

Received January 12, 2019, accepted January 27, 2019, date of publication February 5, 2019, date of current version March 1, 2019.

Digital Object Identifier 10.1109/ACCESS.2019.2897735

Sequence Based Optimization of Manufacturing Complexity in a Mixed Model Assembly Line

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This work was supported by the Ulsan National Institute of Science and Technology through the Development of 3D Printing-based Smart Manufacturing Core Technology Research Fund under Grant 1.190032.01.

ABSTRACT Increasing production variability while maintaining operation efficiency remains a critical issue in many manufacturing industries. While the adoption of mixed-model assembly lines enables the production of high product variety, it also makes the system more complex as variety increases. This paper proposes an information entropy-based methodology that quantifies and then minimizes the complexity through product sequencing. The theory feasibility is demonstrated in a series of simulations to showcase the impact of sequencing in controlling the system predictability and complexity. Hence, the framework not only serves as a tool to quantitatively assess the impact of complexity on total system performance but also provides means and insights into how complexity can be mitigated without affecting the overall manufacturing workload.

INDEX TERMS Mixed model assembly line (MMAL), complexity, sequence, information entropy.

I. INTRODUCTION

In an ever-changing market environment, the need for proper human-machine integration is critical. Furthermore, the role of humans remains, since in spite of advances made in manufacturing automation, humans remain a critical component of adaptable and flexible manufacturing systems [1]. As technological advances accelerate, customer demand gets more sophisticated [2]. To cope with this demand, and to gain competitive advantage, companies have adopted the mixed-model assembly system and modular supply chains capable of handling a large variety of products [3]. On the other hand, the increase in variety worsens the manufacturing performance due to the complexity borne out of creating and handling multiple product models [4], [5].

Thus, there is tradeoff between additional gains from a greater variety of options and higher resources associated with handling the additional manufacturing complexity. From a decision-making standpoint, however, challenges arise when trying to estimate the tradeoff because of the lack of a formal measure of variety induced complexity.

The associate editor coordinating the review of this manuscript and approving it for publication was Ming Luo.

This paper estimates manufacturing complexity by measuring the information content of assembly sequences. We introduce a sequence-based measure of manufacturing complexity in a Mixed Model Assembly Line (MMAL). Note that MMAL is an assembly line system, often human-centered, in which various models of a common base product are manufactured in intermixed sequences. The thought process of the proposed complexity measure is centered on the premise that the operator's performance is likely to be negatively affected by an increase in the complexity. Indeed previous research has already found that the efficiency of operators diminishes as the number of options increases [6], [7].

Thus, the proposed methodology offers a promising tool that ensures higher product variability, while simultaneously maintaining the production efficiency. This paper introduces an entropic measure of complexity that takes into account the product variety distribution, and their respective sequencing in assembly operations. Using the measured complexity, the paper aims to assess the effect of sequencing on assembly complexity. Using stochastic optimization methodologies, namely, the multi-objective genetic algorithm we show how this entropic measure can be used to obtain an optimized sequence of products that ensures a reduced level of complexity while maintaining a balanced workload by penalizing

operator's idle time variation. In this paper, we assume a balanced line, that is the task sequence for a given product assembly is already fixed. Here the task sequence refers to the order at which various components of a given product must be added to the mainframe, given the precedence constraints. Thus, as opposed to task sequence, this paper deals with product sequence which simply refers to the order at which two or more individual products are sequenced on the assembly line.

II. BACKGROUND

A. MANUFACTURING COMPLEXITY

Due to customer sophistication, manufacturers are expected to offer a high product variety to remain competitive. As a result, the industry records show an unprecedented increase in product varieties. For example, Wiendahl and Scholtissek [8] have noted a 400% increase in the number of part variants from 1975 to 1990. This increase in variety led to an increase in complexity and became one of the premier driver of changes in manufacturing industries in sake of containing the said complexity. For instance, to control and contain the variety-induced complexity in the assembly process, manufacturers have shifted from single model to MMAL. Note that a mixed-model Assembly line produces the units of different products or different varieties of the same products in an arbitrarily intermixed sequence.

Despite their reputation as being better equipped for handling the increased variety, a survey by Schleich *et al.* [9], shows the majority of manufactures identifying the complexity resulting from managing variety as a significant cost driver in production in MMAL. While the existence of complexity and its challenges are widely acknowledged, a formal quantification of manufacturing complexity is still a topic for discussion. In fact, complexity is often thought of as “the state of having many different parts connected or related to each other in a complicated way” (Merriam-Webster 2016) with no systematic way to quantify it. In an attempt to formally define complexity in MMAL, Falck *et al.* [10] categorized the assembly complexity into a number of discrete levels according to few defined features of complexity. Likewise, [11] introduced a Likert scale measure of workstation complexity as a function of various elements central to complexity changes. In addition, to the defining complexity, these researchers show how an increase complexity in a manual assembly line often negatively affect the quality and productivity in MMAL [12].

Likert scale as a measure of complexity, while valuable, it is constrictive due to the small scale at which the complexity is defined. To this end, Shannon entropy also known as information entropy has become the most prevalent and commonly accepted theories used as a measure of complexity (For the remainder of the paper, Shannon entropy will be referred to as simply “entropy”). According to Shannon, the entropy is a measure of information contained in a message. This is equivalent to the measure of unpredictability of a random

variable [13], [14]. Notable example use of entropy include Zeltzer *et al.* [15] who proposed an entropic complexity leveling method based on the variation of task cycle time. Similarly, Fujimoto and Ahmed [16] proposed an entropic complexity measure for different stages of process planning, while ElMaraghy *et al.* [17] demonstrate how the entropy function can be used in the quantification of complexity in machining process. While these efforts are worth lauding, the aforementioned studies of complexity measure pay little attention to the operator's choice complexity, its relation to variety, and how it impacts performance in a mixed model assembly line.

The above research into complexity measures does not explain how variety leads to complexity and impacts performance as observed in MMAL [6], [7]. To accommodate variety induced complexity, some studies have proposed entropy models for the computation of operator choice based on Hick's law, that argues that the time it takes for an operator to make a choice is a linear function of the number of possible choices available [6], [7], [18], while [19] added the similarity of options to the mix. For instance, while there is a merit in models based on Hick's law, the entropy calculation is done under the assumption of a random and independent choice processes [19]. In reality, however, manufacturers can opt to sequence the assembly process in a predictable manner, thus rendering the models inapplicable. This paper introduces entropic variety-induced complexity model that considers both part mix along with the assembly sequence.

B. OPTIMIZATION IN A MIXED MODEL ASSEMBLY LINE

There is an overwhelming number of research works that cover the balancing of manual assembly lines [20]. Nearly all their methodologies consider a single-model line with various objective functions such as (i) maximization of profit [21], or minimization of (ii) the number of stations for a given cycle time [22], [23]; (iii) the cycle time for a given number of stations [24]; or (iv) expected total costs [25], [26].

In addition, some researchers have proposed various methodologies to mitigate the complexity of a mixed assembly line. For instance, Wang *et al.* [27] introduce a multi-objective optimization to balance product variety and manufacturing complexity when designing a product family and its mixed-model assembly system. Using the notion of relative complexity, they attempt to find the best set of product variants to be offered while balancing market share and complexity. Wang *et al.* [27] and Wang *et al.* [28] demonstrated how manufacturing complexity can be mitigated through variant differentiation. Wang *et al.* [27] touches on the idea of minimizing the complexity, their approach fails to account for the impact of sequencing, which is one of the major contributors to system complexity. This paper introduces an entropy-based methodology in which the impact of sequencing on complexity is evaluated and controlled.

III. COMPLEXITY MODEL FOR ASSEMBLY SEQUENCING

A. ASSEMBLY SEQUENCE IN MMAL

Short-term sequencing problems are common in MMAL. In fact sequence planning is one of the more critical steps in ensuring an effective assembly process [29]. Therefore, within a planning horizon, managers must set sequences assures that the line do not present a work overload, or the works are well balanced throughout the stations. Due to substantial difference in model variants with regards to assembly difficulty and duration, sequencing rules often specify how many models should contain a specific variant. For instance, a variant whose assembly time is equal to the maximum cycle time of a station of assembly should follow a variant with lower assembly time to balance the work overload at the station.

In the assembly process, an operator makes a series of choices (i.e., module choice, fixture choice, tool choice, etc.). Oftentimes, the choice comes in form of selection of a specific variant of a module from a number of alternatives according to instructions. It follows that for each station, we can define a random variable X describing the outcome of a targeted variant in the outcoming assembly. Here, X can be described as random sequence whose symbols represent all the possible targeted variants.

The sequencing problem can be formulated as a constraint satisfaction problem. For instance, in a MMAL with N types of variants of a given module, each of which has specific part to be assembled, the sequencing in the assembly can be represented using a sequence S with symbols s_i ($i = 0, 1, 2, \dots, \mathbb{N}_+$) from a given alphabet V . For instance, assembly sequencing can be defined as a three-tuple, (V, S, r) where

- $V = \{v_1, \dots, v_N\}$ is the alphabet whose symbols represent different variants of a given module. That is V is a set of all possible variants of the module to be assembled at a given station.
- S with symbols s_i ($i = 0, 1, 2, \dots, M$), $i \in \mathbb{N}_+$, $s_i \in V$. Note that for any sequence S , there exist a subsequence S^L , of length L , with symbols s_j^L ($j = 0, 1, 2, \dots, L$), $L \leq M$
- $r : V \times S^L \rightarrow \{0, 1\}$; that is, if variant $v_i \in s_j^L$, then $r_{v_i s_j^L} = 1$; $r_{v_i s_j^L} = 0$, otherwise. In other words, the function r checks if a given subsequence contains a given variant.

In this paper we consider a MMAL system consisting of multiple stations arranged along a conveyor belt. The conveyor carries workpieces from one station to another with a constant speed v_c and the assembly is done by operators while moving along the conveyor. Thus, the cycle time at the station is fixed, and is determined by the conveyor speed and the length of the station. As previously mentioned, it is recommended that variants associated with high workload should not be successive in a sequence. For instance, this can be conveyed using the following constraint:

$$\sum_j^2 r_{v_i p_{kj}} < 2, \quad v_i \in V \quad (1)$$

Equation (1) would mean that the same variant shall not be requested successively in any sequence. In other words, the constraint imposes that, for any subsequence of two consecutive model on the line, at most one of them may require v_i , for any $v_i \in V$. Assuming the cycle time is fixed, the work overload is marked by conveyor stoppage (i.e., assembly could not be finished within the boundary of the station) or operators' idle time (i.e., concentration of idle time in a section of the sequence could imply an overload at a different segment of the sequence). Thus, to balance the workload of a station, we penalize the conveyor stoppage while we make sure the idle time, if any, is well balanced throughout the sequence.

1) ESTIMATING THE ENTROPY OF ASSEMBLY SEQUENCE

The information content in S is predicated to the predictability of its symbols at any given time. This predictability, which sometimes implies the complexity of the sequence, is measured using entropy [13]:

$$H = - \sum_{s_i \in V} p(s_i) \log_2 p(s_i) \quad (2)$$

Equation (2) gives information about the distribution of the variants on the market. Thus, let $d = d_i$; $i = 1, 2, \dots, N$; where d_i denotes the number of variant type i demanded by customer in a given time horizon. Thus, the total number of demand units (D) in the planning horizon is:

$$D = \sum_{i=1}^N d_i \quad (3)$$

It follows that the probability of producing a given variant in a given time is

$$p(v_i) = \frac{d_i}{D} \quad (4)$$

In a random and independent sequence of production, $p(v_i)$ is equivalent to the probability that a given position of sequence is occupied by module variant v_i . For example, let's reconsider the previous sequence S with symbols s_i ($i = 0, 1, 2, \dots, \mathbb{N}_+$), $s_i \in V$. Here, $p(v_1)$ denotes the probability that s_i takes the value v_1 . Thus, (2) can be rewritten as:

Similar to NSGAI, most of MOGA algorithms struggles to advance toward optimal sequence. As discussed earlier, the sequence complexity is measured using the information entropy. Since the information entropy is in a way a measure of unpredictability of strings of a sequence, it becomes clear that new individuals (i.e., children) obtained by randomly copying parents' strings (genes) will often be as unpredictable as the parents' strings, thus making the algorithm movement toward the optimal value very slow. The introducing of parameter K even at a value as low as 0.1, increase the odds that small subsequence of parents' strings with lower complexity (i.e., low entropy) are copied to children chromosomes; thus, accelerating the improvement objective value.

$$H = - \sum_{v_i \in V} p(v_i) \log_2 p(v_i) \quad (5)$$

Again, H gives information about the distribution of the variants on the market. It does not, however, reflect the order at which these variants are produced, which is an important factor determining the uncertainty of the sequence. In order to incorporate the correlation, (2) has to be generalized to the so-called block-entropies:

$$H = - \sum_{si \in A} p(s_i)^{(m)} \log_2 p(s_i)^{(m)}, \quad (6)$$

where $p(s_i)^{(m)}$ are the probabilities of the combinations of m symbols.

We suppose that the symbolic sequence S is the high-order Markov chain. That is, the probability of symbol s_i to have a certain value $v_k \in V$ under the condition that *all* previous symbols given depend only on M previous symbols. The sequence A is the M -step Markov chain if it possesses the following property,

$$\begin{aligned} P(S_i = \alpha^k | \dots, S_{i-2}, S_{i-1}) \\ = P(S_i = \alpha^k | S_{i-M} \dots, S_{i-2}, S_{i-1}) \end{aligned} \quad (7)$$

To estimate the conditional entropy of stationary sequence S of symbols s_i , one could use (6) to estimate the entropy per block of length L ,

$$H_L = - \sum_{s_1, \dots, s_L \in S} p(s_i^L) \log_2 p(s_i^L) \quad (8)$$

The entropy per symbol, is given by

$$h_L = H_{L+1} - H_L \quad (9)$$

This quantity specifies the degree of uncertainty of the $(L + 1)^{th}$ symbol occurring and measures the average information per symbol if the correlations of $(L + 1)^{th}$ symbol with preceding L symbols are taken into account. The conditional entropy h_L can be represented in terms of the conditional probability function $p(s_1^{L+1} | s_1^L)$

$$h_L = - \sum_{s_1, \dots, s_L \in S} p(s_1^{L+1} | s_1^L) p(s_1^{L+1} | s_1^L) \quad (10)$$

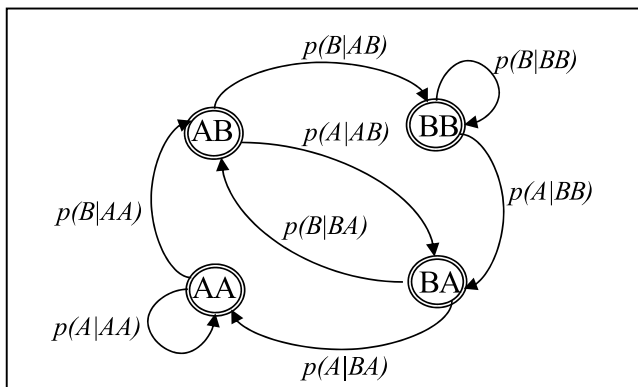


FIGURE 1. A simple illustration of choice process in modular assembly as a Markov sequence of second order. Note that there are two variants of the module (i.e., $v_1 = A, v_2 = B$). This choice process can be represented using a sequence S with symbols s_i ($i = 0, 1, 2, \dots, N_+$) from alphabet $V = \{A, B\}$.

Note that h_L is equivalent to the entropy rate when the sequence length approaches infinity". In addition, the sequence entropy can be estimated through data compression. Assuming a universal compression algorithm (e.g., L-W-Z), the ratio of compression approaches the entropy as the length of sequence grow; converging to the entropy rate when the sequence length goes to infinity.

IV. SEQUENCE BASED OPTIMIZATION OF VARIETY-INDUCED MANUFACTURING COMPLEXITY

A. PROBLEM DESCRIPTION AND FORMULATION

Product family can be divided into two categories: scale-based and module-based. Module-based product family has been one of the better design approaches to satisfy the accelerated demand of product variety. In this approach varieties of a given product family are obtained by "adding, substituting, and/or removing one or more functional modules from the platform architecture" [30].

This problem description is constructed based on MMALs system architecture. Therefore, the following list of assumptions are considered.

- (a). The system consists of multiple stations arranged along a conveyor belt, which is carrying workpieces from one station to another with a constant speed v_c .
- (b). Operators move along the workpiece carrying out distinct tasks, most of which require the "selection of the right module variant" according to the model at hand.
- (c). If the operator reaches the end of station before completing his task, the conveyor is *stopped* until the assembly is completed, after which the operation resumes as usual.
- (d). For simplicity, we assume a serial assembly line in which only one module is assembled at each station.
- (e). The sequence must comply with the customer demand.

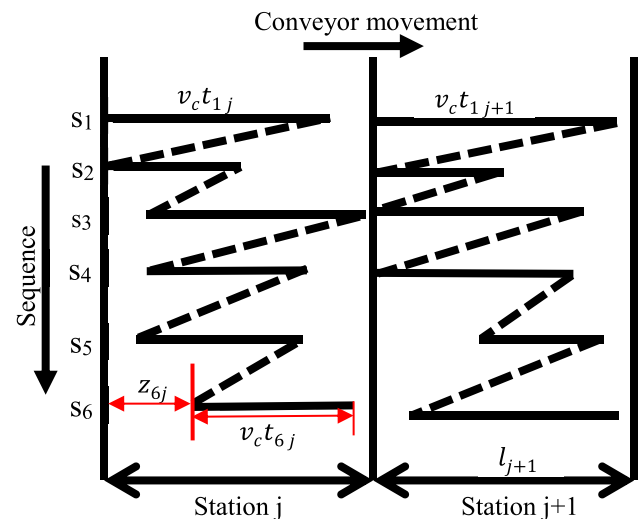


FIGURE 2. Depiction of sequencing, assembly time and station boundary.

(f). Once the operator completes the assembly task, s/he walks toward the left side of the station. The next assembly task starts when the operator meets the next workpiece. If the operator reaches the left edge of the station before encountering the workpiece, s/he waits for it at the left entry of the station.

Thus, the optimization problem can be simply stated as:
Minimize: Manufacturing complexity, idle time variation.
With respect to: Product assembly sequencing.
Subject to: Production balancing requirement.

For a clear understanding, we make use of the notations in Table 1

TABLE 1. List of notations.

Notation	Definition
S :	Sequence with symbols s_i ($i=0, 1, 2, \dots, \square_+$) from a given alphabet V ; $V = \{v_1, v_2, \dots, v_N\}, s_i \in V$
$p(s_i)^{(m)}$:	Probabilities of the combinations of m symbols.
H :	Entropy of sequence, where H_L is entropy per block of length L
s_i^L :	Block sequence of length L
h_L :	Conditional entropy of $(L + 1)^{th}$ symbol given H_L
σ :	The standard deviation of subsequence idle time
D :	Total Demand
N :	Number of variants/models in production
w :	Constant distance between two consecutive units
v_c :	Conveyor speed (a constant)
v_o :	Operator speed (a constant)
z_{ij} :	Distance (i.e., from the left boundary of the station) at which the operator starts the assembly of model i at station j
δ :	Distance interval between two consecutive units
t_{ij} :	Assembly time of model i at station j
t^{stop} :	Total time of stoppage needed to complete assembly
t^{idle} :	Total time the operator waits for the mainframe to arrive in order to start the assembly
l_j :	Length of station j
X_{im}	Binary decision variable (=1 if model m is in the i^{th} position of the sequence, 0 otherwise)

The main objective is to minimize the sequence complexity. This objective function can be reiterated in the following equation.

$$\text{Minimize} - \sum_{s_1, \dots, s_L \in S} p(s_1^{L+1} | s_1^L) p(s_1^{L+1} | s_1^L) \quad (11)$$

As previously noted, this quantity specifies the degree of uncertainty of the $(L + 1)^{th}$ symbol occurring

(i.e., proportional to the probability that a given model variant is next on the assembly sequence) and measures the average information per symbol if the correlations of $(L + 1)^{th}$ symbol with preceding L symbols are taken into account.

To avoid unwanted downtime, product sequence should ensure a well-balanced workload throughout the stations. While It is likely that both the complexity and the work overload correlate, it is possible that the least complex sequence would still lead to work overload. A typical example is when that overload is a result of factors not considered in the computation of sequence complexity (e.g., physical difficulty of a task, task cycle time, etc.). In addition, the proposed sequence-based complexity considers only the variety-induced complexity. Thus, to ensure that the selected sequence does not result in work overload, one more objective function is added: the variation of operator’s idle time. Since the cycle time at the station is fixed by the conveyor speed and the length of the station, one way to reduce the likelihood of work overload is to make sure that variants associated with high workload are not successive in a sequence. Thus, the second objective function ensures a balanced workload by minimizing the variation of idle time of subsequences. The objective function is described in the Eq.(12).

$$\text{Minimize } \sigma = \sqrt{\frac{\sum_i^D (t_{S_k}^{idle} - \bar{t}_{S^L}^{idle})^2}{\frac{D}{L} - 1}} \quad (12)$$

In short, the objective of this optimization is to keep the complexity, and the work overload as low as possible. The constraints of this problem can be formulated as follow:

$$\sum_n^N X_{in} = 1 \quad (13)$$

$$\sum_i^D X_{im} = d_m \quad (14)$$

$$t_{S_i}^{idle} = \frac{-\sum_i^L \frac{\min(z_{ij} + v_c t_{ij} - v_o \frac{w}{v_o + v_c}, 0)}{v_c}}{L} \quad (15)$$

$$l_j, t_{ij}, z_{ij}, d_m \geq 0; \quad X_{im} \in \{0, 1\} \quad (16)$$

Eq. (13) ensures that exactly one unit is assigned to each position in the sequence, while (14) assesses whether the demand requirements are fulfilled for each model type. Eq. (15) compute the total idle time (see(f) in the list of assumption).

B. METHOD

This is a nonlinear multi-objective optimization problem and can be solved using nonlinear optimization methods. However, it is very likely that the non-linear search converges to local optima or takes an unreasonable time to reach to the global optima. In this paper, a multi-objective genetic algorithm is used due to its efficient balance of efficiency and effectiveness. Inspired by natural selection,

it uses a probabilistic search that often overcomes the shortcomings of local optima convergence. Note however that, like individual genetic algorithm, Multi-Objective genetic algorithm (MOGA) does not necessarily return the optimal solution; rather, it ensures a good enough solution in tolerable time [31]. In this paper, we propose a multi-objective genetic algorithm that borrows from some well-known MOGA algorithms with high convergence speed. Recall that the biggest component of evolutionary algorithm reside in how new generations are generated. Thus, we further discuss the algorithm used to solve the problem described above, including the breeding process.

1) CHROMOSOME CODING

Unlike the traditional MOGA, binary coding is rather ineffective in this sequencing problem formulation. In this paper, a chromosome is simply coded as a sequence of strings where each string represent a given variant of the module to be assemble in a given product. The complexity fitness of the chromosome is the entropy of the sequence, while the idle time variation fitness is the standard deviation of subsequence idle time as seen in Eq. (11 & 12).

2) EVOLUTION OF POPULATION

Generally, the population evolves from one generation to another through two major breeding processes: the crossover and the mutation. Unfortunately, traditional crossover shown in Fig.3(1) is not effective since it is likely to produce unfeasible sequence. Assuming both parents are feasible, notice how both children are not feasible. For example, in the one-point crossover, the variant represented by gene ‘‘A’’ is only

seen in the sequence of child1 and child2, twice and four times respectively, instead of three times for both. Due to the product demand requirement, child 1 is not a feasible sequence. Thus, to ensure the feasibility of the offspring, a modified form of two-point ordered crossover is adopted in this paper (see Fig.3 (2)). The crossover is done as follow:

- i. select two non-dominated parents
- ii. randomly select two crossover points
- iii. generate an empty sequence of the same length as the individuals of the populations
- iv. copy the genes of parent2 located between the two crossovers points to the child chromosome
- v. fill the child’s chromosome with the missing genes in the same order as seen in parent 2

While the crossover method in Fig.3(2) produce feasible sequence; the low variability of entropy values of random sequences makes it more likely that most of crossover methods produce new individual with same fitness (i.e., complexity fitness) as that of the parent individuals. To promote the convergence to the sequence with the optimal complexity, a new parameter called convergence parameter ($\kappa, 0 \leq \kappa \leq 1$) is introduced. Therefore, part (v) of the crossover is modified where for each missing gene, with a probability $p = \hat{e}$, a gene from parent 2 with the highest value of $p(s_i^{L+1} | s_i^L)$ is selected and copied to child’s chromosome. Otherwise, fill the missing slot with the missing gene in the same order as seen in parent 2.

Due to its speed and simplicity, the paper uses the Fast Nondominated Sorting Approach proposed in NSGAI. However, due to the elitism that NSGAI entails combined with the lack of variability mentioned above; there is a high probability that new generations retain too many individuals from previous generations, often leading to insignificant progress. Thus, in this paper unless the parent individual dominates the child individual, the parent is removed from the population, thus rending its probability to be selected in the next generation to zero.

Despite the striking similarities between the algorithm used in this paper and NSGAI, the modest difference has a significant improvement due to the nature of the problem. For instance, Fig.6 shows the difference in pareto values of NSGAI against the proposed NSGAI-based algorithm. The general NSGAI consist of a loop where(see Deb et al. [32] for details):

- (a). First, a combined population of size $2N$ is formed.
- (b). The population is sorted according to nondomination and included into different fronts.
- (c). Choose N individuals for new generation. The individuals are chosen from nondominated fronts in the order of their ranking. The crowding distance is used to break the tie for individuals in the same front
- (d) The new population of size N is then used for selection, crossover, and mutation to create a new population of size N . The two new populations are then combined which is equivalent to (a) thus, completing the loop.

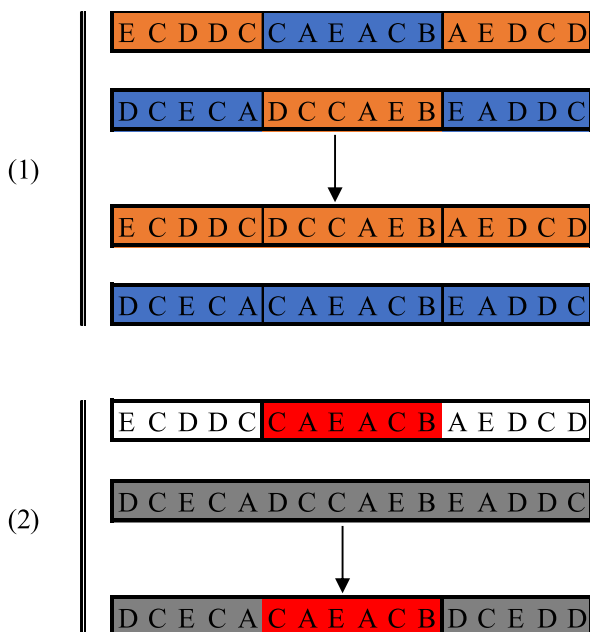


FIGURE 3. Example of traditional crossover method in (1), and the crossover used in this paper (2).

V. ILLUSTRATIVE EXAMPLE

A. PRODUCT SEQUENCING

1) WEATHERSTRIPPING ASSEMBLY SEQUENCING

Let us consider a MMAL where a number of sedan and SUV models are being assembled. For the sake of simplicity, we will only look at one hypothetical station in which, at most, ten variants of weatherstripping are being assembled according to customer demand. For a clear understanding of this illustration, refer to the graphical representation of MMAL offered in Fig 3. In each simulation run, we either assume an equal demand for each variant on the production line, or the demand for each variant is either randomly generated.

Assuming that a company has an obligation to comply with the demand, the scheduling problem of the assembly of weatherstripping that aims to minimize the complexity of the system, can be formulated using (11) – (16). In this example, the demand for car is fixed while the proportion of the car (in the demand) containing a given weatherstripping type is either i) random, provided that each type is represented or ii) uniform; i.e., all types of weatherstripping are demanded on equal (or almost equal) proportion. The number of variants of weatherstripping considered in the simulation were varied from two to ten. In each case, the multi-objective genetic algorithm is used to generate a sequence that minimizes the objective function complexity in accordance with procedure method described in the previous section

2) RESULT

Since the entropy measures the uncertainty or the predictability, it is fair to assume that, all things being equal, a system with many states is less predictable than that of small number of states. The sequencing problem in this paper is represented as a Markov process. Thus, more variants lead to more states resulting in less predictable (more complex) system. As seen in Fig 4 the increase in number of variants in a MMAL undoubtedly increase the complexity of the sequence.

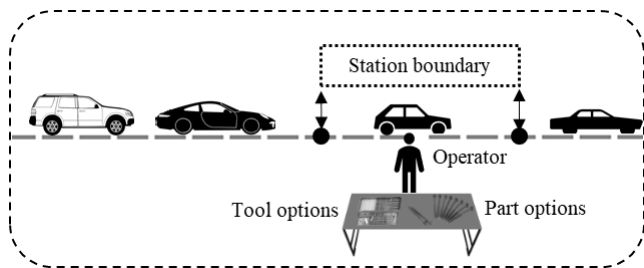


FIGURE 4. Graphical representation of MMAL.

Fig.5 (up) shows the change of complexity as the number of model variants increases. From the same figure (down), notice how a good sequence lowers the complexity, regardless of the number of varieties under production. In addition, the impact of an increased number of varieties in the assembly line is far steeper when the production sequence is not optimized.

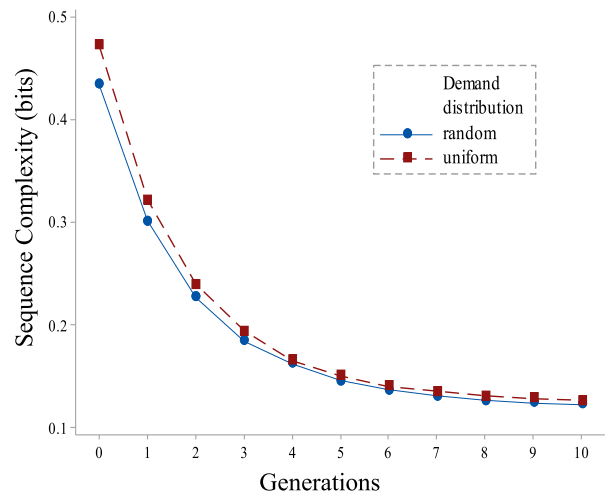
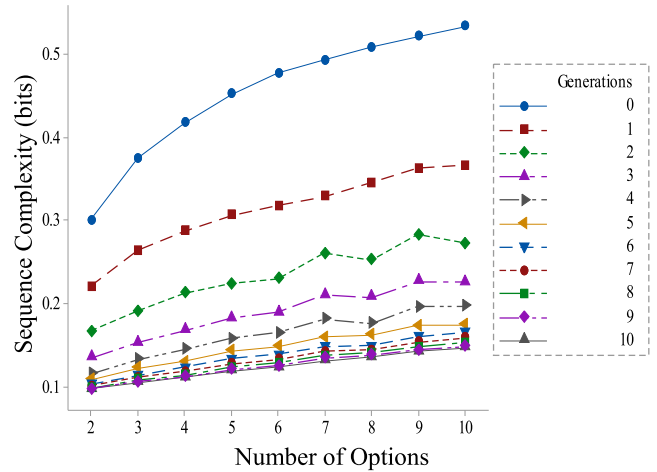


FIGURE 5. Sequence entropy estimates as a function of number of model variants.

Using “Jensen Inequality” shown in Eq(17), it can be shown that the maximum entropy corresponds to the scenario in which the demand for all varieties is equiprobable.

$$h_L = - \sum_{s_1, \dots, s_L \in S} p(s_1^{L+1} | s_1^L) p(s_1^{L+1} | s_1^L) \leq -\log_2 \frac{N}{D} \quad (17)$$

where N is the total number of variant whereas D is the combined demand of all variant. That notion is corroborated in Fig.5 (down) which shows the sequence entropy to be higher when the demand for varieties is uniformly distributed. Notice, however, how in Fig.5 (down) the level of increase of complexity due to the demand distribution can be limited or nullified by optimizing the sequence.

As discussed in the previous section, the nature of this problem makes it difficult for existing evolutionary algorithms to converges to the optimal sequence with regard to the sequence complexity. For instance, the following figure shows the effect of introducing the convergence parameter K. Here with K = 0.1, there is a significant improvement of the pareto results as shown in Fig.6

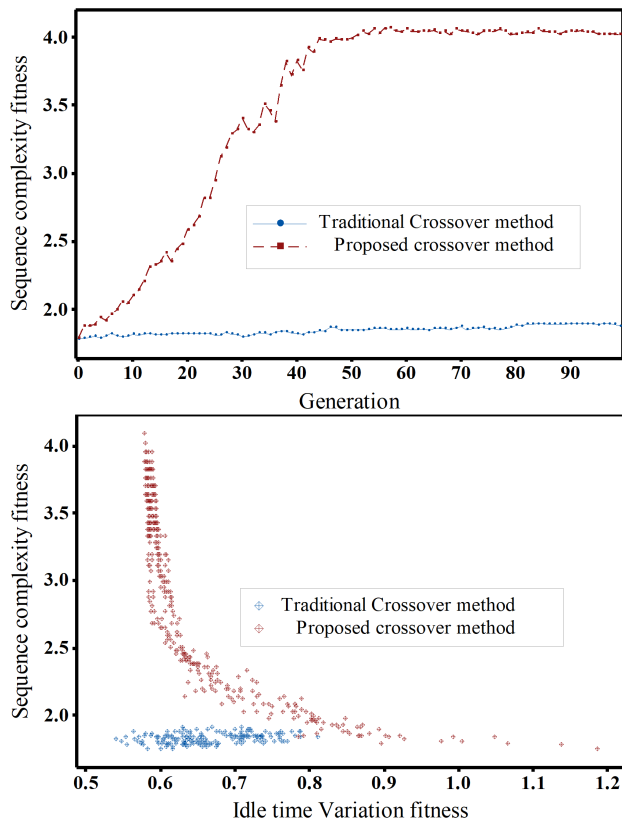


FIGURE 6. Comparison of Pareto fronts obtained using different algorithms.

B. COMPLEXITY AND ASSEMBLY PERFORMANCE

1) OVERVIEW

There is enough evidence that showcases the negative impact of complexity on system performance. For manual assembly, the impact of complexity is manifested in the extra time the operator requires to identify and locate the part or tool for the task at hand. According to Hick’s law [33], [34], the average reaction time (RT) can be approximately formulated as a linear function of the information entropy conveyed by the stimulus

$$RT = a + bh_L \tag{18}$$

where *a* and *b* are ergonomic parameters, while *h_L* is the complexity as shown in (10).

According to (20), as the complexity increases, operators become less effective. That is, in a complex environment, operators have a slower reaction time, prompting an increase in the cycle time of a given task. For example, it takes longer time for the operator to select the right module from a number of options.

2) EXPERIMENT DESCRIPTION

This section aims to demonstrate the relationship between the proposed sequence-based complexity measure and human performance. First, a hypothetical product family was generated. The goal was to optimize the sequencing with respect to

the complexity of the system. We conducted an experiment, in which an operator receives stimuli instructing him or her to perform a given task following certain guidelines. Practically, the form of these stimuli varies from one instance to another. For example, the operator may receive instructions that include a coded name or an image of the part to be assembled with the mainframe. In this experiment, the stimulus was given in the form of an image. Once the operator received the stimulus, he or she had to click on the matching option according to the guidelines (see Fig.7).

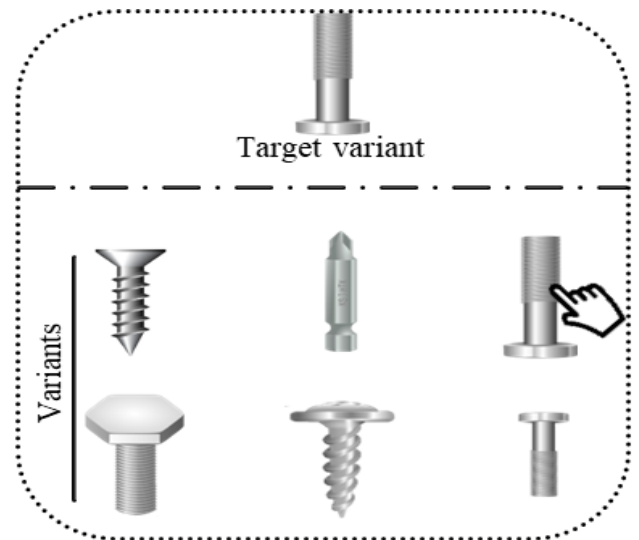


FIGURE 7. Selection task.

The operator (subject) was requested to select the matching image, after which the next matching command appeared. The task began when the stimulus was displayed on top of the options and finished when the subject clicked on one of the options. Once the subject clicked on one of the options, the experiment proceeded by displaying the next stimulus. A stimulus is uniformly selected from the set of all available options. The experiment was run on a desktop with a 21-inch monitor and there was a total of 10 participants each of which took over 25 minutes to finish the experimental runs. We note that number of participants (i.e., 10) in the experiment could be regarded as relatively low; however due to the nature of the analysis, the number of observations is more important to establish the relationship between product sequence and the response speed. In this experiment the data collected consist of more than 3,400 observations which are sufficiently enough to capture the reaction time trends as the sequencing information changes.

3) RESULT

Table 2 summarizes the results of this experiment. As the complexity of the sequence increased, so did the operator’s reaction time. Notice how, rather than the number of module variants, the sequence complexity as measured by the entropy, is the major predictor of an operator’s reaction

TABLE 2. Summary of experimental results.

Number of Variants	Sequencing Mode	Complexity (bits)	Selection time (sec)
2	Randomized	0.3302	0.9085
4	Randomized	0.4484	1.3054
6	Randomized	0.4991	1.4172
8	Randomized	0.5235	1.8216
10	Randomized	0.5497	1.5771
12	Randomized	0.5685	2.0961
15	Randomized	0.5872	2.1373
2	Optimized	0.0901	0.3767
4	Optimized	0.0938	0.3325
6	Optimized	0.0994	0.5042
8	Optimized	0.1032	0.3133
10	Optimized	0.1069	0.2767
12	Optimized	0.1107	0.3000
15	Optimized	0.1163	0.3941

TABLE 3. ANOVA table of entropy vs. reaction time.

Analysis of Variance					
Source	DF	Adj SS	Adj MS	F-Value	P-Value
Regression	7	6.4957	0.92795	26.42	0.000
Entropy	1	5.9361	5.93613	169.04	0.000
Number of Models	6	0.1037	0.01729	0.49	0.795
Error	6	0.2107	0.03512		
Total	13	6.7064			

Model Summary				
S	R-sq	R-sq(adj)	R-sq(pred)	
0.187397	96.86%	93.19%	82.70%	

time, as shown in the ANOVA table (see Table 3). The high correlation between the entropy-based sequence complexity, and the operator’s part selection time is a vindication of the proposed model (see Fig.8. That is, this correlation is a direct

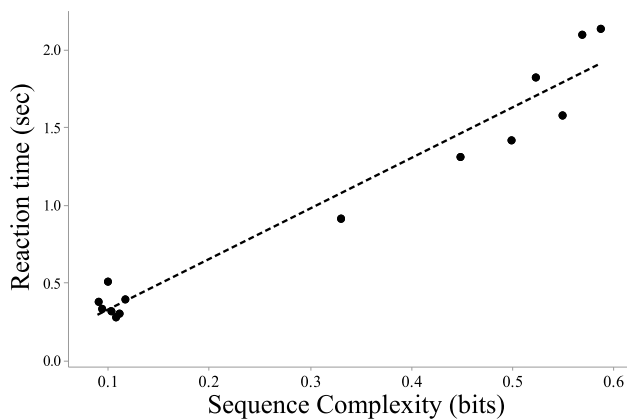


FIGURE 8. Entropy vs. Reaction time.

link between the complexity and the operator’s effectiveness. In comparison to other existing complexity measure in MMAL, the proposed sequence-based complexity measure does a better job predicting the operator’s reaction time. For instance [18] utilized the product mix as the principal factor in the complexity computation while [19] extended on the part mix to include the similarity of variants as two major determinant of operator’s choice complexity. According to our result, our proposed model outperforms both models in predicting the human reaction time: The coefficient of determination (R^2) is 0.48, 0.64 and 0.96 for Hu *et al.* [18], Busogi *et al.* [19], and our proposed model, respectively. While the difference is minimal for a random sequence, the existing model fail to capture the patterns in the sequences that would increase the predictability in the operator’s choice process.

VI. CONCLUSION

Customer driven markets have led to an overwhelming increase in product varieties, thus inducing a wide range of complexities in manufacturing systems. In addition, due to flexible market demands, manufactures are not only required to handle the unprecedented variety, but also the fluctuating demand. However, the lack of formal quantifiable methods of manufacturing complexity puts a limit in the ability to contain that complexity. In this paper, we presented a sequence-based method to compute manufacturing complexity in a MMAL. The complexity measure introduced in this work is based on the well-known information entropy model. Along with a numerical example, we conducted an experimental design to demonstrate the impact of manufacturing complexity on operator’s choice effectiveness.

The use of task sequence as the main input in the computation of complexity is rather compelling since the information (e.g., demand mix) often used in existing complexity computation models is a portion of the information contained in a sequence. For instance, from a given sequence, we can infer the information about the number of modules being assembled, the total demand of each module and the order in which they are being assembled at the station level. Based on the experimental results, the sequence-based complexity has a strong correlation to human reaction time, thus can serve as one of the major predictors of operators’ effectiveness in the assembly process.

The proposed complexity model can potentially serve as a sequence evaluation tool in relation to system complexity. For example, this tool can be used to investigate the state of complexity, and the choice complexity in particular, if a series of policies were to take effect. That is, in an environment where the demand keeps shifting and new variations of a product is often added to the assembly line, this tool allows a decision maker to theoretically assess such scenarios as it relates to choice complexity. The sequence optimization in this paper, while practical, could be extended to include several factors important to decision makers

(e.g., inventory cost). In addition, cost and time impacts on a decision maker should be further explored.

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