialize the location of the bacteria	All possible solutions of Ad_{ij}
The level of nutritional value in the region	The indexes of the solution Ad_{ij}
The degree of bacterial chemo taxis, reproduction and migration	The optimization speed of the solution Ad_{ij}
The best foraging area of bacteria	The best solution Ad_{ij}

There is a limited communication area between the two nodes, and that's to say, we should define the biggest regional communication radius. Hence, we get,

$$0 \leq Ad_{ij} \leq R \qquad (4)$$

It is of great importance for us to optimize the average distance per-hop, and we should find a characteristic function to apply in the BFO algorithm. As our solution is expected to get the minimum value, we have,

$$F_i = \exp(\alpha - G(Ad_{ij}))^2 \qquad (5)$$

α is the coefficient of the function. And the greater the value α is, the less error we get.

3.3 The BFO-DV-HOP algorithm

Step1：Initialize the population S. There are S solutions which distribute randomly and are generated by Eq.6.

$$Ad_{ij} = Ad_{ij\,min} + rand \times (Ad_{ij\,max} - Ad_{ij\,min}) \qquad (6)$$

$rand$ can generate random numbers from 0 to 1.Also, from (4), $Ad_{ij\,max}$ is R, while $Ad_{ij\,min}$ is 0.

Step2：Calculate the fitness value. Calculate fitness value of each Ad_{ij} according to Eq. 5.

Step3：The Escherichia coli migrates and starts chemo taxis, and this procedure can be illustrated by the equation as follows.

$$J(i,j,k,l) = J(i,j,k,l) +$$

$$\sum_{i=1}^{S}[-a \times \exp(-w \times \sum_{n=1}^{Ad_{ij}}(Ad_{ij}(i,j,k,l) - Ad_{ij}(1{:}S,j,k,l))^\wedge 2)] +$$

$$\sum_{i=1}^{S}[h \times \exp(-z \times \sum_{i=1}^{Ad_{ij}}(Ad_{ij}(i,j,k,l) - Ad_{ij}(1{:}S,j,k,l))^\wedge 2)]$$

$$(7)$$

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        ( Start )
            │
     ┌──────────────┐
     │ Initialization │
     └──────────────┘
            │
┌────────────────────────────────┐
│ Anchors broadcast data, packets {location, │
│ hop}, and the unknown codes record packet │
│ with the minimum hop record │
└────────────────────────────────┘
            │
┌────────────────────────────────┐
│ Using the BFO algorithm to calculate the │
│ average distance per-hop  Ad_ij  of anchor nodes │
└────────────────────────────────┘
            │
┌────────────────────────────────┐
│ Calculate the distance between unknown │
│ nodes and each anchors │
└────────────────────────────────┘
            │
┌────────────────────────────────┐
│ Calculate the coordinate of unknown nodes │
│ by the least square procedure │
└────────────────────────────────┘
            │
     ┌──────────────┐
     │ Error analysis │
     └──────────────┘
            │
        (  End  )
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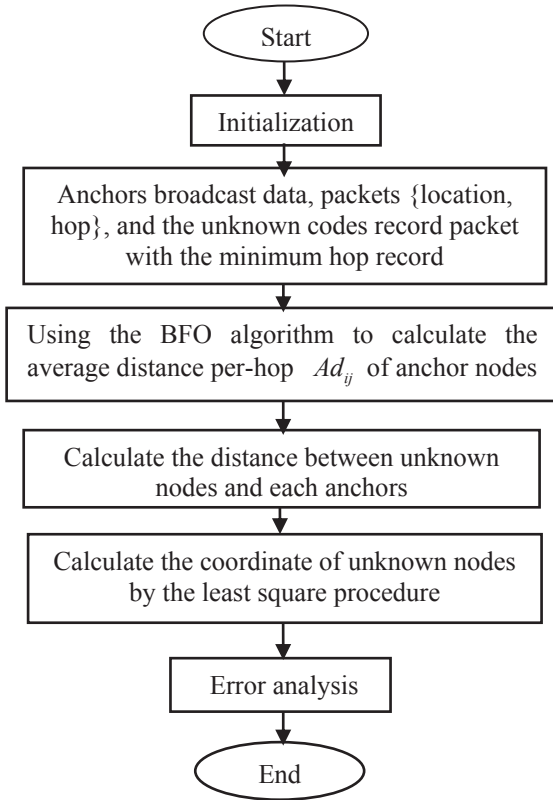
Fig. 2. The process of the BFO-DV-HOP algorithm

Here J represents the degree of adaptation, n is the coefficient of the formula. w is the rate of release of the attracting agent. a represents the number of attractive agents, S is the rate of release of the attracting agent, h represents the number of rejection agents, and z is the rate of release of the rejection agents. In addition, k is the number of chemo taxis, while l is the number of reproduction times.

Step4：Calculate the new generation individual by Eq.5. After several cycles, the loop continues until the optimization reaches the upper limit.

Step5：We get the optimal solution of Ad_{ij}

C. Definition of Positioning Error

The error in positioning can be illustrated as follows, which reflects the accuracy of the localization.

$$Error = \frac{\sum_{i=1}^{E}\sum_{j=1}^{F}\sqrt{(x_i - x_i')^2 + (y_i - y_i')^2}}{EFR} \qquad (8)$$

Here E, F are the number of simulations and the unknown nodes respectively. (x_i, y_i) is the coordinate of the node, while (x_i', y_i') is the estimated coordinate of the node.

IV. SIMULATION AND ANALYSIS

A. Experimental Environment and Conditions

Our algorithm is simulated by the software of MATLAB R2014a. And it runs on the computer with Windows 10 and Intel Core i5 4210 with memory of 4 GB. Firstly, we set the nodes randomly distributed in an area of 100 m × 100 m, and anchors are also selected randomly in this area. All nodes have the same range of R =50m, α =1. Meanwhile, the number of flora is 100 and loops for flora is 25-80. To eliminate the errors caused by the random distribution, we simulated 50 times in the same condition respectively and gained the average value.

B. Simulation Results and Positioning Accuracy Analysis

In this section, we compared the positioning error of DV-HOP algorithm and BFO-DV-HOP algorithm. Specifically, we compared them with two different angles. On the one hand, we assumed that the total number of nodes is constant, but the number of anchors is changed. On the other, the number of anchors is fixed, but the number of nodes is changed.

a) Relationship between anchor and positioning error

We set the total number of nodes is 100, and the anchors changes from 5% to 50%. As shown in Fig. 3, the normalized positioning error decreases with the increasing of the anchors. Also, the error is getting more and more stable. In the same proportion of anchors, the average distance per- hop is getting closer to the actual value. Hence, the error is significantly smaller than the conventional DV-HOP. From TABIE II, we

can clearly come to the conclusion, the BFO-DV-HOP is better than the conventional algorithm, and the accuracy is improved about 10%.

b) Relationship between the position error and the total number of nodes

From Fig. 3, we know the positioning error is stable when the proportion of anchor is 35%. Considering the effect of energy consumption, we set the proportion of anchors is 30% and the total number of nodes is from 60 to 150. With the increasing of the number of nodes, the error decreases and the stability increases. Also, when the number of nodes increases to a certain limit, the error tends to be stable. As shown in

Fig. 4, the positioning accuracy is about 15% higher than that of the conventional DV-HOP. Also, we further show the numerical result in TABLE III.
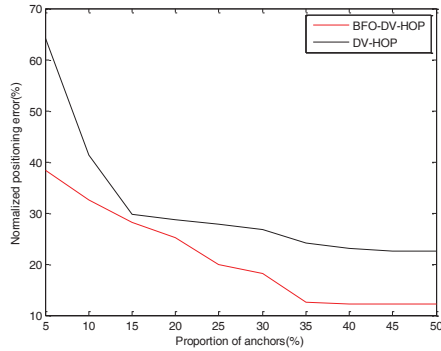

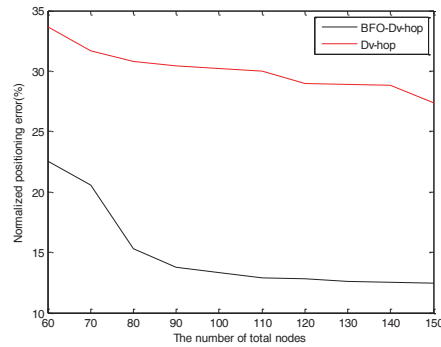Fig. 3. Relationship between anchor and positioning error

Fig. 4. Relationship between the position error and the total number of nodes.

TABLE II.   ERROR OF DV-HOP AND BFO-DV-HOP WHEN THE NUMBER OF NODES IS CONSTANT

Proportion of anchors (%)		5	10	15	20	25
Error (%)	DV-HOP	64.17	41.26	29.71	28.63	27.89
	BFO-DV-HOP	38.27	32.62	28.21	25.23	19.99
Proportion of anchors (%)		30	35	40	45	50
Error (%)	DV-HOP	26.68	24.18	23.04	22.61	22.57
	BFO-DV-HOP	18.25	12.49	12.26	12.26	12.25

TABLE III.   ERROR OF DV-HOP AND BFO-DV-HOP WHEN PROPOETION OF ANCHORS IS CONSTANT

The number of nodes		60	70	80	90	100
Error (%)	DV-HOP	33.68	31.66	30.78	30.45	30.2
	BFO-DV-HOP	22.57	20.53	15.29	13.74	13.3
The number of nodes		110	120	130	140	150
Error (%)	DV-HOP	29.98	28.97	28.93	28.84	27.37
	BFO-DV-HOP	12.92	12.82	12.59	12.54	12.46

V. CONCLUSIONS

In this paper, based on the BFO algorithm, we developed the BFO-DV-HOP algorithm to optimize the indoor positioning accuracy. The BFO-DV-HOP algorithm, which is optimized by the swarm intelligence optimization of BFO, has the higher accuracy and stable operation. It can quickly find the optimal solution based on the characteristic function. This algorithm has higher positioning accuracy by optimizing the average distance per-hop. Simulating results show that BFO-DV-HOP obviously decreases the positioning error. Compared with the conventional DV-HOP algorithm, the indoor positioning precision is improved apparently.

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