JOB SHOP RESCHEDULING USING A HYBRIDIZATION OF GENETIC ALGORITHM AND ARTIFICIAL IMMUNE SYSTEMS

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ABSTRACT. This paper discusses on developing a hybrid model of genetic algorithm and artificial immune systems to tackle the problem of changing environment in the job shop scheduling problem. The main idea is to use the model to develop building blocks of partial schedules that can be used to provide backup solutions when disturbances occur during production. Each partial schedule, also known as antibody, is assigned a fitness value for the selection of final population of best partial schedules. The results of the analysis are compared with a previous work. Future works on this study are also discussed.

Keywords: artificial immune systems, genetic algorithm, job shop scheduling

INTRODUCTION

Job shop scheduling problems is concerned with tackling the problem of assigning *n* jobs to *m* machines. Several local search techniques such as genetic algorithm, simulated annealing, ant colony system and tabu search have been used to address the problem. Fang et al (1993), and Jensen and Hansen (1999) used a genetic algorithm to produce robust schedules for scheduling problems, where Fang also addressed a job shop rescheduling problem. This study specifically focuses on tackling the problem of changes in job shop environments. The changes include unexpected arrival dates of jobs in a factory. When jobs arrive too early, it might lead to jobs being stored for long periods of time and if they arrive late, it could cause delays in processing other jobs. An efficient method of rescheduling is needed to manage the problem.

This study aims to generate a range of partial schedules that could be used to produce backup schedules to maintain smooth flow of manufacturing process. In this paper, genetic algorithm and artificial immune system techniques are used to build these partial schedules. Past, complete schedules (later known as the antigen universe) are used to build this collection of partial schedules. The data stems from (Hart & Ross, 1999) where the number of jobs used is 15 assigned to five machines. These processes will be explained in the next section. Finally, findings from the experiments will be discussed.

A HYBRID GENETIC ALGORITHM AND ARTIFICIAL IMMUNE SYSTEMS MODEL

The solution model for this study is developed from the theory of artificial immune system (AIS), which are then evolved using a genetic algorithm (GA).

AIS are inspired by the study of immunology. The biological immune system protects the body against antigens and generates antibodies that can bind to a specific antigen. A biological antibody evolves to enable it to adapt with new antigens in addition to the common antigens. de Castro and Timmis discussed the classification of systems as artificial immune system. The system developed has to incorporate a basic model of an immune component and has to be designed by drawing upon theoretical or experimental ideas from immunology (De Castro & Timmis, 2002).

Previous works on scheduling has shown that AIS and GA can be used to solve scheduling problems in a manufacturing environment. Different scheduling problems have been addressed including the job shop scheduling problem (Bin et al, 2011; Chandrasekaran et al, 2006; Coello et al, 2003; Ge et al, 2005; Hart et al, 1998; Mohsen & Hadieh, 2012; Ren & Yuping, 2012), flexible job shop scheduling (Bagheri et al, 2010), the hybrid flow shop scheduling problem (Engin & Doyen, 2004) and the job shop rescheduling problem (Hart et al, 1998; Hart & Ross, 1999; Hart & Ross, 1999), which is the main concern of this study. Hart and Ross built a block of partial schedules to tackle the job shop rescheduling problem (Hart & Ross, 1999). There are many definitions given to the antibody and the antigen for the problem. This study employs the definition given by Hart and Ross. The key definitions used are described below:

- An **antigen** is defined as "*the sequence of jobs on a particular machine given a particular scenario*" (Hart & Ross, 1999), which represents a complete schedule for the problem. For the experiments in this study, the antigens are represented by a sequence of numbers of length 15.
- An **antibody** is defined as "*a short sequence of jobs that is common to more than one schedule*" (Hart & Ross, 1999), which is also known as partial schedules. The antibodies are represented by sequences of numbers of length 5, where the length of an antibody is less than the length of an antigen.
- An **antigen universe** is considered to be a collection of antigens to be matched with the antibodies. An antigen universe has to be prepared before we can build an antibody population.
- An **antibody population** is a collection of partial schedules constructed from gene libraries.

The study is divided into three phases; generating the antibody population, evolving the antibody population, and recombine the partial schedules. In this paper, we are mainly concerned with the first two phases only.

Generate Antibody Population

An antigen universe must be created before antibody populations can be generated. The antigen universe for this study is the same used by Hart and Ross (1999), which is based on a benchmark problem by Morton and Pentico (1993). The number of jobs used in this problem is 15 and the jobs have to be assigned to five machines. Hart and Ross created ten test scenarios by mutating the arrival dates of the jobs to a random date between 0 – 300 with a probability of 0.2. The arrival dates must not be less than p_t days before the due date, where p_t is the

processing time of the job. A genetic algorithm developed (Fang et al, 1993) is used to generate five schedules for each of these test-scenarios. This resulted in five sets of ten schedules; one for each machine, and these schedules became the antigen universe for the study. This study uses the antigen universe generated from one of the machines with the assumption that all machines have a similar pattern of jobs.

An antibody population is generated from gene libraries (Coello et al, 2003; Hart & Ross, 1999; Hart & Ross, 1999; Spellward & Kovacs, 2005). The gene libraries in this study are constructed from all the antigens in the antigen universe. The antigens are divided into five libraries, each consisting of ten partial schedules of size 3, also known as components. An antibody for this study is constructed based on a modular design method (Goldsby et al, 2000; Hightower et al, 1995; Oprea & Forrest, 1998; Sompayrac, 2003) where the length of each antibody is 1/3 the length of each antigen.

As an example, assume a set of gene libraries, consisting of four libraries and each library contains three components. Three genes (jobs) are allocated in each component. Following the modular design method, there are several ways to combine the genes from the components to produce an antibody. In For example, the first component from Library 1 can be combined with the second component from Library 2 to produce an antibody. Since the length of an antibody is 5 jobs, a possible combination of

$$P\binom{n_1}{r_1} \times P\binom{n_2}{r_2} = \frac{n_1!}{(n_1 - r_1)!} \times \frac{n_2!}{(n_2 - r_2)!}. \quad (1)$$

can be constructed from this example, where n_1 and n_2 represent the number of jobs in the components from the first and second library, respectively, and r_1 and r_2 represent the number of jobs to be selected from the components. From the example, we can see a combination of three jobs from the first component and two jobs from the second component. We can get other combinations from these two components using Eq. (1) above to generate an antibody population. This process is repeated until all the components in Library 1 have been combined with all the components in Library 2, as well as all the other libraries.

It is also important to ensure no recurring jobs exist in one antibody. Each antibody generated in the population is filtered and antibodies with recurring jobs are eliminated. The process continues until a population of antibodies is generated.

Evolving the Population

A genetic algorithm based on GENESIS (Grefenstette, 1984) is used to evolve the antibody population. Order-based crossover operator is used as it can ensure no job duplication in an antibody for any relationship between two parent antibodies. During crossover, tournament selection is applied to select the best antibody to be included in the next generation. The fitness of the children produced is evaluated and the values are then compared with the fitness of the parents. If the children produced have lower fitness than the parents, they will be discarded, and the parents are selected for inclusion in the next generation. Only the best antibodies, i.e. antibodies with the highest fitness, will be considered for the next generation. A mutation operator, which randomly mutates each gene with a probability of 0.2, is also applied (Hart & Ross, 1999).

The fitness of each antibody in the antibody population is then calculated using a matching function. A sample of antigens is first selected from the antigen universe. Each antibody is then matched against each of the antigens selected by aligning an antigen string with an antibody string and calculating a match score.

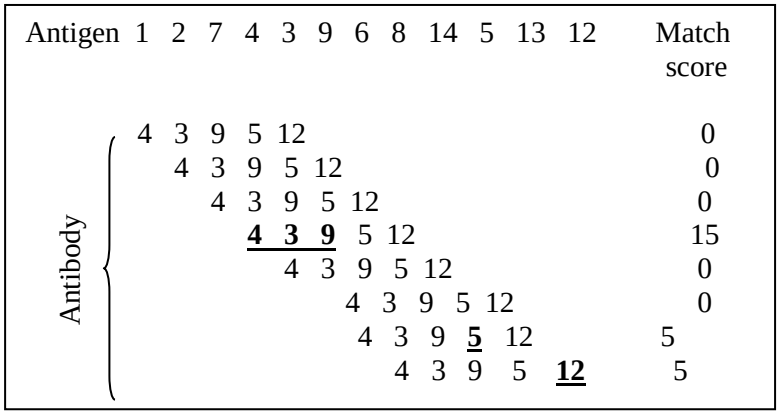

Figure 1. The process of matching an antibody with an antigen by aligning the antibody at every possible alignment position

Based on the example in Figure 1, antibody string '4 3 9 5 12' is aligned at every possible alignment position with the antigen string '1 2 7 4 3 9 6 8 14 5 13 12, job by job in order to calculate a match score. A match score is calculated by summing up the scores from the job matches where a match of each position contributed a score of five. Therefore, based on the number of matches between both the antibody and the antigen, the match score for the example given above is 15, which is the best possible match found (highest match score) by this process. Since an antibody is matched with each of the antigens in the sample, for antibody matched against more than one antigen, a total match score for the antibody is calculated by summing up the highest match scores from its match with each antigen.

Hart and Ross (1999) selected certain samples of antibodies from the antibody population to be matched with a sample of antigens and repeated the matching process for a certain number of iterations based on the number of antigens selected. In this study, all the antibodies in the population are matched with the antigens and the matching process is run only once.

FINDINGS

Using a base problem *jb11*, taken from Morton and Pentico (1993), ten test scenarios have been generated (Hart & Ross, 1999). The schedules generated from the problem became the antigen universe for this study.

The antigen universe generates three types of antibody populations: 1) Type A - Population with antibody duplication (similar antibodies can exist in one population), 2) Type B – Population with no antibody duplication, and 3) Type C – Population with antibody duplication when the antibodies are constructed from different source libraries. These three types of antibody populations are generated as a test to see whether having a large number of similar antibodies in one population would affect the coverage of the antigen universe by the antibody population.

In the first phase, an initial population of size 100 was selected randomly from each type of antibody population. These populations were evolved using a genetic algorithm for 250 generations, with a crossover rate 0.7. Two mutation rates are used in the experiments. A mutation rate of 0.2, which is the same parameter used in (Hart & Ross, 1999) is applied so that it is easier for results comparison purposes. Then, a mutation rate of 0.001 is used as it gives a steady growth of the fitness of the antibodies in the antibody population. The antibodies evolved here were the antibodies with the highest fitness value in each generation. As the antibodies evolve, the average fitness of the antibodies also increases. At the end of the genera-

tion, the final population should consist of a collection of general and specific antibodies, which could either match many antigens or only one specific antigen.

Table 1. Average number of antigens (out of a possible 10) not matched by any antibody as generated by Hart and Ross (1999)

Match Thres-hold	Ag = 1			Ag = 4			Ag = 8		
	Ab			Ab			Ab		
	5	10	30	5	10	30	5	10	30
2	0.9	0.0	0.0	2.2	0.9	0.0	3.5	2.5	0.9
3	5.3	2.6	1.6	5.4	3.2	2.0	5.5	4.7	4.1
4	8.7	7.1	5.2	7.8	7.3	6.3	8.6	8.1	8.2
5	9.7	9.5	8.8	9.5	9.5	8.7	9.7	9.6	9.5

Tables 1 and 2 show the average number of antigens that cannot be matched by any antibody for a match threshold ranging from 2 to 5. A match threshold, t_m, is a guideline to determine whether an antibody and antigen are matched. The number of jobs to bind or match must be greater or equal to the threshold value of t_m (Hart & Ross, 1999). This experiment tests the coverage of the antigen universe by the antibody population. Table 1 shows the results of the experiment by Hart and Ross. Table 2 shows findings from this study performed on final populations generated from the antibody population Type A, Type B and Type C, respectively (Phase I) with a mutation rate of 0.2.

Table 2. Average number of antigens (out of a possible 10) not matched by any antibody (hybrid GA and AIS)

Match Thres-hold	Ab = 100								
	Type A			Type B			Type C		
	Ag			Ag			Ag		
	1	4	8	1	4	8	1	4	8
2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	0.4	0.0	0.0	0.9	0.1	0.0	0.8	0.1	0.0
4	6.5	3.6	1.3	6.2	3.4	1.4	6.6	3.2	1.3
5	8.5	6.3	4.7	8.3	6.6	5.3	8.2	7.1	5.8

In Table 1, the results from Hart and Ross created a trend where the average number of antigens not matched by any antibody decreases as the size of the antibody samples, *s* increases from 5 to 30. The analysis in Table 2 is in line with the trend where the average number of unmatched antigens decreases when the whole population is matched against the antigens. However, in this study, as compared to Hart and Ross, it is found that when the number of antigens increases, the average number of antigens that cannot be matched by any antibody decreases. While the result by Hart and Ross could be interpreted as evidence that more specific antibodies have been produced, it is believed that this study is able increase the fitness of the antibodies when more antigens are exposed to the antibodies. This results in more antigens getting matched or recognized.

The mutation rate used in the study also plays a role in producing antibodies with better fitness. Table 3 also shows the results of the average number of antigens not matched by any

antibody in population Type A, when a mutation rate of 0.001 is used. By using a lower mutation rate, the fitness of the antibodies in the antibody population steadily increases. This also results in more antigens being matched by the antibodies as depicted in the table. Therefore with this study, the partial schedules produced can be used as replacement to an actual schedule when disturbances occur.

Table 3. Average number of antigens (out of possible 10) not matched by any antibody in population Type A (mutation rate 0.001)

Match Thres-hold	Ab = 100		
	Type A		
	Ag		
	1	4	8
2	0.0	0.0	0.0
3	0.6	0.1	0.0
4	6.8	3.0	1.0
5	7.9	6.0	4.4

CONCLUSION

A hybrid model of AIS and GA has been developed to tackle the problem of job shop rescheduling. The findings represent an improvement from those in the previous works. While the results did not show improvement in terms of the coverage of the antigen universe, they did improve the fitness of the antibodies produced in the population. This is important in order to find good search algorithm that could produce a range of good partial schedules to be used as replacement for certain jobs in the actual schedule when changes occur in the arrival dates of the jobs. Further work for this study is to investigate the possibilities of hybridizing the current model developed with local search algorithms to improve the performance of the model.

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