Applying Feature Selection to Rule Evolution for Dynamic Flexible Job Shop Scheduling

Yahia Zakaria, Ahmed BahaaElDin and Mayada Hadhoud
Computer Engineering Department, Faculty of Engineering, Cairo University, Giza, Egypt

Keywords: Feature Selection, Flexible Job Shop Scheduling, Dynamic Scheduling, Genetic Programming.

Abstract: Dynamic flexible job shop scheduling is an optimization problem concerned with job assignment in dynamic production environments where future job arrivals are unknown. Job scheduling systems employ a pair of rules: a routing rule which assigns a machine to process an operation and a sequencing rule which determines the order of operation processing. Since hand-crafted rules can be time and effort-consuming, many papers employ genetic programming to generate optimum rule trees from a set of terminals and operators. Since the terminal set can be large, the search space can be huge and inefficient to explore. Feature selection techniques can reduce the terminal set size without discarding important information and they have shown to be effective for improving rule generation for dynamic job shop scheduling. In this paper, we extend a niching-based feature selection technique to fit the requirements of dynamic flexible job shop scheduling. The results show that our method can generate rules that achieves significantly better performance compared to ones generated from the full feature set.

1 INTRODUCTION

Job Shop Scheduling (JSS) (Brucker and Schlie, 1990) is a popular optimization problem with many practical applications in multiple fields such as cloud computing and manufacturing. JSS aims to assign job operations to machines where each job contains a sequence of operations that can only be processed in a certain order and each operation can only be processed on a certain machine. Since static job shop assumes that all jobs are known before the scheduling starts, it is inapplicable to many realistic use-cases where job arrival times are unknown. Dynamic Job Shop Scheduling (DJSS) is an extension of JSS where jobs can arrive at any point in time and the scheduler has no information about future jobs. JSS also assumes that each operation is processable on only one machine. This assumption is not always true especially in large production environments. Flexible Job Shop Scheduling (FJSS) relaxes the aforementioned assumption by allowing each operation to be processed on any member from a subset of the machines. In this paper, we are only concerned with Dynamic Flexible Job Shop Scheduling (DFJSS).

Due to the scalability and speed requirements in practical DJSS applications, Dispatching Rules (DR) are popular due to their simplicity and scalability (Blackstone et al., 1982). Dispatching rules are heuristics that compute a priority for each operation in the machine queue. In DFJSS, Scheduling is operated by a pair of rules (Dauzere-Peres and Paulli, 1997): A Routing Rule (RR) that routes each operation to a machine queue and A Sequencing Rule (SR) that assigns a priority to each operation in the queue. Scheduling rules can be handcrafted by experts but different environments require customized rules so manual rule design tend to be time and effort-consuming.

Genetic Programming (GP) (Koza, 1992) has been adopted by many recent works for automated rule generation. GP encodes the rules as trees where leaves denote features holding information about the decision situation, and inner nodes denote operators connected via edges to its operands. To search for optimum rules, GP starts from a random tree population and applies a sequence of selection, crossover and mutation operators to generate offspring. However, the probability of finding a good rule degrades with the expansion of the search space. Since adding more features will exponentially expand the search space, irrelevant features should be discarded. In DJSS, feature selection (Mei et al., 2017) was applied to opt out features deemed irrelevant to the rule fitness. To our knowledge, the feature selection method proposed by (Mei et al., 2017) is yet to be applied for DFJSS.

Zakaria, Y., BahaaElDin, A. and Hadhoud, M.
Applying Feature Selection to Rule Evolution for Dynamic Flexible Job Shop Scheduling.
DOI: 10.5220/0007957801390146
In *Proceedings of the 11th International Joint Conference on Computational Intelligence (IJCCI 2019)*, pages 139-146
ISBN: 978-989-758-384-1

To address the issue of irrelevant features, this paper has the following objectives:

- Extend feature selection to routing and sequencing rule generation for DFJSS.
- Analyze the feature selection results and compare the results before and after feature selection.

The rest of the paper is organized as follows: Section 2 briefly reviews the related work. Section 3 explains the proposed method. Section 4 details the experimental setup then Section 5 shows and discusses the experimental results. Finally, conclusions and future work are given in Section 6.

2 RELATED WORK

2.1 Routing and Sequencing Rules

In DJSS, dispatching rules are used exhaustively due to their computational efficiency. At decision time, a dispatching rule calculates a priority for each available operation and the operation with the highest priority is selected for processing. Non-delay dispatching rules are applied whenever the machine is idle and its queue is nonempty. Non-delay rules were proved to perform better than active rules (Nguyen et al., 2013) where decisions can be delayed. Early studies focused on manually-designed rules but these rules failed to generalize so attention was shifted to automatically generated hyper-heuristics. Application of Genetic Programming (GP) for DJSS rule generation was explored in many recent works (Nguyen et al., 2013; Yska et al., 2018).

Unlike DJSS, each operation in DFJSS is processable on multiple machines, so a DFJSS scheduler has two tasks: routing operations to machines (Routing) and ordering the operations in the machine queue (Sequencing). To fit DFJSS, GP has been expanded to generate routing and sequencing rule pairs. To evolve two rules at the same time, Cooperative Coevolution GP (CCGP) was proposed in (Yska et al., 2018) where separate populations were used for routing and sequencing rules. During evaluation, CCGP pairs every rule with the most fit rule from the other type. To evolve routing and dispatching rules in one population, a multi-tree representation for the chromosome was proposed by (Zhang et al., 2018) in addition to a swapping crossover operator where one pair of corresponding rules is mated and the other is swapped. The swapping operator should allow for a more diverse offspring without easily breaking useful blocks.

2.2 Feature Selection

With the latest advances in AI and Machine Learning, Feature Selection was proven to be significant (Guyon and Elisseeff, 2003). As features can be irrelevant and misleading, they may deteriorate the model's performance, therefore properly selected features significantly decrease the search space thus improve performance. Feature Selection techniques are divided into 3 categories (Liu and Yu, 2005): Wrapper techniques that pick features with high variance, Filter techniques that greedily search for feature subsets that improve performance and Embedded techniques that combine the advantages of the aforementioned techniques.

GP exhibits embedded feature selection so relevant features will tend to show up in good individuals. However, using the feature frequency in good individuals as a relevance measure has two main drawbacks. First, it might be biased to a local optima thus fail to generalize. Second, the occurrence might have no effect in the rule such as $(\mathcal{X}-\mathcal{X})$ or $(\mathcal{X}/\mathcal{X})$. Later in (Mei et al., 2016), feature contribution to fitness was introduced and features were ranked then selected according to these contributions. The drawback of this method is that GP must be run many times (30 times in their experiments) to generate a diverse rule set without bias to a singular local optima. To overcome this drawback, A Niching-GP method was proposed in (Mei et al., 2017) to generate a set with diverse phenotypes in a single run using a clearing method.

3 PROPOSED METHOD

3.1 Problem Formulation

In DFJSS, a scenario can be formulated as follows:

- Each scenario $\mathcal{S}$ contains a set of Jobs $\mathcal{J} = \{J_1, J_2, ..., J_n\}$.
- Each job J_j has an arrival time $t_a(J_j)$ and a due time $t_d(J_j)$ and a weight $W(J_j)$.
- Each scenario $\mathcal{S}$ contains a set of machines $\mathcal{M} = \{M_i, M_2, ..., M_m\}$.
- Each job J_j contains a sequence of operations $O(J_j) = (O_{j1}, O_{j2}, ..., O_{jl_j})$.
- Each operation O_{ji} can only be processed by a machine $M_k \in \pi(O_{ji}) \subset \mathcal{M}$ where the processing time on machine M_k is $\delta(O_{ji}, M_k)$. Unlike Classical JSS which assume that $|\pi(O_{ji})| = 1$, FJSS relaxes the assumption to $|\pi(O_{ji})| \geq 1$.
- At any given time, each machine can only process up to one operation.

- Operation processing is non-preemptive, so if a machine M_k starts to process an operation O_{ji} at time $t_s(O_{ji})$, it is ensured that the processing will end at time $t_e(O_{ji}) = t_s(O_{ji}) + \delta(O_{ji}, M_k)$.
- In any job J_j, processing of any operation O_{ji} can only start after operation $O_{j(i-1)}$ has been finished and processing of operation O_{j1} can only start after its job arrival time $t_a(J_j)$.

During the simulation, the scheduler is responsible for applying two rules: routing rule $r_r(O_{ji}, M_k)$ and sequencing rule $r_s(O_{ji}, M_k)$. When a new operation O_{ji} becomes available for processing, it is routed to the machine $M_k = \arg\min r_r(O_{ji}, M), M \in \pi(O_{ji})$ then it is added to the machine's queue $Q(M_k)$. Whenever a machine M_k is idle and its queue $Q(M_k)$ is not empty, the operation $O_{ji} = \arg\min r_s(O, M_k), O \in Q(M_k)$ is assigned to the machine M_k and removed from its queue $Q(M_k)$.

The goal of genetic programming is to find a pair of routing and sequencing rules that minimizes a given fitness function $f(r)$ where $r = (r_r, r_s)$. The work in this paper will only focus on minimizing the maximum ($f(r) = maxF(J_j)$), mean ($f(r) = E[F(J_j)]$) and weighted mean ($f(r) = E[W(J_j) \times F(J_j)]$) of the objective function $F(J_j)$ across all jobs $J_j \in \mathcal{J}$ in any given scenario $\mathcal{S}$. The objective functions, used in this paper, are:

- *Tardiness* $T(J_j) = t_e(O_{jl_j}) - t_d(J_j)$ which is the delay in finishing the job beyond its due time.
- *Flow-time* $C(J_j) = t_e(O_{jl_j}) - t_a(J_j)$ which is the total amount of time that the job spends in the system.

3.2 Multi-tree Genetic Programming

In this paper, we use the multi-tree chromosome and the swapping multi-tree crossover operator proposed in (Zhang et al., 2018). Each multi-tree chromosome contains a pair of trees: routing rule tree and sequencing rule tree. Figure 1 shows an example of a rule tree. The swapping multi-tree crossover operator is described in Algorithm 1. As a method for bloat control, the crossover operator is followed by static limit check to replace any offspring that exceeds the height limit with one of their parents (Koza, 1992).

Algorithm 1: Swapping Multi-Tree Crossover.

Input: Chromosomes C1, C2
1: Randomly pick $r \sim \{0,1\}$ with probability 50%
2: $C1[r], C2[r] \leftarrow TreeCrossover(C1[r], C2[r])$
3: $C1[1-r], C2[1-r] \leftarrow C2[1-r], C1[1-r]$

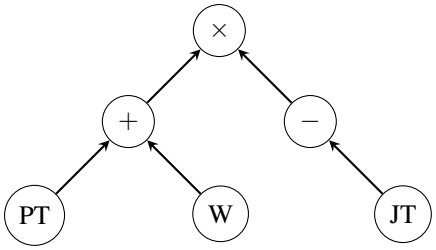


Figure 1: Rule Tree Example $(PT + W) \times (-JT)$.

3.3 Niching-GP Feature Selection

We use the Niching-GP Feature Selection Framework (NiSuFS) proposed in (Mei et al., 2017) which consists of four main steps:

1. Apply Genetic Programming with clearing applied after every generation to prevent the population from converging to a single phenotype.
2. Extract the best diverse set from the final population.
3. Calculate the performance degradation of each rule after opting out each feature, then vote for features whose absence cause a significant degradation.
4. Filter features based on votes to create the final feature subset.

Step 3 follows the assumption that a feature's significance is proportional to the rule fitness degradation after opting out the feature. Since DFJSS contains two rules, step 3 and 4 are extended so that it is applied once to sequencing rules without modifying routing rules and vice versa. The result will be two feature subsets: significant features for routing and significant features for sequencing.

There are four components in NiSuFS which are as follows:

3.3.1 Phenotype Similarity

In order to measure a chromosome phenotype, a set of discriminative situations are required. The set of situations are randomly sampled from multiple simulations which are scheduled by a benchmark rule-pair (Least-Work-in-Queue for routing and Maximum-Operation-Waiting-Time for Sequencing). Situations that contain options (machines or operations) fewer than a certain threshold are filtered out due to their low discriminative properties. Two sets of situations are sampled: Routing Situations and Sequencing Situations. In each situation, the options are sorted by their benchmark priorities and stored for later use in the clearing method. To calculate the chromosome phenotype, its rules are applied to each situation, then

a phenotype vector is composed of the new ranks for the options which was given rank-1 by the benchmark rules. The distance between any two chromosomes is the euclidean distance between their phenotype vectors. The phenotype calculation steps are shown in Algorithm 2.

Algorithm 2: Calculate Phenotype.

Input: Rule r, Benchmark-Sorted Situation Set S
Output: Phenotype P

for $i = 0$ to $length(S)$ **do**
  $priorites \leftarrow ApplyRule(r, S[i])$
  $indices \leftarrow ArgSort(priorities)$
  $P[i] \leftarrow FindIndex(indices, 0)$
end for

3.3.2 Clearing Method

Clearing is a niching technique applied after each generation to prevent crowding. First, the chromosomes are sorted by fitness (best fitness first). Then, each chromosome will iterate through weaker siblings within a certain phenotype distance σ, keep the best k siblings and set the fitness of the rest to ∞. The cleared chromosomes stay in the population but will have a very low chance of being picked by selection. The steps are shown in Algorithm 3.

Algorithm 3: Clearing Method.

Input: Population P

$SortByFitness(P)$
for $i = 0$ to $length(P) - 1$ **do**
  if $P[i].fitness = \infty$: **Continue**
  $size = 1$
  for $j = i + 1$ to $length(P) - 1$ **do**
    if $Distance(P[i], P[j]) \leq \sigma$ **then**
      if $size = k$ **then**
        $P[j].fitness \leftarrow \infty$
      else
        $size = size + 1$
      end if
    end if
  end for
end for

3.3.3 Best Diverse Set

The best diverse set algorithm is exactly the same as the clearing method except that only the best R rule pairs are kept. The best diverse set is picked from the final population in order to supply the feature selection with the best generated rule pairs from different phenotypic proximities.

3.3.4 Voting for Features

Each feature's significance to a rule is assumed to be proportional to the rule fitness degradation after the feature has been set to a fixed value. If the fitness degradation exceed a certain threshold ε, the rule votes for the feature. The fitness of the rule pair $f(r)$ is measured as the mean fitness on a set of reference scenarios which are randomly generated once before the feature selection. Each rule has a different voting weight from 0 to 1 based on its fitness as shown in Equation 1. Any feature, that collect votes greater than a certain ratio α of the total weights, is added to the selected subset.

$$w(r') = \frac{\max_r(f(r)) - f(r')}{\max_r(f(r)) - \min_r(f(r))} \tag{1}$$

During degradation calculation, The feature t is set to 1 for either the routing rule or the sequencing rule. After that, the degraded fitness of the rule pair $f_n(r|t = 1)$ is measured where $n \in \{routing, sequencing\}$. The significance $\zeta_n(r,t)$ is calculated as shown in Equation 2. Based on the significance, the feature selection algorithm is applied as shown in Algorithm 4. The fixed feature is set to 1 since it is the multiplicative and divisive identity value. Although 1 is not the additive or subtractive identity, it will not affect the overall ranking.

$$\zeta_n(r,t) = f(r) - f(r|t = 1) \tag{2}$$

Since the scenario lengths in our experiments are short, the fitness function tends to be noisy, thus some insignificant features may be selected by some diverse sets. To increase the quality of the selected feature, we run the experiments multiple times and select only the features that has selected by a certain number of diverse sets.

Algorithm 4: Feature Selection.

Input: Rule Pairs R, Features T, Rule type n
Output: Selected Feature $\tilde{T}$

$W \leftarrow CalculateWeights(R)$
$w_{threshold} \leftarrow \alpha \sum_{w \in W} w$
$\tilde{T} \leftarrow \{\}$
for t in T **do**
  $v \leftarrow 0$
  for r in R **do**
    if $\zeta_n(r,t) \geq \varepsilon$ **then**
      $v \leftarrow v + W[r]$
    end if
  end for
  if $v \geq w_{threshold}$ **then**
    $\tilde{T} \leftarrow \tilde{T} \cup \{t\}$
  end if
end for

4 EXPERIMENTAL SETUP

This section details the experimental steps and the configuration for each step. The experiments were conducted 6 times; once for each objective: maximum, mean and weighted mean of tardiness and flowtime. We do not clamp the tardiness of early-finished jobs to zero in order to reward the rules that finish as early as possible. Before running the feature selection, we generate and store 20 situations for each rule type (routing and sequencing) and each situation must have at least 5 options available. We also generate 5 reference scenarios for feature selection and 21 test scenarios for performance comparison. All the scenarios used for situation generation, training, feature selection and testing have the same configuration. For each objective, The NiSuFS algorithm is run 5 times followed by feature aggregation to generate an aggregated feature set. The significance threshold ε is set to 0.0001 and the voting threshold ratio α is set to 0.25. Setting the voting threshold ratio to 0.5 as in (Mei et al., 2017) led to selecting only one or two features per run. We hypothesize that fixing the feature in only one rule from the pair undermines its perceived significance. Any feature that has been selected less than 2 times are removed by the aggregation step. The regular Multi-tree GP without niching is run twice per objective: once with full feature set and once with selected features only.

4.1 Scenario Generation Configuration

Due to time and parsimonious constraints, the scenario length is set to be very short. Since short scenarios will rarely contain situations that discriminate between rules, we added a short spike in the job arrival schedule at the start of the simulation and set the warm up jobs to zero. The scenario generation configuration is detailed in Table 1.

Table 1: Scenario Generation Configuration.

Parameter	Value
#Machines	10
#Jobs	50 + (10 with $t_a(J_j) = 0$)
#Ops per job	$U(1,10)$
#Machines per op	$U(1,5)$
Op processing time	$U(1,99) \in \mathbb{Z}$
Utilization	0.99
Job arrival	Poisson process
Due time factor	U(1,1.3)
Job weight	1(20%), 2(60%), 4(20%)

4.2 GP Configuration

The Niche-GP configuration is based on a combination of the configurations in (Mei et al., 2017; Zhang et al., 2018) with some settings toned down to fit our resource constraints. The configuration is detailed in table 2. The operators used in our experiments are $\{+,-,\times,\div,negative,mininmum,maximum\}$. All the operators are binary except *negative* which is unary. Each feature has a corresponding terminal as shown in Table 3. The feature set include the features used by (Zhang et al., 2018) in addition to time-invariant versions of some features used by (Mei et al., 2017).

The Regular GP configuration is based on the configuration in (Zhang et al., 2018) with toned-down settings to fit our resource constraints. The configuration is detailed in table 2. The same operators and terminals as in Niche-GP are used in Regular-GP.

4.3 Rule Comparison

To compare two rule pairs, each pair is applied to the 21 test scenarios and the fitness is supplied to Wilcoxon signed-rank test at 5% level. The fitness of the rule pair for each scenario $f(r,s)$ is normalized relative to the benchmark rule-pair fitness for the same scenario $f_b(s)$ before applying the Wilcoxon test. In our implementation, tardiness can be negative so dividing by the benchmark tardiness can flip the objective from minimization to maximization. To solve this problem, we subtract a lower-bound fitness $f_l(s)$, that can never exceed the fitness of any rule, from the rule-pair and benchmark fitness before normalization. The lower bound is calculated by assuming that each operation will be processed as soon as it is available and that it will be assigned to the machine with the least processing time. The normalized fitness $\hat{f}(r,s)$ is calculated as shown in Equation 3.

$$\hat{f}(r,s) = \frac{f(r,s) - f_l(s)}{f_b(s) - f_l(s)} \tag{3}$$

5 RESULTS AND ANALYSIS

Figure 2 shows the results of feature selection. The horizontal axis denotes the terminals and the vertical axis denotes the Niche-GP run. From the figure, we can conclude the following:

- *PT* was selected in nearly every routing and sequencing rule which shows that it has great significance in the rules' performance.
- *WIQ* is selected in every routing rule since it is a significant indicator of the expected operation

Table 2: GP Configuration.

Parameter	Niche-GP	Regular-GP
#Generation	51	51
Population Size	512	512
Selection Method	Tournament of Size 7	Tournament of Size 7
Crossover Probability	0.8	0.8
Mutation Probability	0.15	0.15
#Elites	-	32
Generated Tree Size	$U(1,2)$	$U(1,2)$
Maximum Tree Size	8	8
#Simulation Replication per Evaluation	1	1
Clearing Distance σ	5	-
Clearing Set Size k	1	-
Best Diverse Set Size R	32	-

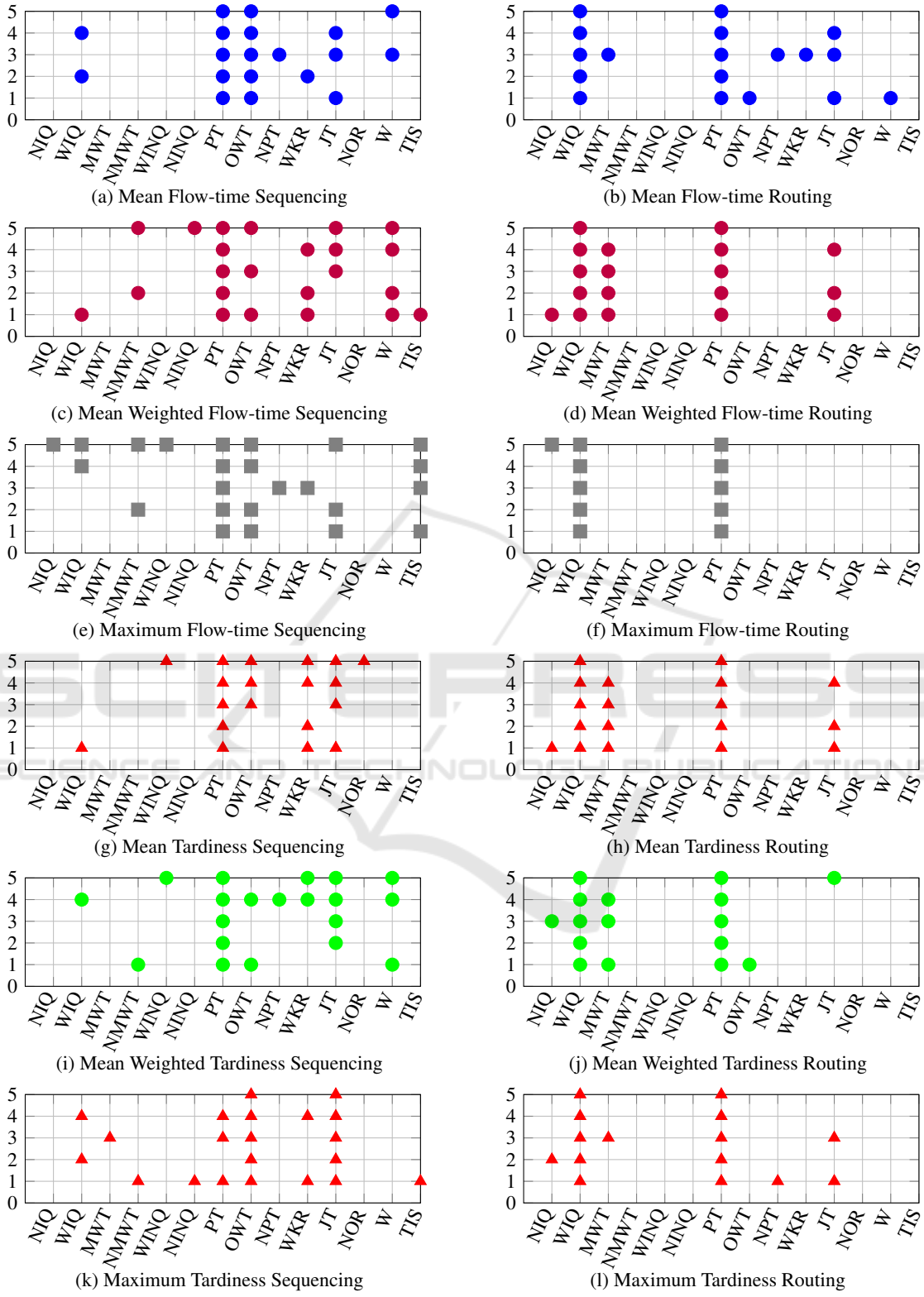
Table 3: Feature Set.

Feature	Description
NIQ	Number of Operations in Machine Queue
WIQ	Current Work in Machine Queue
MWT	Machine Waiting Time
NMWT	Median Waiting Time for Next Operation Machines
NINQ	Median Operation Count in Next Operation Machines Queues
WINQ	Median Work in Next Operation Machines Queues
PT	Operation Processing Time
OWT	Operation Waiting Time
NPT	Next Operation Median Processing Time
WKR	Sum of Median Processing Time for Remaining Operations
JT	Current Delay After Job Due Time
NOR	Number of Remaining Operations in Job
W	Job Weight
TIS	Time Spent by Job in System

waiting time and aids in load balancing. However, *NIQ* is rarely selected, probably due to its redundancy with the more informative feature *WIQ*.

- *OWT* is highly relevant to sequencing and mostly irrelevant to routing.
- *MWT* is sometimes important for routing rules and never relevant to sequencing.
- *JT* is relevant in most sequencing rules but its significance is fluctuating in routing rules.
- *W* is heavily selected by sequencing rules in Mean Weighted Flow-time and Tardiness but it is rarely selected otherwise, which is intuitively expected.
- *TIS* is very relevant to sequencing for Maximum Flow-time only, otherwise, it is rarely selected.
- *NPT*, *NOR*, *NINQ* and *WINQ* are mostly deemed to be irrelevant as they were rarely selected. *NMWT* barely passed the threshold for sequencing in mean weighted and maximum flow-time.

It is noteworthy that the selected features after aggregation do not exceed 6 features for sequencing rules and 4 features for routing rules. Since the number of selected features is always below half the full feature set, we can expect that the search space will be much smaller and efficient to explore. Table 4 shows the comparison results between using the selected feature set and using the full feature set. In half the tests, using the selected features yields significantly better results and in the remaining cases, it is either insignificantly better or worse. Applying GP in a smaller search space should increase the probability of converging to good rules. However, opting out important features will create a search space with no good rules and GP will only converge to weak solutions. Since the results show that our method has a higher probability of finding good rules, we can conclude that the feature selection does keep important features while tightening the search space.



(a) Mean Flow-time Sequencing

(b) Mean Flow-time Routing

(c) Mean Weighted Flow-time Sequencing

(d) Mean Weighted Flow-time Routing

(e) Maximum Flow-time Sequencing

(f) Maximum Flow-time Routing

(g) Mean Tardiness Sequencing

(h) Mean Tardiness Routing

(i) Mean Weighted Tardiness Sequencing

(j) Mean Weighted Tardiness Routing

(k) Maximum Tardiness Sequencing

(l) Maximum Tardiness Routing

Figure 2: Selected Features.

Table 4: Performance Comparison Results.

	Using The Selected Feature Set			Using The Full Feature Set			Wilcoxon
Objective	Average	Min	Max	Average	Min	Max	p-value
Mean flow-time	**0.28238**	0.18709	0.36727	0.31201	0.20618	0.41312	**00.10%**
Mean weighted flow-time	**0.28278**	0.19737	0.44225	0.29387	0.20499	0.43446	05.82%
Maximum flow-time	**0.58983**	0.47137	0.72148	0.67963	0.54417	0.83272	**00.02%**
Mean tardiness	**0.28217**	0.19048	0.38080	0.28607	0.20464	0.38240	35.70%
Mean weighted tardiness	0.30408	0.18893	0.47572	**0.29339**	0.20966	0.42190	16.97%
Maximum tardiness	**0.55338**	0.44895	0.70544	0.60615	0.41829	0.81957	**00.19%**

6 CONCLUSION AND FUTURE WORK

This paper proposed an extension to Niching-GP Feature selection (NiSuFS) to be compatible with multi-tree genetic programming for Dynamic Flexible Job Shop Scheduling. NiSuFS was applied to DJSS in (Mei et al., 2017) and the results proved its effectiveness in improving rule generation. However, it was not applied to DFJSS in other works. The results in this paper showed that the extended NiSuFS can enhance the rule generation in multi-tree genetic programming. The improvement was significant in 50% of our tests and the generated rules were never significantly worse than the baseline. For future work, we plan to investigate the assumption that feature significance can be measured on routing and sequencing separately despite the rule pair interaction. We also plan to study information redundancy in features and the applicability of feature reduction techniques such as PCA. Since situation sampling for phenotype measurement is completely random, different components of the phenotype may be dependent, so phenotypes with orthogonal components is worth exploring. Moreover, other discriminative phenotype measurement methods will be investigated in future work.

REFERENCES

Blackstone, J. H., Phillips, D. T., and Hogg, G. L. (1982). A state-of-the-art survey of dispatching rules for manufacturing job shop operations. In *International Journal of Production Research*, pages 27–45.

Brucker, P. and Schlie, R. (1990). Job-shop scheduling with multi-purpose machines. *Computing*, 45:369–375.

Dauzere-Peres, S. and Paulli, J. (1997). An integrated approach for modeling and solving the general multiprocessor job-shop scheduling problem using tabu search. In *Ann. Oper. Res*, pages 281–306.

Guyon, I. and Elisseeff, A. (2003). An introduction to variable and feature selection. *Journal of Machine Learning Research*, 3:1157–1182.

Koza, J. (1992). Genetic programming: on the programming of computers by means of natural selection. In *MIT press*, volume volume 1.

Liu, H. and Yu, L. (2005). Toward integrating feature selection algorithms for classification and clustering. *IEEE Transactions on Knowledge and Data Engineering*, 17(4):491–502.

Mei, Y., Nguyen, S., Xue, B., and Zhang, M. (2017). An efficient feature selection algorithm for evolving job shop scheduling rules with genetic programming. *IEEE Transactions on Emerging Topics in Computational Intelligence*, 1(5):339–353.

Mei, Y., Zhang, M., and Nyugen, S. (2016). Feature selection in evolving job shop dispatching rules with genetic programming. In *GECCO*.

Nguyen, S., Zhang, M., Johnston, M., and Tan, K. (2013). A computational study of representations in genetic programming to evolve dispatching rules for the job shop scheduling problem. *IEEE Transactions on Evolutionary Computation*, 17(5):621–639.

Yska, D., Mei, Y., and Zhang, M. (2018). Genetic programming hyper-heuristic with cooperative coevolution for dynamic flexible job shop scheduling. In *Proceedings of the European Conference on Genetic Programming*, pages 306–321. Springer.

Zhang, F., Mei, Y., and Zhang, M. (2018). Genetic programming with multi-tree representation for dynamic flexible job shop scheduling. In *Australasian Joint Conference on Artificial Intelligence*, pages 472–484. Springer.