



The Flowshop Scheduling Makespan by the ACO-GA Algorithm

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ABSTRACT

Flow shop scheduling could be a scheduling model where all jobs that are processed flow within the same direction / path. the matter is usually faced if n jobs are processed on m machines, where what must be done first and what allocates jobs on the machine in order that a scheduled production process are obtained. To validate this algorithm a computational test was done employing a dataset of 60 examples from the Taillard Benchmark. HS algorithm with a comparison of two constructive heuristics from the literature, namely the NEH heuristic and stochastic greedy heuristic (SG). The average results obtained for dataset sizes are 20 x 5 to 50 x 10, that the ACO-GA algorithm has smaller makespan compared to the opposite two algorithms, except for large dataset sizes the ACO-GA algorithm has larger makespan compared to the 2 algorithms above with difference of 1.4 units of your time

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1. Introduction

Market development contributors are manufacturing companies, there are many problems within the field of scheduling companies to take care of efficiency and productivity where the corporate requires the allocation of information sources for future activities, to extend company productivity. Companies are required to take care of efficiency in reducing production costs with a brief interval [1] - [4].

Flowshop scheduling may be a scheduling model where work is completed for all processes flowing within the same direction [5],[6], problems often arise if there are n jobs being processed on m machines [7] - [11].

Scheduling flow plays a crucial role to produce optimal solutions to the corporate, with the aim of scheduling flowshop to attenuate the time of labor completion [5] - [7]. Shabtay, 2012 [18] minimizing the makespan within the flowshop problem using Johnson's algorithm, disbursed with an analytical approach to resolve n-jo with 2 machine problems. supported testing and comparison with relevant [9] [10]. Rajendra and Ziegler (2013) [13] flowshop problem using ACO and M-MMAS, the effectiveness of ACO is taken into account within the problem useful limits, the results of the experimental performance shown in ACO are better than in 83 out of 90 cases. Ta's research, 2015 [12], determines work production and delivery for groups, so procrastinators may be minimized, Heuristic Algorithms are proposed on random data to point out increased tabo search. Hybrid GA and ACO to supply TSP and evaluated to some random data and samples from the TSP data set [3], [13], during this case the results of the hybrid method are proposed to extend, but specialise in the mixture of GA and ACO from two sides optimal [4].

2. Methodology

The algorithmic process is as follows:

1. Cell data input
2. ACO data initialization
3. Calculate job time for each job (GA)
4. Calculate changes between points





5. Update the intensity of the trail between points
6. If it stops or the maximum number is finished, then sort the job, if not return to step – 2.

3. Results and Discussion

Determine Make span time using the following steps:

3.1. Population Initialization

Flow shop scheduling representation with the following process:

- a. Determine the jobs and machines used.
- b. Determine the job processing time on each machine.
- c. Determine the sequence of job processes from 1 to n.

For example, Chromosome 1 job 1 on machines 1 to 3 machines with the time machine-1 = 80, machine-2 = 70, machine-3 = 60 are as follows: K-1: 1.1 1.2 1.3 210

Chromosome 2 jobs 2 on machines 1 to 3 machines with time machine 1 = 40, machine 2 = 30, machine 3 = 50 are as follows: K-2: 2.1 2.2 2.3 120

Chromosome 3 job 3 on machine-1 to machine-3 with a time machine-1 = 40, machine-2 = 30, machine-3 = 60 are as follows: K-3: 3.1 3.2 3.3 130

Chromosome 4 job 4 in machines 1 to 3 machines with the time machine-1 = 75, machine-2 = 50, machine-3 = 65 are as follows: K-4: 4.1 4.2 4.3 190

Henceforth, a crossover is performed.

3.2. Crossover

Crossover is a combination of parent genes to produce new offspring. Crossover used in this study was two points. This is done by exchanging gene values at the same gene position of the two parents. The following are the stages of the crossover process:

- a. The crossover between chromosomes in Parent 1 is chromosomes 1 with chromosome 2 by exchanging the values of randomly selected genes:

K-1: 1.1 1.2 1.3 with the value of makespan 210

K-2: 2.1 2.2 2.3 with the value of makespan 120

Chromosome 1 Parent 1 with Chromosome 2 Parent 1 in positions 1 and 3:

Table 1.

Simulations on two crossover points

1.1	1.2	1.3
2.1	2.2	2.3

The result of the generation of the crossover process from two individual parents:

Child 1 Parent 1

2.1	1.2	2.3
-----	-----	-----

Makespan = 40 + 70 + 60 = 170

Child 2 Parent 1

1.1	2.2	1.3
-----	-----	-----

Makespan = 80 + 30 + 60 = 170

- b. The chromosome crossover process of two individual parent-3 to parent-4 exchanges gene values:

K-3: 3.1 3.2 3.3 the value of makespan 100

K-4: 4.1 4.2 4.3 the value of makespan 160

Chromosome 1 Parent 2 with Chromosome 2 Parent 2 at position 1 and 3:

3.1	3.2	3.3
4.1	4.2	4.3





the results of the generation of the crossover process from parent 2:

Child 1 Parent 2

4.1	3.2	4.3
-----	-----	-----

$$\text{Makespan} = 75 + 30 + 65 = 170$$

Child 2 Parent 2

3.1	4.2	3.3
-----	-----	-----

$$\text{Makespan} = 30 + 40 + 50 = 120$$

3.3. Mutations

The mutation process uses the reciprocal exchange mutation method with random numbers (Pm). Chromosomes mutate as much as 10% randomly selected mutation probability values. This process is done by exchanging two genes without the help of another chromosome to avoid being stuck.

2.1	1.2	2.3
-----	-----	-----

$$\text{Makespan} = 40 + 70 + 60 = 170$$

Furthermore, the chromosomes are carried out mutations in gene number 3

2.1	1.2	1.1
-----	-----	-----

$$\text{Makespan} = 40 + 30 + 80 = 150$$

3.4. Termination

Termination is repeating the initial steps of population initialization for chromosome formation in line with genetic parameters. Furthermore, the chromosomes formed are sequences of the scheduling process which can be further processed with the ACO algorithm.

Table 2
First Generation Genetic Chromosome Populations

Kr/Gen	Gen-1	Gen-2	Gen-3	Make span
Kromosom-1	2.1	1.2	1.1	190
Kromosom-2	1.1	2.2	1.3	170
Kromosom-3	4.1	3.2	4.3	170
Kromosom-4	3.1	4.2	3.3	150

The data that is processed is the process scheduling matrix of the genetic process with 4 jobs on 3 machines with different times.

For example, Chromosome 1 job 1 on machines 1 to 3 with engine time 1 = 70, machine 2 = 60, machine 3 = 50 are as follows:

$$1.1 = 80, 1.2 = 70, 1.3 = 60$$

Chromosome 2 jobs 2 on machines-1 to machines 3 with engine-time = 30, machines-2 = 20, machines-3 = 40 are as follows:

$$2.1 = 40, 2.2 = 30, 2.3 = 30$$

Chromosome 3 job 3 on machine-1 to machine-3 with time machine-1 = 30, machine-2 = 20, machine-3 = 50 are as follows:

$$3.1 = 40, 3.2 = 30, 3.3 = 60$$

Chromosome 4 job 4 on machines-1 to machines-3 with the time machine-1 = 65, machine-2 = 40, machine-3 = 55 are as follows:

$$4.1 = 65, 4.2 = 40, 4.3 = 55$$

From Table 3.10 above, it can be seen that the Job sequence in the form of Chromosomes is:





Chromosome 1:

Job-2 = engine-1 (40)

Job-1 = engine-2 (70)

Job-1 = engine-1 (80) makespan = 190

Chromosome 2:

Job-1 = engine-1 (80)

Job-2 = engine-2 (30)

Job-1 = engine-3 (60), makespan = 170

Chromosome 3:

Job-4 = engine-1 (75)

Job-3 = engine-2 (30)

Job-4 = engine-3 (65) makespan = 170

Chromosome 4:

Job-3 = engine-1 (40)

Job-4 = engine-2 (50)

Job-3 = engine-3 (60) makespan = 150

Table 3.

Spacing between points (dij) on a G-chromosome graph

Titik	M-1	M-2	M-3
J-1	80	70	-
J-2	40	-	50
J-3	40	30	60
J-4	75	50	65

Table 4

Matriks *Flow Shop*

Node	M-1	M-2	M-3
J-1	80	70	-
J-2	40	-	50
J-3	40	30	60
J-4	75	50	65

Table 5.

Visibility between Points (η_{ij})

Node	M1	M2	M3
J1	1/80	1/70	-
J2	1/40	-	1/50
J3	1/40	1/30	1/60
J4	1/75	1/50	1/65

Table 6.

Visibilitas between node (η_{ij}) pada Graf *G*

Node	M1	M2	M3
J1	0.014	0.016	-
J2	0.033	-	0.025
J3	0.033	0.050	0.020
J4	0.015	0.025	0.018

Table 7

Feromon between node pada Graf *G*

Titik	M1	M2	M3
J1	0,01	0,01	-
J2	0,01	-	0,01
J3	0,01	0,01	0,01
J4	0,01	0,01	0,01





The visibility (η) and pheromone (τ) values are employed within the probability equation and so the parameters stricken by the ant within the subsequent point selection.

Search for the subsequent destination node using probability:

Probability on Chromosome-1 = 2.1 1.2 1.1

Cycle -1:

Fill out the initial Taboo:

2.1 1.2 1.1

at $t = 1$

The number of ants per node =

$M-1 = 1$

$M-2 = 1$

$M-3 = 1$

1st Ant:

- Taboo list = 2.1

- The probability from node 2.1 to each subsequent node is:

$= (0.1 * 0.33) + (0.1 * 0.16) + (0.1 * 0.14)$

$= 0.063$

By calculating the probability of node 2.1 on each node as follows:

Point 2.1 = 0

Point 1.2 = $(0.1) \cdot 1.0 \cdot (0.16) \cdot 1.0 / 0.0063 = 0.253$

Point 1.1 = $(0.1) \cdot 1.0 \cdot (0.14) \cdot 1.0 / 0.0063 = 0.222$

Cumulative Probability: 0 0.253 0.475

Random numbers generated: $r = 0.399$

Checking qk-1

Fill Tabu List = 2.1 1.1

Pheromone local update

$t_{ij} \leftarrow (1-\rho) \cdot \tau(i, j) + \rho \cdot \Delta i(i, j)$

With $\Delta(i, j) = 1 / (P_{ij} \cdot C)$

Where,

P_{ij} = time job i on machine j ,

C = number of machines

ρ = parameter from 0 to 1,

$\Delta \tau(i, j)$ = change in pheromone

$\Delta \tau(\text{Chromosome-1}) = 1 / 3.60 = 1/180 = 0.055$

$\tau(\text{Chromosome-1}) = (1-0.5) \cdot 0.01 + (0.5 * 0.055)$

$= 0.077$

2nd Ant:

Calculate the probability of Chromosome 2 = 1.1 2.2 1.3.

- Taboo list = 1.1

- The probability from node 1.1 to each subsequent node is:

$= (0.1 * 0.14) + (0.1 * 0) + (0.1 * 0)$

$= 0.014$

So that the probability of node 1.1 is calculated for every node as follows:

Point 1.1 = 0

Point 2.2 = $(0.01) \cdot 1.00 \cdot (0) \cdot 1.00 / 0.063 = 0$

Point 1.3 = $(0.01) \cdot 1.00 \cdot (0) \cdot 1.00 / 0.063 = 0$

Cumulative Probability: 0 0.0 0

Random numbers generated: $r = 0.012$

Checking qk-1

Contents of Taboo List = 1.1 2.2

Pheromone local update

$\Delta \tau(\text{Chromosome-2}) = 1 / 3.0 = 1/3 = 0$

$\tau(\text{Chromosome-2}) = (1-0.5) \cdot 0.01 + (0.5 * 0)$

$= 0.05$





3rd Ant:

Calculate the probability of Chromosome 3 = 4.1 3.2 4.3.

- Tabu list = 4.1

- The probability from node 4.1 to every subsequent node is:

$$= (0.01 * 0.15) + (0.1 * 0.5) + (0.1 * 0.18) \\ = 0.0245$$

Thus the probability of node 4.1 is calculated for every node as follows:

Point 4.1 = 0

$$\text{Point 3.2} = (0.1) \cdot 1.00 \cdot (0.5) \cdot 1.00 / 0.0245 = 0.24$$

$$\text{Point 4.3} = (0.1) \cdot 1.00 \cdot (0.18) \cdot 1.00 / 0.0245 = 0.734$$

Cumulative Probability: 0 0.204 0.277

Random numbers raised: $r = 0.80$

Checking qk-1

Fill Tabu List = 4.1 4.3

Feromone renewal

$$\Delta\tau (\text{Chromosome-1}) = 1 / 3.55 = 1/165 = 0.60$$

$$\tau (\text{Chromosome-1}) = (1-0.5) \cdot 0.1 + (0.5 * 0.60) \\ = 0.015$$

The 4th Ant:

Calculate the probability of Chromosome-4 = 3.1 4.2 3.3.

- Tabu list = 3.1

- The probability from node 3.1 to every subsequent node is:

$$= (0.01 * 0.033) + (0.1 * 0.25) + (0.1 * 0.02) \\ = 0.078$$

Thus the probability of node 3.1 is calculated for every node as follows:

Point 3.1 = 0

$$\text{Point 4.2} = (0.1) \cdot 1.00 \cdot (0.33) \cdot 1.00 / 0.078 = 0.423$$

$$\text{Point 3.3} = (0.01) \cdot 1.00 \cdot (0.25) \cdot 1.00 / 0.078 = 0.32$$

Cumulative Probability: 0 0.423 0.743

Random numbers raised: $r = 0.45$

Checking qk-1

Fill Tabu List = 3.1 4.2

Feromone renewal

$$\Delta\tau (\text{Chromosome-1}) = 1 / 3.40 = 1/120 = 0.0083$$

$$\tau (\text{Chromosome-1}) = (1-0.5) \cdot 0.01 + (0.5 * 0.0083) \\ = 0.020$$

Table 8
ACO Results Cycle 1

Ant to	Chromosom	Make span
1	2.1 1.1	110
2	1.1 2.2	100
3	4.1 4.3	130
4	3.1 4.2	80

Produced a chromosome with the littlest make span value on the 4th chromosome that's 80

Table 9.

The Value of Make Chromosome Span (job)

Kr	Node-1	Node-2	Node-3	Make span
1	2.1	1.2	1.1	110
2	1.1	2.2	1.3	100
3	4.1	3.2	4.3	130
4	3.1	4.2	3.3	80

Chromosome-4 (Job-4) features a smaller make span. Then the calculation continues until the ant completes its journey visiting each node. This can repeat until it matches the Ncm.

4. Conclusions





In this study an analysis was performed on the hybrid performance of the ACO algorithm with Genetics to attenuate the makespan of Flowshop scheduling. The results of this study showed that the general performance of the ACO-GA algorithm dataset produced smaller makespan compared to the NEH Heuristic and Stochastic Greedy Heuristic (SG) algorithms, except some for larger datasets than.

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