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Rapid sequence optimization of spot welds for improved geometrical quality using a novel stepwise algorithm

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ABSTRACT

Joining sequence optimization is a combinatorial problem, requiring extensive computational time. The significance of determination of an optimal sequence for improved geometrical quality is substantial. Previously, genetic algorithms have been studied for defining the optimal sequence. However, these algorithms are highly dependent on the internal parameters, requiring additional computational analysis and thereby extended evaluation time. In this article, a novel robust stepwise algorithm is introduced to determine the optimal weld sequence. Application of the proposed algorithm leads to drastic time improvements for defining the optimal weld sequence of each assembly. Three industrial assemblies are evaluated. Comparison with the previously applied population-based optimization algorithms indicates that the optimization time can be reduced drastically with the proposed stepwise algorithm. The stepwise algorithm is intended to be applied in a geometry assurance digital twin, where the assembly parameters are being optimized for each individual assembly.

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Joining; sequence; optimization; deformation; stepwise algorithm

1. Introduction

Controlling the geometrical outcome of manufactured goods is a common challenge within the manufacturing industry. Today, complex products are designed from several sub-assemblies. These sub-assemblies often consist of two or more components joined with different joining methods. The inconsistencies between the geometry of each component during the manufacturing processes result in part geometrical variation. Assembly process variations are derived from the fixture, material handling, joining, and other interacting processes. The assembly sequence, *i.e.* the order in which the parts are mated together, is of importance for the final manufacturing cost and also the assembly outcome (Bahubalendruni and Biswal 2016, 2018). The process variation, together with the part variation, are the sources resulting in the non-nominal produced products (Wärmefjord, Carlson, and Söderberg 2016; Camelio, Hu, and Ceglarek 2003).

To handle the geometrical variation, geometry assurance activities such as locator design, and matching are performed. To support the decision making during these activities in all the product realization phases, Söderberg *et al.* have proposed a virtual geometry assurance process and toolbox (Söderberg *et al.* 2016). In this process, joining simulations are performed on the transition between the concept and verification phase. Later in the production phase, real-time adjustments of assembly parameters are performed using digital twins (Söderberg *et al.* 2017).

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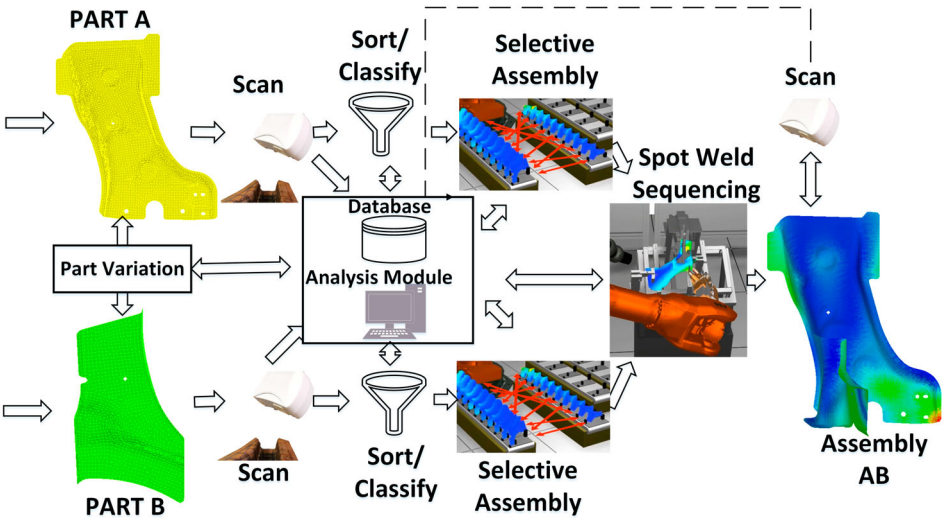

Figure 1. Schematic view of a self-compensating assembly line.

For real-time adjustments of the assembly parameters for sheet metal assemblies, a self-compensating assembly line, or the geometry assurance digital twin, is introduced (Söderberg *et al.* 2017). Figure 1 presents the layout of such a concept for an assembly of two parts. Each part is being scanned, and the deformations are captured (Wärmefjord *et al.* 2017). Later the parts are being sorted, classified, and selectively chosen to be assembled (Aderiani *et al.* 2019). In the assembly cell, the parts are positioned in the fixture, and the adjustments of the assembly parameters are proposed by the analysis module. In the analysis module, a Computer-Aided Tolerancing (CAT) tool is interacting with an optimizer. The CAT-tool evaluates the geometrical outcome of the assembly, given the part deviations from the scanned data. The optimizer uses the outcome of the CAT-tool to propose improvements for the assembly parameters.

Within the assembly process parameters, the joining process has been shown to have a significant effect on the final geometrical outcome of the assembly (Wärmefjord *et al.* 2016). The sequence of joining is one of the aspects the importance of which for the final assembly has been addressed in previous studies (Liao 2005; Tabar, Wärmefjord, and Söderberg 2019; Xie and Hsieh 2002). Finding the optimal sequence for each assembly using physical experimentation is economically infeasible. Therefore, numerical simulations are used for this purpose. In the concept of the presented self-compensating assembly line, an optimal spot welding sequence needs to be proposed for each individual assembly using numerical simulations. Using CAT-tools together with FEM calculations to evaluate the outcome of each individual exhaustively for all possible permutations of sequences requires extensive calculation time (Tabar, Wärmefjord, and Söderberg 2018). Previous studies have mainly focused on time-dependent Genetic Algorithms (GAs) to find the optimal sequence (Liao 2005; Xie and Hsieh 2002; Tabar, Wärmefjord, and Söderberg 2018). These algorithms require adjustments of the algorithm operators for higher efficiency, which makes them unsuitable for application in environments with a limited optimization time frame, such as the proposed geometry assurance digital twin concept, see Figure 1. Even with the optimal algorithm operator parameters, GAs and other population-based algorithms require several assembly deformation evaluations to converge, which again makes them more time-consuming. Therefore, there is a preeminent need for a rapid algorithm to propose an optimal spot welding sequence with a lower number of assembly evaluations by the CAT-tool.

1.1. Compliant variation simulation

Predicting the geometrical outcome of the assemblies, given the part tolerances, has been realized by CAT-tools. These tools often use transformation matrices to transfer the nominal part, by rotations and translations, to the allocated tolerance form with different approaches (Hong and Chang 2002; Zheng *et al.* 2011; Rao and Wu 2005). The effect of part deviations is often modelled using Monte Carlo (MC) simulations (Söderberg *et al.* 2016). For compliant assemblies such as sheet metals, the parts are bent and deformed during assembly. Therefore, to represent this behaviour, the Finite Element Method (FEM) is often used for modelling. FEM is used for structural and topology optimization in several applications (Kuczek 2016; Li *et al.* 2016).

The Method of Influence Coefficients (MIC) is proposed to evaluate the outcome of sheet metal assemblies (Liu and Hu 1997). MIC builds linear relationships between part deviation, stiffness matrix, and assembly deviation. In the geometry assurance digital twin concept presented Figure 1, the 3D scanned data of the parts are used for part deviations, representing the physical deviated parts. Using the MIC method, the assembly response to the existing part deviation is retrieved (Söderberg *et al.* 2017).

The MIC method has been complemented by a contact modelling algorithm for more accurate simulation outcomes. During the assembly of the compliant parts, they may cut through each other in the adjacent areas virtually. To avoid this behaviour during the simulation, contact points are defined on the nodes in the adjacent areas. In cases where penetration happens, these contact points apply negative forces to bring the parts back to their mating condition (Lindau et al. 2016).

Joining operations are included in the assembly model, with the small local deformation assumption (Liu and Hu 1997). Assuming the parts are in their elastic zone during assembly, the local deformation in the joint is considered to be small and negligible compared to the total assembly deformation. At the location of the joints, a stiff element is added to the weld nodes, forcing them to contact and lock them in all degrees of freedom. The simulation of the variation of the spot-welded assembly taking the sequence into account has been developed by introducing the sensitivity of the assembly to part deviation (Lorin *et al.* 2019, 2018).

1.2. Spot weld sequence optimization

Spot welding sequence optimization is about finding the best sequence among all the possible alternatives for the objective. The problem is a combinatorial one. By increasing the number of the welds that are included in the sequence, the number of possible solutions increases drastically, which puts the problem in the category of NP-hard combinatorial problems.

Several objectives and approaches are considered for this purpose. A neural network approach has been proposed for finding the optimal path of continuous welding with respect to local shrinkage of the material (Fukuda and Yoshikawa 1990). A surrogate modelling approach using neural networks with an efficient sampling strategy has been introduced for sequence optimization of spot welds with CAT-tools (Tabar, Wärmefjord, and Söderberg 2020). Huang *et al.* have proposed a genetic algorithm for finding the optimal sequence with respect to geometrical displacements (Huang, Hsieh, and Arora 1997). Other studies have also implemented GAs to optimize the sequences with respect to deformations (Liao 2005; Xie and Hsieh 2002). Using CAT-tools, general guidelines and strategies for the welding sequence of sheet metals are proposed for reduced geometrical variation (Wärmefjord, Söderberg, and Lindkvist 2010a). Identifying the most important weld points for geometrical quality, weld point geometry, and their sequence are evaluated using CAT-tools and GAs (Tabar, Wärmefjord, and Söderberg 2019). Evolutionary algorithms, Ant Colony Optimization (ACO) and Particle Swarm Optimization (PSO) are implemented and compared on three different assemblies to reduce geometrical variation (Tabar, Wärmefjord, and Söderberg 2018). Based on the GA, a rule-based algorithm has been proposed to find the optimal sequence of welding individualized assemblies with respect to geometrical deviation (Tabar *et al.* 2019). In a series of physical tests, it has been

identified that considering the sequence of weld points in the CAT-tool and compliant variation simulation with contact modelling increases the accuracy of the simulations (Wärmefjord, Söderberg, and Lindkvist 2010b). Considering state-of-the-art variation simulation, see Lorin *et al.* (2019, 2018), where contact modelling is combined with the MIC approach, optimizing the sequences for each assembly is time consuming. The rule based approach introduced by Tabar *et al.* (2019) has been shown to be more time efficient compared to standard evolutionary algorithms. However, the dependency of these algorithms on the internal parameter settings results in different performance with different parameters. Identifying the optimal parameter settings for these algorithms adds another layer of time-consumption to the problem. Therefore, in this article a novel robust algorithm is proposed for finding the optimal welding sequence, in which the number of evaluations by the CAT-tool is significantly lower compared to GAs and the previously introduced algorithms. Moreover, the algorithm does not involve additional internal parameters, making it more robust compared to previously introduced algorithms.

1.3. Scope of the article

In this article, a novel search algorithm has been proposed for finding the optimal sequence of welding using CAT-tools combined with contact modelling. The proposed algorithm is intended to reduce the number of assembly evaluations by the CAT-tool, and thereby reduce the optimization time. Section 1 provided an introduction to the problem. The rest of the article is structured as follows. Section 2 presents the modelling approach and the proposed optimization algorithm. Section 3 presents three reference assemblies to be evaluated by the proposed approach. Section 4 evaluates the efficiency of the proposed algorithm and compares the results with previously applied GA, PSO, a hybrid GA-PSO, and the rule-based GA. Finally, in Section 5, conclusions are drawn based on the evaluation presented.

2. Optimization approach

In this section, the assembly modelling approach using the MIC method is presented for retrieving the assembly deviation. This is followed by the presentation of the proposed algorithm.

2.1. Assembly model evaluation

To evaluate the assembly's geometrical outcome, the CAT-tool RD&T (RD&T Technology AB 2017) is used. This tool follows the MIC and contact modelling introduced in Section 1.1 to retrieve the assembly's response to part deviation and imposed forces during assembly. The following steps are followed to retrieve the geometrical outcome of the assembly.

(1) *Positioning in the fixture and clamping*. Considering an assembly, including parts x and y, with the small strain assumption, the following linear relation holds:

$$\boldsymbol{F}^x = \boldsymbol{K}^x \boldsymbol{d}^x \qquad \boldsymbol{F}^y = \boldsymbol{K}^y \boldsymbol{d}^y, \tag{1}$$

where $\boldsymbol{F}^x$ and similarly $\boldsymbol{F}^y$ are the forces needed to close the gap between the clamps in the part fixture. The stiffness matrices for each part are $\boldsymbol{K}^x$ and $\boldsymbol{K}^y$. The gaps to be closed in the fixture by the clamps are represented by $\boldsymbol{d}^x$ and $\boldsymbol{d}^y$.With this information, the part deformations are calculated. A sensitivity matrix $\boldsymbol{S}$ is built based on the response of the assembly to a unit disturbance of the clamping points. Now, this sensitivity matrix can be used to retrieve the assembly response to part deviation, when they are positioned in the fixture and clamped:

$$\boldsymbol{d}^c = \boldsymbol{S}\boldsymbol{d}^p, \tag{2}$$

where $\boldsymbol{d}^c$ is the deformation of the assembly when the clamps are applied in the assembly fixture. The gaps that need to be closed when the deviated parts are positioned in the fixture are represented by $\boldsymbol{d}^p$.

(2) *Joining*. The next assembly step is joining. In this step, to model the behaviour of the joints, a stiff beam is added to the model locking the joint nodes together. The updated stiffness matrix of the assembly is represented by $\boldsymbol{K}^j$. Then, the forces that are needed to weld the parts together can be calculated by

$$\boldsymbol{F}^j = \boldsymbol{K}^j \boldsymbol{d}^j, \tag{3}$$

where $\boldsymbol{F}^j$ is the force required to lock the joining nodes together. The displacements in the joining nodes are represented by $\boldsymbol{d}^j$.

(3) *Release from the fixture and springback*. The springback, when the assembly is released from the fixture, can be calculated by

$$\boldsymbol{K}^j \boldsymbol{d}^r = -\boldsymbol{F}^c, \tag{4}$$

where $\boldsymbol{d}^r$ is the displacement after the assembly is released from the fixture. Negative forces, equal to the forces needed to close the clamps, are applied to the assembly. These forces are denoted as $\boldsymbol{F}^c$. The final assembly response to the part deviation after joining is calculated by the summation of the displacements of the part deviations (Equation 1), clamping displacement (Equation 2), and springback displacements (Equation 4).

During all the steps mentioned above, a contact algorithm evaluates the assembly to avoid penetration of the parts virtually, see Section 1.1. The contact forces needed to bring the parts back to their mating condition is calculated by

$$\boldsymbol{F}^m = \boldsymbol{K}^j \boldsymbol{d}^m, \tag{5}$$

where the forces needed to bring the parts back to their mating condition is $\boldsymbol{F}^m$. The penetration displacement is denoted by $\boldsymbol{d}^m$. To avoid iteration of the contact algorithm and reduce the calculation time, a new method for building the sensitivity matrices and for retrieving the contact and joining forces is introduced (Lorin *et al.* 2019, 2018).

To evaluate the deformation of the assembly after welding in a sequence, the deformation of all nodes (from the mesh model) of the assembly in the normal direction is calculated. The Root Mean Square (RMS) of the deformations among all the nodes is considered for minimization between different sequences. The RMS of the deformation of all the nodes is chosen owing to its generic form to represent the whole assembly. Any other critical measure can also be evaluated for the minimization of the assembly deviation. Defining d^i as the deviation of node i of the assembly, $i = \{1, \ldots, k\}$, then the RMS of the deviation of the assembly (D) is calculated by

$$D = \left(\frac{1}{k} \sum_{i=1}^{k} d^{i2} \right)^{1/2}. \tag{6}$$

2.2. Problem formulation

With the MIC and contact modelling approach presented above, assembly deviation after joining in a sequence can be retrieved. The CAT-tool RD&T is used to evaluate the geometrical outcome of the assembly D (from Equation 6) after spot welding in a sequence.

With N weld points on the assembly, there are $N!$ possible permutations that need to be evaluated. Evaluating all the possible sequences to find the best sequence for minimized geometrical deviation of the assembly is not feasible. The assembly deviation can only be retrieved when all the weld points are set on the assembly. Therefore, running all the primary and pairwise combinations of the sequence

elements with a branch and bound approach is not applicable. This is due to the non-cumulative aspect of the welding sequence, for which the summation of the deformation after each welding step cannot be considered. To describe this point further, consider an assembly of four weld points. An array of numbers creates a sequence, and each member of this array is referred to as an element of the sequence. All the possible alternatives for the first element are {[1], [2], [3], [4]}. At the first level, the assembly is evaluated with only one weld point with each of these alternatives, and the minimum assembly deviation is found. Assuming that weld point 4 results in the minimum deviation, in the second level the assembly is evaluated with alternatives {[4, 1], [4, 2], [4, 3]}. With this approach, since the deformation cannot be added at each level, and weld point 4 does not get the chance to appear in other sequence elements, the geometrical deviation of the optimization will be outside the boundaries of the problem.

Previous research (Huang, Hsieh, and Arora 1997; Liao 2005; Tabar, Wärmefjord, and Söderberg 2018) provided the GA approach to solve this optimization problem wherein only complete solutions are evaluated, such as [1, 2, 3, 4] or [4, 2, 3, 1] on the example with four weld points. However, population-based algorithms like GAs require several evaluations of complete sequences to converge, which is time-consuming.

In general, the formulation of the problem for an assembly with N weld points can be expressed as

$$\begin{aligned} \underset{D}{\text{minimize}} \quad & D(W_i) \\ \text{subjectto} \quad & \boldsymbol{W} : \{1, \ldots, N\} \rightarrow \{N, \ldots, 1\}, \quad N \in \mathbb{N} \\ & W_i \subseteq \boldsymbol{W}, \quad i \in \mathbb{N} : 1 \leq i \leq |\boldsymbol{W}| \\ & W_i = \{a_{i1}, \ldots, a_{ij}\}, \quad a_{ij} \in \mathbb{N} : 1 \leq j \leq N \\ & |W_i| = N. \end{aligned} \tag{7}$$

The problem considers minimizing the RMS of the assembly deviation (D from Equation 6) among all possible permutations, $\boldsymbol{W}$. For an assembly with N weld points, only complete sequence combinations of welds 1 to N should be considered to build the permutations. In other words, no sub-sequences with less than N elements are allowed for evaluation.

2.3. Proposed stepwise algorithm

To increase the efficiency, *i.e.* save evaluation time, a stepwise algorithm is proposed here.

With the formulation provided in Equation (7), the proposed algorithm suggests evaluation of the complete sequences, while the optimization is performed stepwise for each element. An algorithm with N weld points will have $N-1$ steps at its elementary form. The steps of the algorithm are as follows.

Step 1

(1.1) Generate all possible complete solutions.

(1.2) Evaluate all possible alternatives of the primary 's' elements of the sequence. The parameter s can be defined as one or more depending on the number of elements in the sequence. In the example of the assembly with four weld points, if $s = 1$ the first level is built with {[**1**, 2, 3, 4], [**2**, 1, 3, 4], [**3**, 1, 2, 4], [**4**, 1, 2, 3]}. The rest of the elements can be chosen in any arbitrary order. To increase the accuracy of the algorithm, these primary elements can be defined as two, $s = 2$. In this approach, the initial step starts by generating all the combinations of the first two elements, [**1**, **2**, 3, 4], [**2**, **1**, 3, 4], [**4**, **3**, 1, 2], [**3**, **4**, 1, 2] and so on.

(1.3) Find the sequence with minimum deviation (D from Equation 6) among the evaluated sequences.
For explanation, assume that the sequence $[4, 1, 2, 3]$ results in the minimum D.
(1.4) Set the first element of the sequence equal to the first element of the sequence with minimum D. From $[4, 1, 2, 3]$, if $s = 1$ the primary element of the sequence is set to $[4]$, and if $s = 2$ the primary elements of the sequence are $[4, 1]$.

Step 2

(2.1) Generate an updated set of solutions with the determined elements. All the possible combinations should be contained in the next element after the decided elements.
f $s = 1$, the solutions $\{[4, \mathbf{1}, 2, 3], [4, \mathbf{2}, 1, 3], [4, \mathbf{3}, 1, 2]\}$ are built for evaluation. For $s = 2$, $\{[4, 1, \mathbf{2}, 3], [4, 1, \mathbf{3}, 2]\}$ are created.
(2.2) Evaluate the created solutions.
(2.3) Find the sequence with minimum D.
(2.4) Set the next element according to the sequence with the minimum D.

Steps 3 . . . (N − 1)

(3) Iterate Steps (2.1) to (2.4) until the complete sequence is set.

With this algorithm, the problem is identifying s elements among all possible N alternatives in the first step,

$$\binom{N}{s},$$

and

$$\binom{N-k+1}{1}$$

at the other steps, where k is the step number. Therefore, instead of evaluating $N!$ sequences,

$$\binom{N}{s}s! + \sum_{n=2}^{N-s}\binom{n}{1}, \tag{8}$$

sequences need to be evaluated. This number of evaluations for reaching an optimum is considerably lower than $N!$. For instance, in $s = 1$, the multiplication of the elements $\prod_{n=2}^{N} n$ turns into the summation $\sum_{n=2}^{N} n$. For longer sequences, Step 1 can be conducted multiple times, with larger s values to reach a higher accuracy.

The overall optimization approach is that the stepwise algorithm generates the feasible solutions and calls the CAT-tool RD&T to evaluate the assembly deviation for each sequence, at each step. The proposed stepwise algorithm is realized in MATLAB® and the connection to the CAT-tool is built. Algorithms 1 and 2 are the pseudocodes of the presented stepwise algorithm.

In Algorithm 1, the input of the algorithm is the number of weld points, or joints, N, in the assembly. The number of primary elements to be considered to generate the first step sequences s, as mentioned in is Step (1.2), is also an input. The optimal weld sequence and the corresponding assembly deviation (Equation 6) evaluated by the CAT-tool are the outputs of this algorithm. In the initialization phase, the required variables are being created. In Step 1, the algorithm calls a function to create the required sequences at each step. This function is referred to as Generate Step Sequences (GSS). This function is presented in Algorithm 2, where, based on the number of welds and the step number and the defined s, the sequences at each step are created. The assembly deviation D of the

Algorithm 1 Stepwise spot weld sequencing algorithm

Input: N Number of welds in the assembly
s Desired number of primary elements in the sequence
Output: W_s^* Optimal weld sequence
D^* Assembly deviation of the optimal sequence

Initialization
Define N
Define s
$W_s \leftarrow [1:N]$, define the sequence W_s
$l \leftarrow 0$, number of sequences to be evaluated
for $i = 1$ to $N - s$ **do**
    $l \leftarrow l + 1$
end for
$l \leftarrow \binom{N}{s} s! + l$, calculated number of sequences to be evaluated
$[Step_{all}] \leftarrow \mathbf{[0]}_{\,l \times N+1}$, pre-define the matrix of all steps

Step 1
$[Step_1]_{u \times v} \leftarrow GSS\,(W_s, 1, s)$, generate Step 1 sequences, see Algorithm 2
$[Step_{all}]_{(1:u)\times(1:N+1)} \leftarrow Evaluate(Step_1)$, evaluate each sequence in the first step and save the corresponding assembly deviation D in the $(N+1)$th column.
$[\sim, y] \leftarrow Min(Step_{all}((1:u), (N+1))$, find the row of the sequence with minimum D.
$W_s \leftarrow Step_{all}(y, (1:N+1))$, assign the sequence with the minimum D

Main loop
for $k = s + 1$ to $N - 1$ **do**
    $[Step_k]_{u \times v} \leftarrow GSS(W_s, k, 1)$, create the step sequence
    $[Step_{all}]_{(1:u)\times(1:N+1)} \leftarrow Evaluate(Step_k)$, evaluate each sequence in Step k
    $[\sim, y] \leftarrow Min(Step_{all}((1:u), (N+1))$, find the minimum row
    $W_s \leftarrow Step_{all}(y, (1:N+1))$, assign the sequence
end for
$W_s^* \leftarrow W_s$, assign the last evaluated sequence as the optimum
$D^* \leftarrow Step_{all}(l, N+1)$, assign the last evaluated assembly deviation as the optimum

generated sequences are evaluated by the CAT-tool RD&T. After all the elements of the sequence are determined, Algorithm 1 returns the optimal sequence and the corresponding assembly deviation.

3. Reference assemblies

Three automotive sheet metal assemblies are evaluated for optimal welding sequence with the proposed approach. The material in all the assemblies is steel. The elastic modulus is 210 GPa, the density 7800 kg/m^3, and the thicknesses of the sheets vary for each assembly. The thicknesses are specified in the description of each assembly. The assembly models are prepared using the CAT-tool RD&T. The mesh models of the parts are used in the model. The part deviations are introduced into the model with the deformed part meshes. The positioning systems of the parts and the assemblies are introduced to the models. The locations of the welding points are introduced, and contact modelling is performed on the models. All weld points are functional and locking all the degrees of freedom in the position of the weld.

Changing the positioning system and the clamping positions results in different model behaviours. The same applies to changes in the material properties. The proposed stepwise algorithm is applicable

Algorithm 2 *GSS*, Generate Step Sequences (GSS)

Input: W_s Weld sequence generated at the previous step
k Step number from Algorithm 1
e number of elements, s or one, to be included in the sequence generation
Output: Seq Weld sequence sample

$[Seq]_{u\times v} \leftarrow perms(W_s(k, end))$, generate all the possible permutations of the not assigned elements.
for $i = 1$ to u **do**
  $E \leftarrow Seq(1, e)$, assign the primary elements of the sequence
  if $E \neq Seq(i, e)$ **then**
    $c \leftarrow i - 1$, calculate the interval number, when the corresponding element changes
  end if
end for
$[z]_{x\times y} \leftarrow Seq(1 : c : end, :)$, assign the sequences, without the decided elements
$d \leftarrow [\mathbf{0}]_{x\times k-1}$, pre-define the decided elements matrix
for $j = 1$ to $k - 1$ **do**
  $d(:, j) \leftarrow W_s(j)$, assign the decided elements
end for
$Seq \leftarrow [d, z]$, concatenate the decided element to the new step sequences

to all models with different assembly properties and changes to the reference system and clamping positions.

To compare the evaluation time, each assembly is evaluated using the CAT-tool on a workstation with a 2.7 GHz CPU and 32 GB of RAM, and the time is recorded. In the following, the details of each assembly are presented.

3.1. Assembly I

Assembly I consists of two sheet metal parts joined together with seven weld points. The sheet thickness for Part 1 is 1.6 mm and Part 2, 1.2 mm. Figure 2(a) shows the CAT model of the assembly. The position of the weld points and their numbering are depicted. The positioning system and the locking directions are shown by arrows. Contact modelling is performed using 154 contact points. With these model properties, each simulation of assembly deviation, for a specific welding sequence, requires 7.2 seconds on the specified workstation.

3.2. Assembly II

This assembly consists of three sheet metal parts joined together with seven weld points. The sheet thickness for Part 1 is 0.76 mm, Part 2, 0.75 mm, and Part 3, 0.8 mm. Figure 2(b) shows the CAT model of this assembly. The positioning system, the weld points with the spheres, and their corresponding numbering are shown. This model is prepared with 62 contact points. This model requires 3.73 seconds to evaluate the assembly deviation for a specific welding sequence, using the CAT-tool.

3.3. Assembly III

This assembly consists of three sheet metal parts joined together with nine weld points. Seven weld points are set in a sequence $\{W_1, \ldots, W_7\}$. Two weld points, $\{W_8, W_9\}$, are set simultaneously after the first seven weld points are welded. The model is prepared with 194 contact points. The sheet

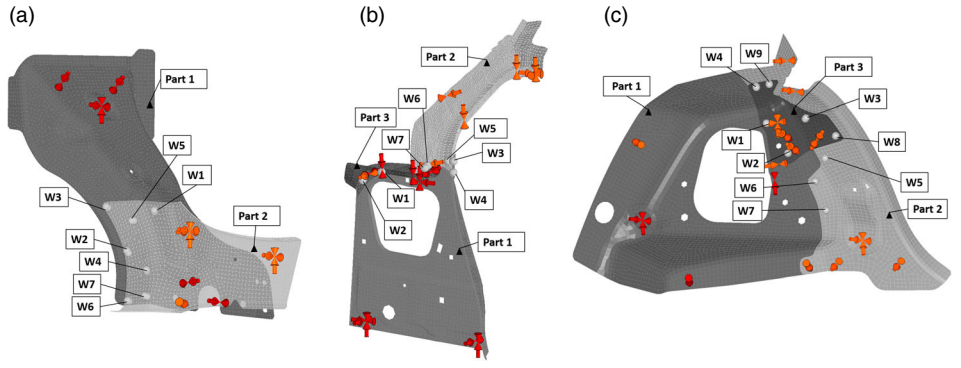

Figure 2. Three sheet metal reference assemblies. (a) Assembly II, (b) Assembly III.

thicknesses for Parts 1–3 are 0.8 mm. Figure 2(c) shows the CAT model of the part. The positioning system, the weld points, and their corresponding numbering are shown in this figure. With the above settings, the model requires 12.35 seconds to evaluate the assembly deviation for a specific welding sequence.

4. Method evaluation

To evaluate the accuracy and time efficiency of the proposed algorithm, and provide a comparison, an exhaustive search method, the previously applied GA, the PSO described in Tabar, Wärmefjord, and Söderberg (2018), a hybrid GA-PSO, and a rule-based GA presented in Tabar *et al.* (2019) are applied to the three reference assemblies. In the following, descriptions of the applications of these methods to the problem are presented.

4.1. Exhaustive search

To identify the optimum sequence, and the corresponding assembly deviation (D), as the point of comparison, all the possible sequences on the three reference assemblies are evaluated using the CAT-tool RD&T. Table 1 presents the global optimum sequence with the minimum assembly deviation. The efficiency of the algorithms has been compared with the achieved results, presented in this table. For Assembly III, there are 60 sequences that result in the minimum RMS of geometrical variation, while in Assemblies I and II there is a single optimum with several near-optimum sequences. The sequence presented in Table 1 for Assembly III is one of the 60 sequences and their corresponding assembly deviations.

Table 1 also presents the single evaluation time for each assembly in seconds. Total evaluation times to find the sequence with the minimum assembly deviation are also presented in hours. The total evaluation time is the product of the number of available sequences ($7! = 5040$) and the single evaluation time.

Table 1. Optimal sequence, assembly deviation (in millimetres) and evaluation time of the reference assemblies from the exhaustive search.

Assembly	Optimal sequence	Assembly deviation (D)	Single Eval. Time (s)	Total Eval. Time (h)
I	{1-4-2-5-3-6-7}	0.32	7.2	10.08
II	{3-5-7-2-4-6-1}	0.08	3.73	5.22
III	{3-4-6-7-2-5-1-(8, 9)}[a]	0.655	12.35	17.29

[a] The sequence of welds are represented by the weld numbers, where {W1-W4-W2-W5-W3-W6-W7} is represented by {1-4-2-5-3-6-7}. In Assembly III, welds W8 and W9 are welded simultaneously at the end of the sequence, represented by (8,9).

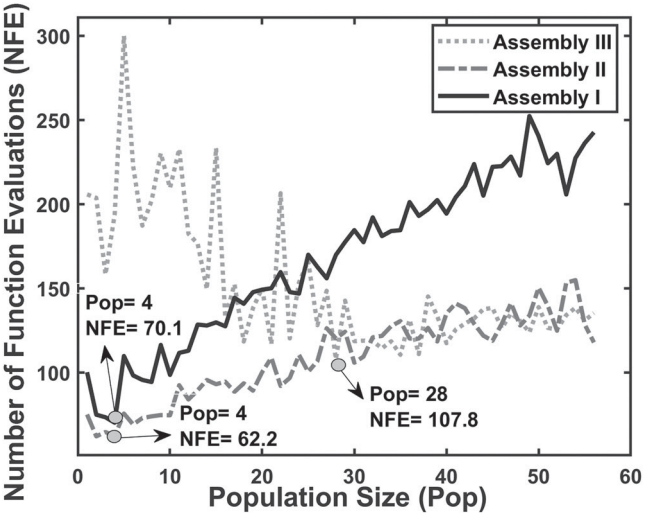

Figure 3. Mean number of function evaluations (NFEs) for different population sizes in 100 trials.

4.2. Genetic algorithm

A standard GA, which has been applied previously to this problem (see Tabar *et al.* [2019]), is applied to the three assemblies for comparison. In the GA, a single-point crossover with a roulette wheel selection method for selecting the offspring is used. The mutation operator consists of inversion, insertion and swapping operators. The crossover rate is 0.5 and the mutation rate 0.9. Population sizes 1 to 56 are evaluated. Since, at the maximum, the stepwise algorithm requires 56 evaluations from the CAT-tool, the GA at population size 56 will have a minimum of 56 evaluations. Thereby, population sizes 1 to 56 are evaluated. At each population size, the GA algorithm is run 100 times to reach the assembly deviations, mentioned in Table 1, as the ending condition to compare the computational efficiency. The mean Number of Function Evaluations (NFEs) are depicted in Figure 3 for time comparison. The required time for each single evaluation (one NFE) for each assembly is reported in Table 1. Using the GA, to retrieve a sequence with the assembly deviation mentioned in Table 1, Assembly I requires at least 70.1 NFEs from the CAT-tool. Each NFE is equivalent to one instance when the GA calls the CAT-tool to evaluate the assembly deviation. Assembly II requires 62.2 NFEs, and Assembly III requires 107.8 NFEs on average. Using the GA, these evaluation times vary based on the population sizes that are used in the algorithm. Finding out which population sizes are the most suitable for each assembly is not known prior to the evaluation of many sequences, which makes the approach time-consuming.

Moreover, to evaluate the accuracy of the algorithm compared to the stepwise algorithm, GA has been run 100 times at each population size with the end condition of reaching 56 NFEs. This is equal to the maximum NFEs that the stepwise algorithm requires to find the optimum for the three assemblies. The ranges of the retrieved assembly deviations at each population size in the 100 trials are depicted in the first row, right column of Figure 4 for Assembly I. The corresponding figures for Assemblies II and III are presented in the Supplemental data for this article (which can be accessed at https://doi.org/10.1080/0305215X.2020.1757090). As can be seen, the variability of the retrieved optimum in all population sizes are high with 56 evaluations. In Assembly I, Figure 4, the error of the retrieved optimum of assembly deviations can be up to 40% of the global optimum, retrieved from the exhaustive search (see Table 1). In Assembly II, this error is up to 25%, and in Assembly III, 2.3%. This means that the GA is not robust at 56 NFEs and fails to provide satisfactory accuracy with this NFE, or in other words evaluations from the CAT-tool RD&T.

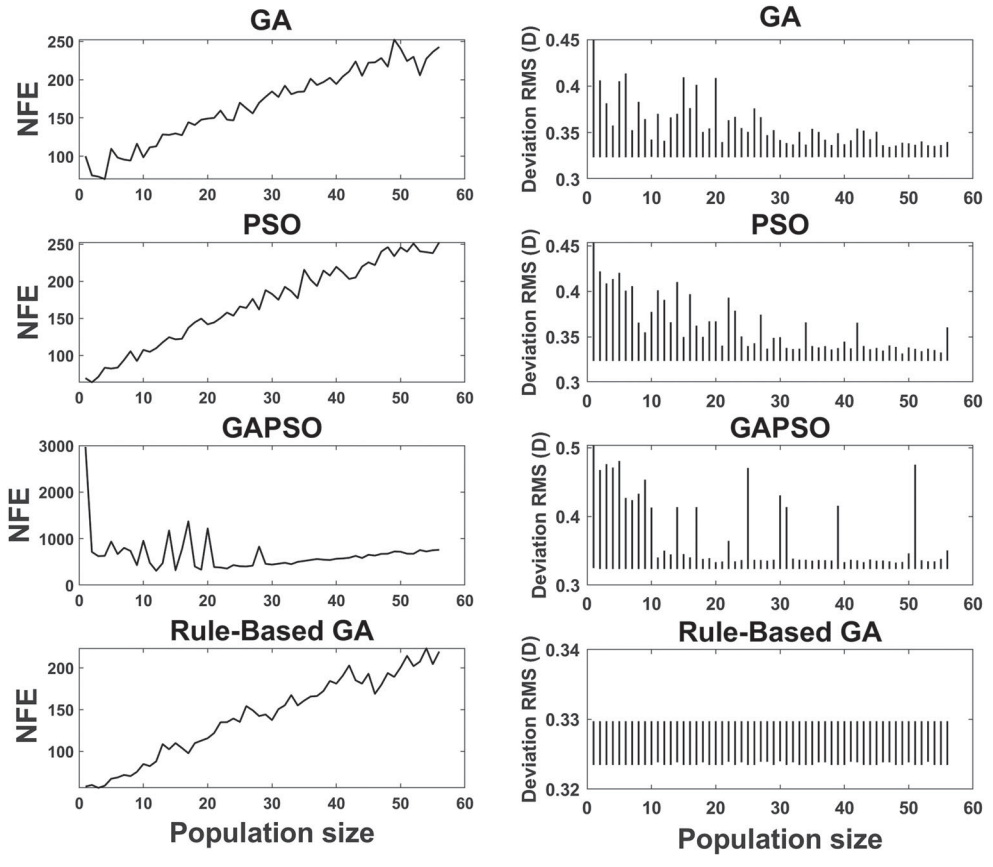

Figure 4. Mean number of function evaluations (NFEs) (left column) and assembly deviation range (right column) for different population sizes in 100 trials between the compared algorithms for Assembly I.

4.3. Particle swarm optimization

A particle swarm optimization algorithm has been setup to compare the accuracy and the time consumption to the proposed stepwise algorithm. This type of swarm-based optimization approach has been a competitor of the GA and previously applied to the problem (Tabar, Wärmefjord, and Söderberg 2018). The same analysis as for the GA is performed. The results are presented in the second row of Figure 4 for Assembly I. PSO requires at least 64 NFEs to reach the optimum in Assembly I. For Assembly II, 60 NFEs, and 111 NFEs for Assembly III, see the Supplemental data.

The accuracy of the algorithm is also evaluated. For Assembly I, the error is up to 40% of the global optimum, for Assembly II, 30%, and for Assembly III, 2%.

4.4. Hybrid evolutionary algorithm

A combined GA and PSO hybrid algorithm, referred to as GAPSO, is also applied to the assemblies for comparison. The number of required NFEs to reach the optimum and the range of the retrieved optimum with a maximum of 56 evaluations are shown in the third row of Figure 4 for Assembly I. The minimum number of NFEs using this algorithm is 307 for Assembly I, 216 for Assembly II, and 370 for Assembly III.

The errors of the method among all population sizes, from the collected ranges of RMS assembly deviation (D), compared to the exhaustive search result are 57% for Assembly I, 137% for Assembly II and 8% for Assembly III.

4.5. Rule-based GA

A rule-based GA has been previously applied to the problem and showed improved results compared to the stand-alone GA (Tabar *et al.* 2019). This algorithm is also included in the comparison between the algorithms presented above.

The results of the above evaluations are depicted in the last row of the Figure 4 for Assembly I. For Assemblies II and III, see the Supplemental data. The minimum average number of NFEs required to reach the global optimum is 56 for Assembly I, 42 for Assembly II and 21 for Assembly III.

The range of the retrieved optimum by having a maximum of 56 NFEs as the ending condition, in 100 trials, shows the error among the trials. These errors are up to 2% of the global optimum for Assembly I, 27% for Assembly II and 1.2% for Assembly III.

4.6. Stepwise algorithm sequence evaluation

To evaluate the sequence of welding in an assembly, the stepwise algorithm suggests deciding the elements of the sequence based on their position in the sequence array. The first step is to define the primary elements. As the algorithm states, the first and/or second elements can be chosen as the primary elements. Figure 5 shows the evaluations of the first elements of the three assemblies and compares them with the exhaustive search results. The left column represents the stepwise algorithm with $s = 1$ in the initialization step. The right column of Figure 5 depicts the initial first step with all combinations of the primary two elements, $s = 2$. With this information, the primary elements of the sequence are determined based on the sequence that results in the minimum RMS geometrical deviation of the assembly (D) in this step. Following the algorithm, in Step 2 the sequences are updated, and a new set of sequences are generated and evaluated. This process is continued until all the elements of the sequence are determined. Figure 6 shows the evaluated sequences in each step until convergence is achieved. Table 2 presents the optimal sequence and the corresponding assembly deviation obtained using the stepwise algorithm when one element and two elements are evaluated in the initial step of the algorithm. The algorithm results in the optimum sequence in all cases by evaluating the primary two elements of the sequence in the initial step, with negligible errors from the global minimum of assembly deviation. When $s = 1$, the accuracy of the retrieved convergence values has been optimal in Assemblies I and II, and near-optimal in Assembly III. Considering that the stepwise algorithm with $s = 1$ requires half of the evaluations of $s = 2$, the convergence values are accurate. For Assemblies I and II, the first four elements of the sequences are the same as the optimal sequence achieved by the exhaustive search presented in Table 1. While in Assembly III, since 60 sequences result in the minimum assembly deviation, the sequence elements vary between the exhaustive search and the stepwise algorithm.

4.7. Evaluation time comparison

To compare the evaluation time, the number of times that algorithms call the CAT-tool to evaluate a sequence is considered. The NFEs for all the compared algorithms (see Sections 4.2 to 4.5) and the stepwise algorithm are counted. The stepwise algorithm needs a fixed number of evaluations, NFE, for $s = 1$ and $s = 2$. These numbers are presented in Table 3. The GA's and PSO's performances are close to each other, while the hybrid algorithm requires a longer evaluation time to converge.

Using the stepwise algorithm with $s = 1$ saves 57 to 75% of the evaluation time in the evaluated assemblies compared to the GA. Considering that the stepwise algorithm results in near-optimal

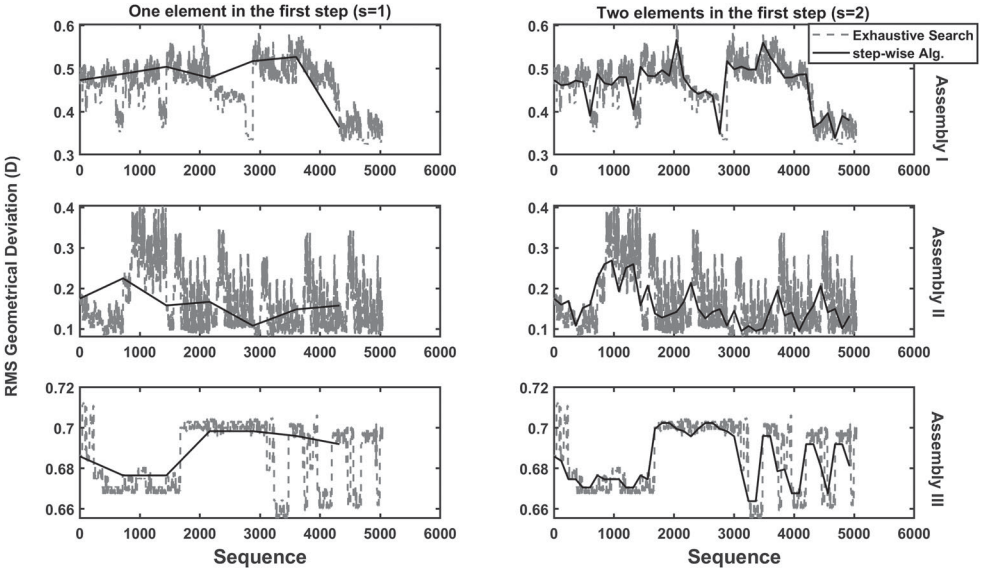

Figure 5. First step of the stepwise algorithm with one and two elements compared to the exhaustive search.

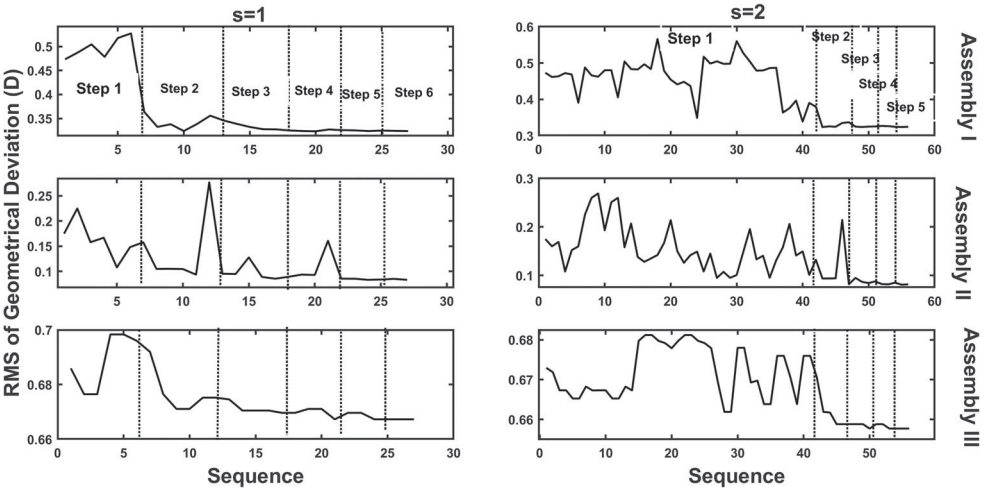

Figure 6. Optimization steps using the stepwise algorithm.

results with 27 evaluations, the improvements are drastic compared to the GA, PSO and GAPSO algorithms. When $s = 2$, 56 evaluations are required to reach the optimum, saving 10 to 48% of the evaluation time compared to the GA. By increasing the s value, the accuracy of convergence increases; however, the evaluation time also increases, since a larger set of sequences needs to be evaluated in the initial step of the algorithm. Having $s = n$ in an N weld-point assembly increases the NFEs to

$$\binom{N}{n} n!$$

Therefore, $s = 1, 2$ is recommended in the stepwise algorithm. It is shown that the stepwise algorithm with $s = 1$ identifies the near-optimal with negligible errors from the global optimum sequence with the lowest NFEs possible (see Table 3).

Table 2. Optimal sequence and the assembly deviation (in millimetres) of the reference assemblies retrieved from the stepwise algorithm with $s = 1$ and $s = 2$.

	Optimal sequence		Assembly deviation (D)	
Assembly	$s = 1$	$s = 2$	$s = 1$	$s = 2$
I	{1,4,2,5,6,7,3}	{1,4,2,6,7,5,3}	0.32	0.32
II	{3,5,2,7,4,6,1}	{3,5,7,2,4,6,1}	0.08	0.08
III	{6,2,1,5,4,3,7,(89)}	{3,4,5,2,6,7,1,(89)}	0.667	0.655

Table 3. Evaluation time comparison.

	Assembly I		Assembly II		Assembly III	
Algorithm	NFEs	Time (s)	NFEs	Time (s)	NFEs	Time (s)
GA	70.1	504.7	62.2	232	107.8	1331.3
PSO	64	460.8	60	223.8	111	1370.8
Hybrid GAPSO	307	2363.9	216	805.7	370	4569.5
Rule-based	56	403.2	42	156.7	21	259.4
Stepwise ($s = 1$)	27	194.4	27	100.7	27	333.45
Stepwise ($s = 2$)	56	403.2	56	208.9	56	691.6

The advantage of the algorithm is that it tends to identify the critical weld points stepwise for each element of the sequence. This approach takes into consideration the previous weld points of the sequence element and the weld points after. In other words, the problem turns into the summation of the combination of possible elements that need to be evaluated, rather than the multiplication of possible elements. This helps to reduce the evaluation time considerably compared to the previous GA applications, where the sequences are evolved based on the evaluation of the random sequences in each population generation. Moreover, the algorithm is free from extra operators and parameters. Therefore there is no requirement for fine tuning prior to the optimization procedure, *i.e.* of population size or mutation and/or crossover operators in the GA. This advantage is more tangible comparing the evaluation time of the stepwise algorithm and the rule-based GA. Although the evaluation times are close to each other (as shown in Figure 4), the optimal parameter settings of the rule-based GA are not known initially, and to find these requires extensive evaluation time.

Unlike the population-based algorithms, the proposed stepwise algorithm requires the same number of evaluations (NFEs) at each trial. This means that the stepwise algorithm performs the same steps at any trial, evaluating identical sequences compared between the trials, and converges to the same optimum. This makes the algorithm more robust and insensitive to parameters compared to the the evaluated population-based algorithms. Independent of the number of trials of the algorithm on an assembly, the same computational time is expected. To clarify this point further, the plot of the number of trials to the number of evaluations (NFEs) for the stepwise algorithm will be a straight line for either 27 or 56 NFEs.

The other advantage of the algorithm is that the evaluations in each step are independent of each other. Therefore, in each step, the evaluations can be performed in parallel. This is similar to the parallel algorithms, such as parallel GA, where the evaluations are performed in parallel in several steps.

4.8. Accuracy comparison

The accuracies of the retrieved optimum by different algorithms are compared against each other. The results of this comparison are shown in Table 4. For each population-based algorithm—GA, PSO and GAPSO—and the rule-based algorithm, the population size that results in the lowest mean NFEs is chosen for this comparison. As mentioned in Sections 4.2 to 4.5, at each population size the algorithms are run 100 times with a maximum of 56 NFEs. The generation that results in 56 NFEs is considered

Table 4. Accuracy comparison.

	Assembly I		Assembly II		Assembly III	
Algorithm	Mean D	Range D	Mean D	Range D	Mean D	Range D
GA	0.33	0.03	0.08	0.01	0.657	0.012
PSO	0.33	0.10	0.08	0.02	0.657	0.012
Hybrid GAPSO	0.33	0.03	0.08	0.02	0.656	0.007
Rule-based	0.33	0.01	0.08	0.01	0.656	0.005
Stepwise ($s = 1$)	0.32	0	0.08	0	0.667	0
Stepwise ($s = 2$)	0.32	0	0.08	0	0.655	0

in the reported results. The mean and the range of the retrieved optimal assembly deviation (D) over 100 trials at the population size with the minimum NFEs is reported in Table 4 for each algorithm. All the population-based algorithms—GA, PSO and GAPSO—and the rule-based algorithm involve inaccuracies in the retrieved optimal value. It is worth mentioning, once more, that to retrieve the population size that results in the minimum NFEs for these algorithms, extensive evaluations are performed over population sizes 1 to 56, with 100 trials at each population size.

For Assembly I, all the population-based algorithms fail to retrieve the global optimum, while GA, PSO and the hybrid GAPSO lie in the higher ranges from the optimum compared to the rule-based algorithm. However, the stepwise algorithm identifies the optimum without any errors compared to the exhaustive search results reported in Table 1. Since at any trial the stepwise algorithm performs the same steps, the retrieved optimum is always the same. Therefore, the stepwise algorithm involves zero range in the retrieved optimum (see Table 4).

The same comparison applies to Assemblies II and III, where the population-based algorithms GA, PSO and GAPSO, and the rule-based algorithm, fail to retrieve the global optimum, having larger ranges from it in 100 trials. While the stepwise algorithm finds the global optimum at $s = 2$ for all the assemblies.

The stepwise algorithm is more robust, insensitive to parameters, and results in the same accuracy at any trial, while the population-based algorithms are shown to be sensitive to the internal parameters and to result in different optimum values at any trial and any population size.

5. Conclusion

A rapid stepwise algorithm for optimization of the spot welding sequence with respect to the geometrical deviation of the assembly is proposed. The proposed stepwise optimization algorithm is applied to three sheet metal assemblies. The accuracy of the algorithm is compared to an exhaustive search performed on all the assemblies, and also four other population-based algorithms—GA, PSO and GAPSO—and a rule-based GA. The evaluation times of the algorithms to reach to the optimum are also compared. The results show that the presented stepwise algorithm results in an accurate optimal geometrical deviation of the assembly while requiring considerably lower, up to 75%, evaluation time compared to the population-based algorithms. The algorithm is parallelizable and does not require internal operators. This aspect makes the algorithm require no fine tuning of the parameters, leading to less preparation time. By a comparison performed between the stepwise algorithm and other population-based algorithms, it is shown that the stepwise algorithm is more robust, insensitive to parameters, and results in identical and accurate optima on each trial. Thereby, the algorithm is specifically well suited to the presented self-compensating assembly line, where a sequence is proposed for each individual assembly rapidly to improve the geometrical quality.

Future research includes developing a sensitivity analysis approach based on the presented optimization method to identify the critical areas to be improved by an optimal sequence. Accurate identification of the essential weld points for geometrical quality, known as geometry weld points, is

also within the scope of future research. Application of the proposed sequence optimization approach to other assembly aspects, such as clamping sequences, also lies within the scope of future research.

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