Application of Achieve-Based Genetic Algorithm for Consequence Management of Contaminant Entering in Water Distribution Networks

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ABSTRACT: In this research, for the first time, finding the optimal operation actions in WDN to decrease the optimization time is taken into consideration. Valve(s) and hydrant(s) are also employed for isolating and flushing the contamination out of the network. The proposed embedded simulation-optimization approach for consequence management in this study is compromised EPANET simulation model and archive-based non-dominated sorting genetic algorithm-II (NSGA-II). Two objective functions are considered in this paper. The first objective function, minimized numbers of field operational actions related to expenses of the optimal solutions, whereas the other one minimized "consumed contamination mass" take into account for public health and safety. 20 valves and 31 hydrants are designed to insulate the network and discharge pollution, respectively. Without a follow-up management program, the total amount of contamination consumed in the event of network contamination would be 81.3 kg. Using 15 reactive activities, the mass of contamination consumed has reached 60.6 kg. For extracting the Pareto front between these objective functions with general NSGA-II which is a constraint to a maximum of 15 operational actions, approximately 73 minutes is required. To decrease this optimization time, archive-based NSGA-II is taken into account. With an archiving concept, it is possible to not implement a simulation model for similar chromosomes. Sensitivity analysis on the archive capacity of 0, 100, 200, 500, 1,000, 2,000, 3,000, 4,000, and 5,000 chromosomes has been investigated. As an example, with an increase in archive capacity from 0 to 5000, the required time for extracting the optimal Pareto front is reduced from 73 to about 35 minutes, indicating a decrease of more than 50%. The results showed that if a small amount is selected for the archive capacity, for example, 50 or 100, the time required to extract optimal activities increases slightly relative to the base state. The reason for this is that if a small amount is selected for the archive capacity, part of the implementation time of the simulation-optimization model will be spent on finding similar chromosomes, and due to the low capacity of the archive, t is time to use the archive capacity. Using the archive, it is possible to reduce the time optimization and consequence management of the network in real-time operation.

1. INTRODUCTION

So far, a lot of research has been done on the recovery of urban water networks after the occurrence of pollution. In this study, contamination refers to any chemical, biological or radiological contamination that has adverse effects on public health. The studies on consequential management in urban water distribution networks are very limited. This includes researches by Baranowski and LeBoeuf [1], Ostfeld [2], Alfonso *et al.* [3], and Bashi Azghadi *et al.* [4]. In this study, the use of archive-based genetic algorithms to reduce the time required to extract optimal reactive activities is considered. The study of the previous articles shows that the use of archive-based genetic algorithms has been widely used in other topics in water engineering. For example, we can refer to Knowles and Corne's [5] and Fieldsend *et al.*
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[6] researches, but so far the reduction in the extraction time of these optimal activities has not been considered yet. Accordingly, the use of archive-based genetic algorithms to reduce the extraction time of optimal management activities is the main innovation of this research.

2. METHODOLOGY

In this study, EPANET software and its library file have been used in MATLAB program as a quantitative and qualitative simulation model, multi-objective archived-based genetic algorithm as an optimization model and example number 3 of EPANET software has been used as a case study. In this study, the optimal reaction activities are selected from the potential hydrants to discharge contamination from the network and valves to isolate the contamination zone in the network. Fig. 1 shows the steps of the proposed approach.
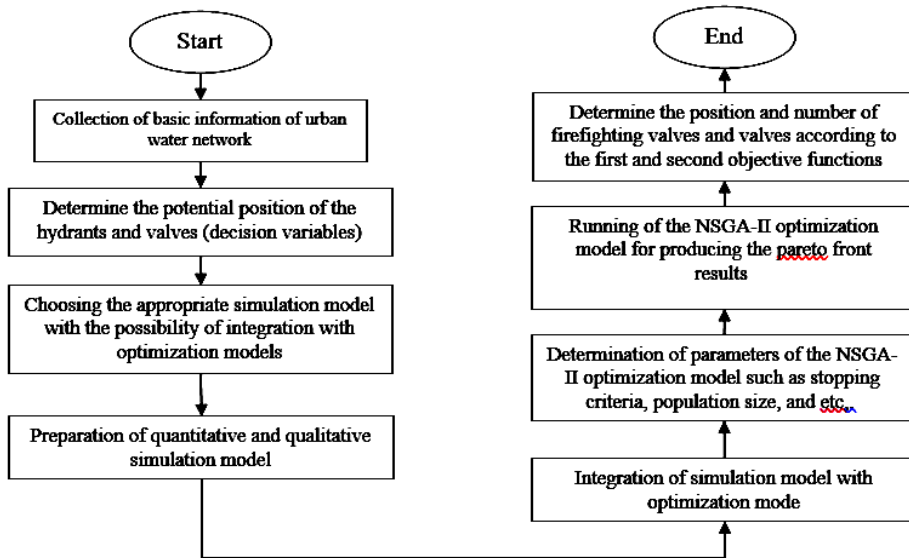
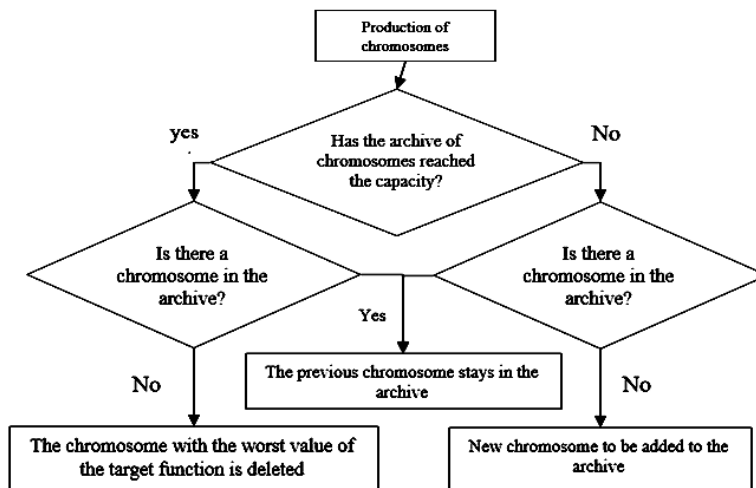**Fig. 1. The proposed approach structure in the management of the consequence**

Fig. 2. Structure of achieve-based genetic algorithm

2.1. Objective functions

In this study, the objective functions used include minimizing (1) the number of reaction activities, and (2) the amount of contamination consumed, which are described below.

2.1.1. Minimize the number of reaction activities (Z1)

$$Z1 = \sum_{i=1}^{V} VA_i + \sum_{j=1}^{H} HY_j \qquad (1)$$

In which, i is the indicator of valves, V is the total number of valves, j is the indicator of hydrants, H is the total number of hydrants, and VA_i and HY_j are the binary decision variables.

2.1.2. Minimize the amount of contamination consumed (Z2)

$$Z2 = \sum_{k=1}^{N} \sum_{t=td}^{EPS} C_{kt} \times V_{kt} \qquad (2)$$

In which, K is the node indicator, t is the time index, td is the time elapsed after the time of contamination detection in the network, and EPS is the total time. C_{kt} is the pollution concentration in node K in time t, and V_{kt} is the consumed polluted water in node K in time t.

2.2. Archived-based genetic algorithm

The structure of the multi-purpose genetic algorithm based on the archive considered in this study is shown in Fig. 2.
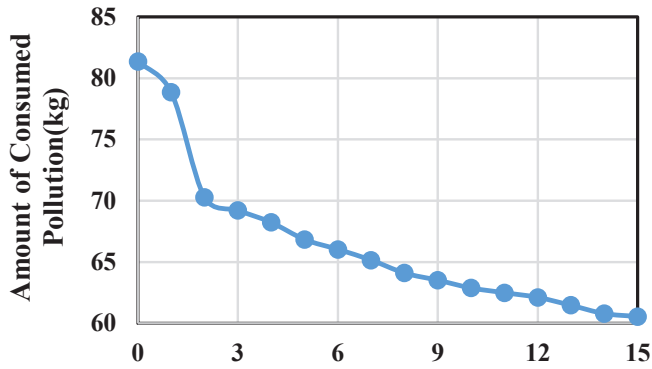
Fig. 3. The Curve of Interaction between the Various Goals of Consequence Management

Fig. 4. Time to extract the curve of interaction between goals for different archive capacities

Based on this Figure, an archive with a specific capacity for storing different chromosomes is first prepared. Then, due to the production of each new chromosome in the multi-generational genetic algorithm in each generation, if the archive capacity has not reached its maximum value and this new chromosome is not already in the archive, it will be added to the archive and if it is in the archive, the previous chromosome will be saved in the archive. Also, if the archive has reached its maximum capacity and there is no new chromosome in the archive, the chromosome will be removed with the worst value of the objective function. The above solutions make the archive have unique and appropriate chromosomes from the perspective of the objective function.

3. RESULTS AND DISCUSSION

Example 3 EPANET software has been used in this study as a case study. In this study, five sensors were identified in nodes 15, 35, 145, 225, and 255 to detect pollution based on maximizing the correctness of spatial detection. Fig. 3 displays the optimal interaction curve between the number of reactive activities and the amount of contamination used. As shown in this Figure, without performing a consequence management program, the total amount of contamination consumed in the event of network contamination would be 81.3 kg. Using 15 reactive activities, the mass of contamination consumed has reached 60.6 kg.

It takes about 73 minutes to extract the interaction curve between the goals presented in Fig. 4. In this Figure, the time required to extract optimal activities (the interaction curve between different goals) is shown. As can be seen, as the capacity of the archive increases, the time required to extract optimal response activities also decreases. For example, increasing the capacity of the archive from zero to 5,000 will reduce the time required from 73 to about 35 minutes, indicating a reduction of more than 50 percent. This reduction in time, and consequently in the reduction of the response time of reactive activities, will have a significant effect on increasing the effect of optimal reactive activities extracted in reducing the mass of contamination consumed.
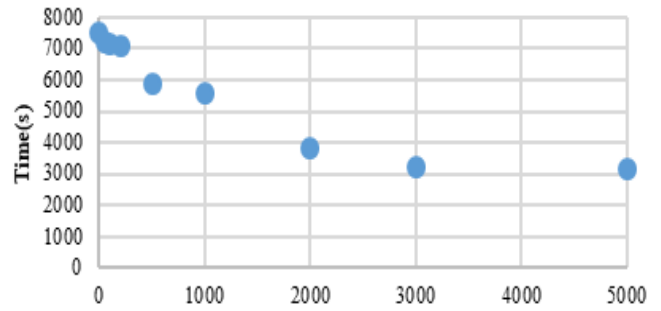
4. CONCLUSION

In the proposed approach, using the archive capacity, it is possible not to run the simulation model for similar chromosomes, which leads to a significant reduction in the execution time of the model without reducing the model results. In the proposed approach, the archive capacity with 0, 100, 200, 500, 1000, 2000, 3000, 4000, and 5000 chromosome numbers was examined, which also had good results. For example, in general, as the archive population increases from 0 to 5,000, the time required to extract the interaction curve between goals decreases from 73 to 35 minutes, indicating a decrease of more than 50 percent.

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