

THESIS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY

JOINING SEQUENCE ANALYSIS AND
OPTIMIZATION FOR IMPROVED
GEOMETRICAL QUALITY

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Gothenburg, Sweden 2021

JOINING SEQUENCE ANALYSIS AND OPTIMIZATION FOR IMPROVED GEOMET-
RICAL QUALITY

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ISBN 978-91-7905-438-0

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Doktorsavhandlingar vid Chalmers tekniska högskola

Ny serie nr: 4905

ISSN 0346-718X

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Cover: Assembly geometrical deviation for different sequences in one of the reference
assemblies, see Papers A-D

Printed in Sweden by
Chalmers Reproservice

Gothenburg, Sweden 2021

Abstract

Disturbances in the manufacturing and assembly processes cause geometrical variation from the ideal geometry. This variation eventually results in functional and aesthetic problems in the final product. Being able to control the disturbances is the desire of the manufacturing industry.

Joining sequences impact the final geometrical outcome in an assembly considerably. To optimize the sequence for improved geometrical outcome is both experimentally and computationally expensive. In the simulation-based approaches, based on the finite element method, a large number of sequences need to be evaluated.

In this thesis, the simulation-based joining sequence optimization using non-rigid variation simulation is studied. Initially, the limitation of the applied algorithms in the literature has been addressed. A rule-based optimization approach based on meta-heuristic algorithms and heuristic search methods is introduced to increase the previously applied algorithms' time-efficiency and accuracy. Based on the identified rules and heuristics, a reduced formulation of the sequence optimization is introduced by identifying the critical points for geometrical quality. A subset of the sequence problem is identified and solved in this formulation.

For real-time optimization of the joining sequence problem, time-efficiency needs to be further enhanced by parallel computations. By identifying the sequence-deformation behavior in the assemblies, black-box surrogate models are introduced, enabling parallel evaluations and accurate approximation of the geometrical quality. Based on this finding, a deterministic stepwise search algorithm for rapid identification of the optimal sequence is introduced.

Furthermore, a numerical approach to identify the number, location from a set of alternatives, and sequence of the critical joining points for geometrical quality is introduced. Finally, the cause of the various deformations achieved by joining sequences is identified. A time-efficient non-rigid variation simulation approach for evaluating the geometrical quality with respect to the sequences is proposed.

The results achieved from the studies presented indicate that the simulation-based real-time optimization of the joining sequences is achievable through a parallelized search algorithm and a rapid evaluation of the sequences. The critical joining points for geometrical quality are identified while the sequence is optimized. The results help control the assembly process with respect to the joining operation, improve the geometrical quality, and save significant computational time.

Keywords: Joining, Sequencing, Optimization, Efficiency, Non-Rigid Variation Simulation, Geometrical Quality.

Acknowledgments

This research project is carried out in collaboration with Wingquist Laboratory and the Area of Advance Production at Chalmers within the project Smart Assembly 4.0, financed by the Swedish Foundation for Strategic Research. I gratefully acknowledge the support.

I would like to express my gratitude to the academic supervisors Professor Kristina Wärmeffjord, Professor Rikard Söderberg and Associate Professor Lars Lindkvist for their help and guidance through the course of the research project.

I am grateful for the help of Björn Lindau, providing the test models in this thesis, and the help with the study visits at Volvo Cars. Dr. Samuel Lorin, thank you for the discussions around the topic. I also appreciate Dr. Timo Kero's help with the planning of a study visit at Volvo Trucks.

I wish to thank the colleagues at the research group Geometry Assurance and Robust Design, and at the Department of Industrial and Materials Science at Chalmers.

Last but not least, my special thanks goes to my family, including Zahra, Masoud, Reza, Hanna, and all my friends for their support, understanding, and patience.

ROHAM SADEGHI TABAR

Gothenburg, January 2021

List of Publications

This thesis is based on the following appended papers:

Paper A. Roham Sadeghi Tabar, Kristina Wärmefjord, Rikard Söderberg, Lars Lindkvist 2019, *A novel rule-based method for individualized spot welding sequence optimization with respect to geometrical quality*. Journal of Manufacturing Science and Engineering, 141 (11), 111013.

Paper B. Roham Sadeghi Tabar, Kristina Wärmefjord, Rikard Söderberg, 2019, *A method for identification and sequence optimisation of geometry spot welds in a digital twin context*. Journal of Mechanical Engineering Science, Proceedings of the Institution of Mechanical Engineers Part C, 233 (11), pp. 3701-3711.

Paper C. Roham Sadeghi Tabar, Kristina Wärmefjord, Rikard Söderberg, 2020, *A new surrogate model based method for individualized spot welding sequence optimization with respect to geometrical quality*. The International Journal of Advanced Manufacturing Technology, 106 (5), pp. 2333-2346.

Paper D. Roham Sadeghi Tabar, Kristina Wärmefjord, Rikard Söderberg, 2020, *Rapid sequence optimization of spot welds for improved geometrical quality using a novel stepwise algorithm*. Engineering Optimization, Published Online (May), DOI:10.1080/0305215X.2020.1757090.

Paper E. Roham Sadeghi Tabar, Kristina Wärmefjord, Rikard Söderberg, Lars Lindkvist, 2020, *Critical joint identification for efficient sequencing*. Journal of Intelligent Manufacturing, Published Online (September), DOI:10.1007/s10845-020-01660-4.

Paper F. Roham Sadeghi Tabar, Samuel Lorin, Christoffer Cromvik, Lars Lindkvist, Kristina Wärmefjord, Rikard Söderberg, 2021, *Efficient spot welding sequence simulation in compliant variation simulation*. Journal of Manufacturing Science and Engineering, Published Online (January), DOI:10.1115/1.4049654.

Additional Publications

- AP 1. Roham Sadeghi Tabar**, Kristina Wärmefjord, Rikard Söderberg, 2018, *Evaluating evolutionary algorithms on spot welding sequence optimization with respect to geometrical variation*. Procedia CIRP, 75, pp. 421-426.
- AP 2. Roham Sadeghi Tabar**, Kristina Wärmefjord, Rikard Söderberg, Lars Lindkvist 2019, *Efficient spot welding sequence optimization in a geometry assurance digital twin*. Journal of Mechanical Design, 142 (20), 102001. Selected as a featured article by the journal.
- AP 3. Roham Sadeghi Tabar**, Samuel Lorin, Christoffer Cromvik, Lars Lindkvist, Kristina Wärmefjord, Rikard Söderberg, 2020, *Efficient spot welding sequence simulation in compliant variation simulation*. In ASME The International Mechanical Engineering Congress and Exposition, November 16-19, Virtual Conference, Online.

Distribution of Work

The distribution of the work for each paper is as follows:

Paper A. Sadeghi Tabar initiated the idea and carried out the studies with some guidance from Wärmefjord. Lindkvist supported building the interface between the simulation software and the optimization algorithm. Sadeghi Tabar wrote the paper, with Wärmefjord and Söderberg acting as reviewers.

Paper B. Sadeghi Tabar initiated the idea and carried out the studies with some guidance from Wärmefjord. Sadeghi Tabar wrote the paper, with Wärmefjord and Söderberg acting as reviewers.

Paper C. Sadeghi Tabar initiated the idea and carried out the studies. Sadeghi Tabar wrote the paper, with Wärmefjord and Söderberg acting as reviewers.

Paper D. Sadeghi Tabar initiated the idea and carried out the studies. Sadeghi Tabar wrote the paper, with Wärmefjord and Söderberg acting as reviewers.

Paper E. Sadeghi Tabar initiated the idea and carried out the studies. Lindkvist supported the study with the simulation software. Sadeghi Tabar wrote the paper, with Wärmefjord, Söderberg, and Lindkvist acting as reviewers.

Paper F. Sadeghi Tabar and Lorin initiated the idea and carried out the studies. Lindkvist supported the study with the simulation software. Cromvik supported the verification of the method. Sadeghi Tabar wrote the paper, with Cromvik, Wärmefjord, Söderberg, and Lindkvist acting as reviewers.

List of Acronyms

AP	–	Additional Publication
ACO	–	Ant Colony Optimization
BIW	–	Body In White
CAD	–	Computer-Aided Design
CAT	–	Computer-Aided Tolerancing
DoF	–	Degrees of Freedom
DMC	–	Direct Monte Carlo
DRM	–	Design Research Methodology
DS	–	Descriptive Study
EA	–	Evolutionary Algorithm
GD&T	–	Geometrical Dimensioning and Tolerancing
GMAW	–	Gas Metal ARC Welding
FEA	–	Finite Element Analysis
FEM	–	Finite Element Method
GA	–	Genetic Algorithm
LSL	–	Lower Specification Limit
MADS	–	Mesh Adaptive Direct Search
MIC	–	Method of Influence Coefficients
NFE	–	Number of Function Evaluations
NN	–	Neural Network
NP	–	Non-deterministic Polynomial-time
PS	–	Prescriptive Study
PSO	–	Particle Swarm Optimization
RBGA	–	Rule-Based Genetic Algorithm
RC	–	Research Clarification
RMS	–	Root Mean Square
RQ	–	Research Question
RSS	–	Root Sum Square
RSW	–	Resistant Spot Welding
RD&T	–	Robust Design and Tolerancing
SVM	–	Support Vector Machines
SA	–	Simulated Annealing
TSP	–	Traveling Salesman Problem
USL	–	Upper Specification Limit

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II Appended Papers

- A** A novel rule-based method for individualized spot welding sequence optimization with respect to geometrical quality.
- B** A method for identification and sequence optimisation of geometry spot welds in a digital twin context
- C** A new surrogate model based method for individualized spot welding sequence optimization with respect to geometrical quality
- D** Rapid sequence optimization of spot welds for improved geometrical quality using a novel stepwise algorithm
- E** Critical joint identification for efficient sequencing
- F** Efficient spot welding sequence simulation in compliant variation simulation

Part I

Introductory Chapters

Chapter 1

INTRODUCTION

In the following, the introduction to the research is provided and the scope of the presented study is defined.

1.1 Background

Product development has always been integrated into human life, from understanding a need to realizing a product. Concept development, verification, and production are the fundamental phases of the product realization cycle. Initially, the awareness of the need is raised, and ideas for satisfying it are generated in the concept phase. These notions are then tested to fulfill functionality requirements during the verification phase, and are finally made for consumption in the production phase.

For producing physical products, raw materials are transformed into a consumable through manufacturing processes. These processes often take place in the transition between the concept and verification phases until the conclusion of production. Like any aspect of the product development cycle, the manufacturing processes have been advanced to achieve more effective and efficient products. A logical requirement of such a procedure is that the manufactured product complies with the intended design. In other words, it is expected that the geometrical shape after manufacturing matches the design. However, with the industrial revolution and higher production rates, a larger number of products had to be delivered within shorter time frames. Therefore, the technological capability and the cost required were delimiting manufactured goods to be within certain specification limits. Eventually, mass production and customization resulted in products to be assembled using several components. In this way, complex shapes could be broken down into manufacturable smaller parts. Ever since this period, the assembly process has been an inevitable part of the manufacturing processes, until the product reaches the hands of the end-user.

Geometric Dimensioning and Tolerancing (GD&T) and the quality control methods, i.e., Taguchi and six-sigma, are developed to among other applications, secure the geometrical outcome of the produced assemblies. Nevertheless, tighter tolerance

allocations on individual products exponentially increase manufacturing cost. The challenge is indeed to decide on the tolerance without prior knowledge of the outcome of the assembly. Therefore, Computer-Aided Tolerancing (CAT) virtual tools have been developed supporting decision-making during the product specification development, enabling the simulation of the geometrical variation of assemblies. These tools are not only used for the sole purpose of early fault detection but also to reduce production costs and achieve the environmental sustainability demands of future manufacturing.

To assemble single parts of a product, joining operations are required. Among other acting assembly parameters, the joining parameters affect the final geometrical outcome. Today, in a highly automated production set-up for complex assembled products, there could be up to several hundreds of robots organized into lines and stations for assembly and joining operations. Geometry related problems caused by these actors result in late design and manufacturing changes and production delays, constituting a significant part of the total cost of low quality. While the industrial implementation of CAT tools and variation simulation have been shown to improve geometrical quality in the early product development phases, further investigations are needed for deploying such tools at their highest potential for quality improvement.

In this thesis, non-rigid, also referred to as compliant assemblies, are studied. In these assemblies, parts are bent and deformed during the assembly. Thereby, predicting the assembly's outcome is more challenging compared to rigid assemblies, where the traditional linear tolerance stack-up analysis is applicable. Simulation methods based on the finite element method (FEM) have been developed, allowing this prediction, whereas they increase the calculation time. The more complex the assembly, the more the calculation time to simulate the geometrical outcome. Assembly complexity is defined as the size of parts, number of parts, the mating conditions between the adjacent deviated surfaces of parts, and the requirements needed to be satisfied. Product optimization strategies based on simulations are directly affected by this assembly complexity.

For non-rigid assemblies, the complexity of the assembly, as defined above, determines the joining parameters affecting the geometrical outcome, namely the number of joints, their position, and also the sequence of joining. The position of the joining points affects the strength requirements of the assembly. Joining sequences have shown to have a significant effect on the final geometrical outcome. The joining sequence influences the mechanistic behavior of the parts during assembly, independent of the joint type. Choosing the right joining sequence can help reduce the geometrical deviation in the assembly. However, the choice of the right sequence may require extensive further investigations. Choosing the best sequence among all possible sequences, for a specific objective, is a non-deterministic polynomial-time hard, also referred to as NP-hard, problem¹. This aspect, together with the assembly complexity, and the non-linear function of the deformation simulation, makes the sequencing a time-consuming and challenging task.

¹The time required for a computer to solve a problem, where the time is a simple polynomial function of the input size, is referred to as polynomial time.

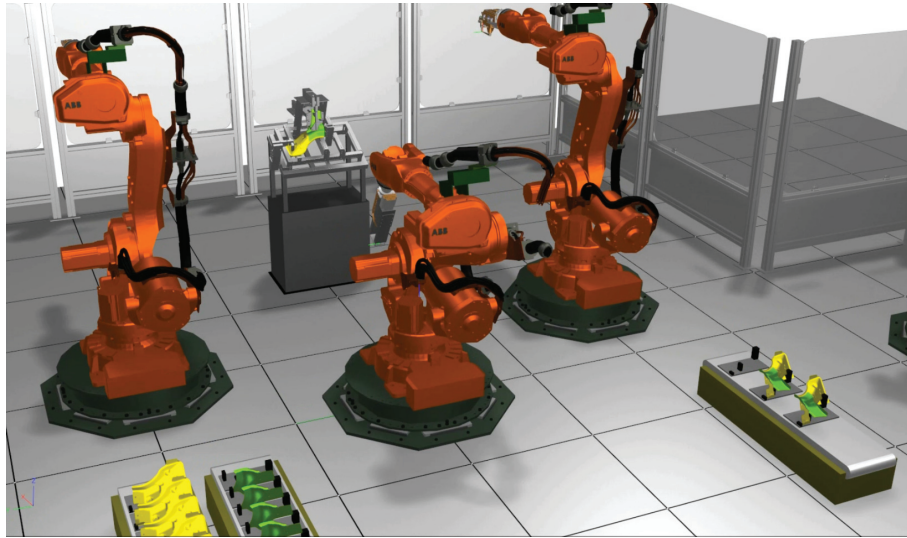


Figure 1.1: Assembly Cell

While the assemblies' non-rigid behavior depends on the different material properties of individual parts, the fundamental approach to model this behavior is common among different material types. The contribution of this thesis is mainly focused on the sheet metal assemblies. The assembly process of such assemblies is further described in the following section.

1.1.1 Sheet metal assemblies

Sheet metal is the dominant material for body structures of transportation means, such as automobiles and airplanes. Sheet metals are assembled using different joining techniques in which spot welding and riveting are among the most common point-based joining operations. In these operations, ideally, at the exact location of the joint, the parts are being connected. All degrees of freedom (DoF) are being locked at the joint position. Joining sequences of such joints on non-rigid assemblies are taken into consideration for further evaluation. In a typical body in white² (BIW) production line, the joining stations are organized into geometry stations and re-spot stations. In the geometry stations, individual parts and sub-assemblies are assembled by spot welding. In the aerospace industry, this process is referred to as pre-joining of the riveted assemblies. In this station, the assembly's geometrical quality is determined and later reinforced in the downstream re-spot station. In the re-spot station, a larger number of joining points are usually set on the assembly.

Figure 1.1 shows the schematic view of a geometry assembly cell, where multiple robot arms operate, assembling the parts. In this setup, the parts are being picked by a gripper and positioned into the fixture. The welding is performed by a robot arm holding a welding gun. After welding, the assembly is being transferred to the transportation rack.

²Body in white is referred to as a joined unpainted body frame of a car.

This process can be divided into four generic steps:

1. *Placement of parts in a fixture*: Fixtures are used for repeatability and accuracy of the produced batch assemblies. Since the fixtures are rigid and stable, they enable repeatable processes, allowing the assembly process to be automated.
2. *Clamping parts together*: In this step, the parts are forced into their nominal shape in the location of the clamps. The clamps also constrain the movements of the individual parts due to external forces, such as gravity or welding gun forces. Bending occurs, and internal stresses are built up in this step.
3. *Joining parts together*: In this step, the parts are joined together. Similar to the clamping step, bending, deformation, and internal stresses are imposed on assemblies during this operation. The number, location, and sequence of the joining-points significantly impact the geometrical deviation of the assembly. Therefore, determining and optimizing these parameters are essential for improved geometrical quality.
4. *Release from the fixture and spring-back*: After the joining process has been completed, the assembly is released from the fixture. The internal stresses built up during the steps above result in the spring-back of the assembly.

Within such a setup, non-nominal parts and processes result in deviated assemblies, causing functional and aesthetic problems in the final product. Previous manufacturing processes that individual parts have been through, i.e., stamping and forming, cause variations from the parts' nominal shape. Besides, the assembly process itself contributes to the final variation, with disturbances stemming from fixtures, robots, operators, and other involved actors. As a result, these variations in form and dimension stack up and the final assembly varies from nominal geometry. With the variation in sub-assemblies, assembly process issues may also arise while connecting the sub-assemblies in the downstream processes.

The main challenge is controlling the assembly process so that the final product does not get influenced by the deviations and, ultimately, variation.

1.1.2 Geometrical quality

The focus of this thesis is on improving the geometrical quality through joining sequence analysis and optimization. To distinguish the term geometrical quality in the context of this thesis, it needs to be defined. The term *quality* is defined by the Oxford English dictionary as "*the standard of something as measured against other things of a similar kind*" (Oxford English Dictionary, 2020). Using this definition, from a subjective point of view, geometrical quality describes how good the geometry is compared to the other geometries of the same type.

To understand this state of being better in quality, requirements are specified during the design phases, with a metric connected to the shape of the product. The

dimensional specification and form of the geometrical features are controlled to fulfill such requirements. The deviations from the nominal geometry are measured and tracked with respect to a point of reference. The positioning system is often used as the reference point for defining the form deviations. Upon controlling such attributes of geometry, functional, aesthetic, and assembly requirements can be assured to be met. Geometrical quality is therefore defined as conformance to the geometrical requirements.

In a mass production setup, a sample of products is measured to fulfill the geometrical requirements. Therefore, statistical methods are used to calculate the mean deviations and variability among the produced units. Hence, the term geometrical variation is defined as the mean and dispersion of the deviations from the nominal geometry. In this thesis, geometrical deviation and variation of the assembly are associated with geometrical quality. In non-rigid assemblies, the geometrical deviation and variation after joining is measured at certain critical points, dimensions, and across the entire assembly. The focus is therefore on analysis and optimization of the joining sequence to minimize geometrical variation or deviation, thus, improving geometrical quality.

1.1.3 Geometry assurance and robust design

Satisfying the geometrical requirements specified on the designed products is one of the main challenges of the manufacturing industry. Anomalies in part geometry and the disturbances during the assembly process lead to non-nominal assembly geometries. Geometry assurance refers to the activities practiced to secure the products' geometry during the development phases. Within the verification phases and production, the joining simulation is performed, Figure 1.2. The joining simulation for the geometrical outcome is often performed whereas the sequence is neglected, and the joining is conducted simultaneously in the virtual tool. The time requirement of the sequencing task is the main reason for the simultaneous welding simulation approach, in which no sequence is considered for welding. The traditional methods for spot welding sequencing in the automotive industry are based on the line balancing requirements and tacit manufacturing knowledge deciding on which critical weld points are to be welded first.

Theoretically, the simulation-based optimization of the joining sequences requires time-consuming and comprehensive FEM calculations. Integrating the sequence analysis in the simulation is necessary to represent the assembly process accurately, cloning the physical assembly setup, and identifying the improvement potential in the geometrical quality.

To handle variation and allow mass production with interchangeability among parts, the designer specifies tolerances on all critical dimensions: the tighter the tolerances, the more precise are the processes required to achieve the final demands on the assemblies. A design that is insensitive to variation, a robust design, is desired to evade tighter tolerances and exponential cost growth. In other words, although geometrical variation exists in parts and processes, the final geometrical demands

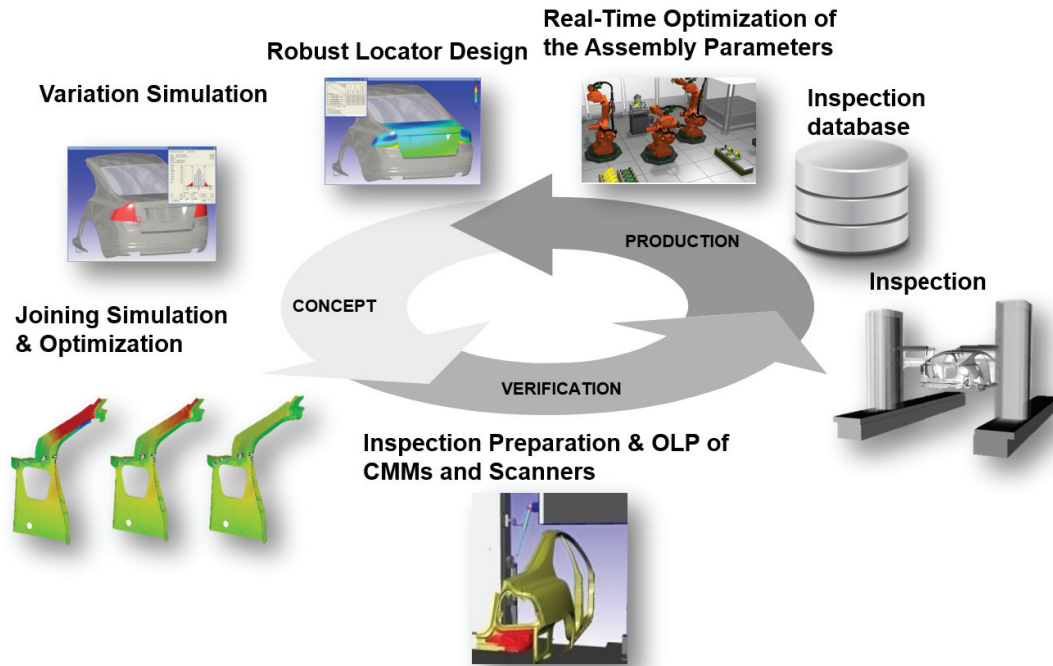


Figure 1.2: Virtual geometry assurance toolbox. Adapted from (Söderberg et al., 2016)

can be met with a robust design. From the robust design perspective, identifying the optimal joining sequence allows controlling the assembly outcome to compensate for the existing variation, thus achieving a robust assembly.

1.1.4 Self-compensating assembly line

In the manufacturing industry, geometrical problems are often discovered during the pre-production and physical prototyping phase. Late identification of the geometrical problems gives rise to several design and manufacturing changes, causing massive delays and costs as a result. To be able to adjust and steer the assembly line based on the fabrication errors of the parts, Söderberg et al. have introduced the concept of a self-compensating assembly line for real-time geometry assurance in an individualized production (Söderberg et al., 2017). Figure 1.3 presents the overall layout of such an assembly cell. The incoming parts are initially scanned. The parts are sorted and classified based on their quality criteria using the scanned geometries. Later, the parts are being selectively chosen for optimal matching based on quality criteria. Within the assembly cell, the assembly parameters are being optimized for the improved geometrical quality. Spot welding sequence optimization takes place within the assembly cell. To perform the real-time optimization, a CAT tool interacts with an optimizer within the analysis module. The sequence of the welding is being optimized for each assembly. The outcome of the assembly is later being scanned and used for the feedback process.

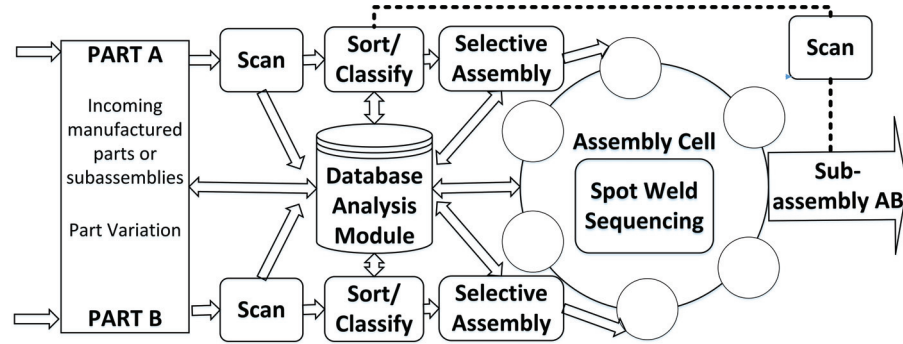


Figure 1.3: Self-compensating assembly line. Adapted from (Söderberg et al., 2017)

The self-compensating assembly process is in line with the concepts of cyber-physical systems and industry 4.0 for sorting and self-adjusting equipment, which improves the quality without tightening the tolerances. The concept utilizes information about individual parts to be joined (sensing), to optimize the parameters for each individual (thinking) and to perform the assembly process with the optimal parameters provided (acting), and feedback for eventual automatic adjustments. The smart system utilizes product and process knowledge as inputs to an interlinked approach, in which the conditions for each product are optimized to reach the highest quality with limited resource consumption.

In this thesis, geometry assurance expertise will be exploited to develop an assembly cell that can adjust to individual parts to optimize geometrical quality in assembled products through efficient joining processes.

1.2 Research Project

The research project, in which this research is carried out, is entitled *Smart Assembly 4.0*, conducted within the Wingquist Laboratory and Area of Advance Production at Chalmers, financed by the Swedish Foundation for Strategic Research. The vision of the project is an autonomous, self-optimizing robotized assembly factory, which maximizes quality and throughput while maintaining flexibility and reducing cost by sensing, thinking, and acting strategies. The primary project goal is to develop new methods, a demonstrator showing the vision of the Smart Assembly 4.0 and self-compensating assembly lines for complex products. Additionally, the goal is to show and quantify the positive impact of such a setup on quality, throughput, equipment utilization, flexibility, and cost.

1.3 Scope

In line with the vision of the research project, the purpose of this thesis is to show the vision of a self-optimized robotized smart assembly for complex products through the

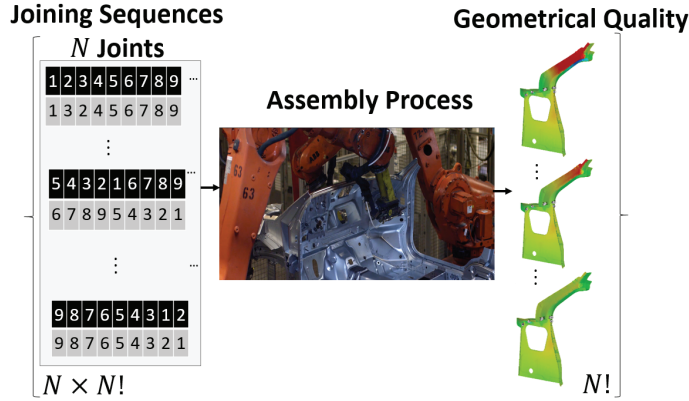


Figure 1.4: The overview of the joining sequence problem

applications of self-optimized joining processes. The purpose is also to minimize the geometrical deviations for each assembly. From the joining parameters in the non-rigid variation simulation, the joining sequence is studied for real-time applications. The overview of the joining sequence problem is visualized in Figure 1.4.

Theoretically, joining sequence optimization for geometrical quality is an NP-hard combinatorial problem, in which exhaustive search and time-consuming FEM calculations are needed to explore the problem. To solve such a problem in real time, with a simulation-based approach, to optimize the geometrical quality of non-rigid assemblies, is the research goal. Application of the proposed analysis and optimization approaches, within the context of a self-compensating assembly cell, is also within this research scope.

1.4 Research Questions

Based on the research scope and goals presented earlier, the following Research Questions (RQ) are formulated:

- RQ 1:** *What problem formulations can be considered for joining sequence evaluation with respect to the geometrical quality of assembly?*
- RQ 2:** *How can joining sequence be time-efficiently optimized with respect to the geometrical quality of assembly in a non-rigid variation simulation?*
- RQ 3:** *How can critical joining points be identified with respect to the geometrical quality of assembly in a non-rigid variation simulation?*

1.5 Delimitation

The joining sequence analysis and optimization are the focus of this research. Within the joining processes, only point-based methods, i.e., spot welding or riveting, have been analyzed. For generalization, these methods are modeled using a stiff beam locking all the DoF in the joining nodes, and the mechanistic assembly behavior is studied, when joining in a sequence. Within these operations, several parameters are affecting the assembly geometrical outcome. The heat exerted on parts during the welding will cause local deformation in the joining points and eventually result in material shrinkage. The applied simulation method is built based on linear FEM, using linear material models and infinitesimal strain assumptions in this research. With these assumptions, negligible local weld deformation compared to the entire assembly is assumed. Non-linear material models and thermal effect, depending on the joining technique, can be considered while retrieving the assembly geometrical outcome in the simulation, with the trade-off of the simulation time. Today, for sequence optimization in a digital twin context, lower simulation times are desired.

Moreover, in all studies, the assembly geometrical outcome is retrieved while the sound weld quality is considered for all the weld points. All the weld points are assumed to be functional, locking all the DoF in the joining point. In reality, force losses during welding result in weld bead defects, making them non-functional. Joint defects might also arise in the riveting process, avoiding the degrees of freedom to be fully constrained in the points to be joined. Such behaviors are not taken into analysis in the sequence evaluation.

Due to the combinatorial nature of the problem, the proposed optimization and analysis approach is simulation-based. Performing physical experiments for all the possible alternatives is infeasible. However, experimental data can also be used in the proposed methods and algorithms to retrieve the assembly geometrical outcome.

Other joining methods on different types of material have not been analyzed in the studies presented.

1.6 Structure of the thesis

This thesis is structured into two parts, Part I Introductory Chapters, and Part II Appended Papers.

In the Introductory Chapters, the first chapter provides the background to the research topic, research scope, and questions are presented. The second chapter discusses the frame of references on which this thesis is based and critically addresses relevant research. Chapter 3 introduces the research methodology and the methods applied to this thesis. Chapter 4 presents and summarizes the results achieved in the research presented. Chapter 5 discusses the results achieved and provides the answers to the research questions. In Chapter 6, the conclusions are drawn based on the analysis of the results presented, and future work is discussed.

Part II presents the appended papers upon which this thesis is built. The details

of the results can be found in the corresponding papers.

FRAME OF REFERENCE

Joining sequence analysis and optimization for improved geometrical quality fundamentally integrate three main scientific domains, Design, Manufacturing and optimization. Simulation-based design optimization for the joining processes is in the intersection of these domains, revolving around the product realization loop, and the related activities securing product geometry, as introduced in Section 1.1.3, Figure 1.2. In this Chapter, the areas of relevance and contribution in this thesis, based on Figure 2.1, is presented.

Geometry assurance aims to assure the geometrical quality of the products. The fundamental pillar of this process is based on robust design principles. Thereby, initially, robust design is addressed. The robustness and the geometrical variation of a part are closely interconnected with the positioning of a part in space, often referred to as a locating scheme, which directly influences the assembly process and consequently the geometrical outcome of the joining operation.

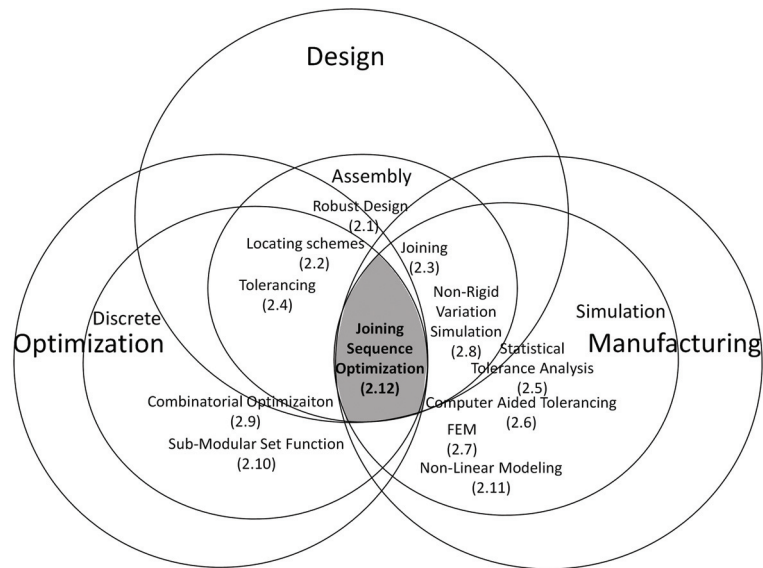


Figure 2.1: Areas of relevance and contribution in this thesis

The second section introduces locating schemes, followed up by an overview of the joining operations considered in this thesis, Section 2.3. The goal of having more robust products is to satisfy requirements. The definition of geometrical requirements is achieved by geometrical tolerances, addressed in Section 2.4. The ultimate challenge is to estimate the geometrical outcome of the assembly, with the specified assembly setup, for compliance with geometrical requirements. Followed up by the statistical basics and definitions, the traditional statistical methods to estimate the assembly outcome is addressed, Section 2.5. The computer-aided tolerancing principles, estimating the geometrical outcome for rigid bodies, is presented in Section 2.6. Followed by a short description of FEM in Section 2.7, non-rigid variation simulation to retrieve the assemblies' geometrical outcome after joining is presented in Section 2.8.

The nature of the problem under study in this thesis lies within the combinatorial optimization category, addressed in Sections 2.9 and 2.10. Non-linear modeling is introduced, explaining the relation between joining sequence and geometrical outcome, Section 2.11. Finally, the main contribution of this thesis lies in joining sequence analysis and optimization, addressed in Section 2.12.

2.1 Robust Design

The design that is insensitive to geometrical variation is defined as a robust design. Based on the Taguchi quality principles, control factors and noise factors are affecting the design concept (Taguchi, 1986). Figure 2.2 is a block diagram representation of a product or process. The response of product to the inputs is the output. This output in the robust design context can be considered to be the quality characteristics. The signal factors are the inputs to the system by the users. The noise factors are the parameters that cannot be controlled by designers. The control factors can be specified and manipulated by designers and are easily controlled. The control parameters should be chosen at a level where the expected loss of the noise factors is minimized (Taguchi, 1986). In other words, to optimize the quality characteristics in the robust design process, the control parameters are optimized.

Disturbances and noise factors, which may result in geometrical variation, exist in all manufacturing processes. Therefore, the control factors in the design concept should be chosen in a manner so that the product, here the assembly, is robust. However, the manipulation of these factors depends on the existing processes and interlinked parameters. Figure 2.3a shows the input-output perspective on the robustness curve. The variations in the inputs are equal at the two segments of the horizontal axis. In contrast, the variation in the output is reduced, minimizing the effect of noises by the right choice of control factors. Considering the assembly process, the optimal locating and joining parameters, with the given equal part and process variation, result in lower assembly geometrical variation.

As mentioned previously, Section 1.1.3, geometry assurance activities are designed to reduce the effect of variation in the products, to achieve better geometrical quality.

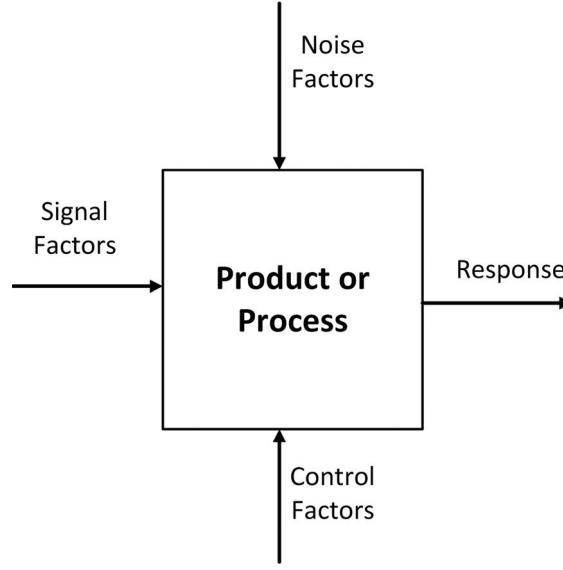


Figure 2.2: Robust design in a system perspective. Adapted from (Phadke, 1995)

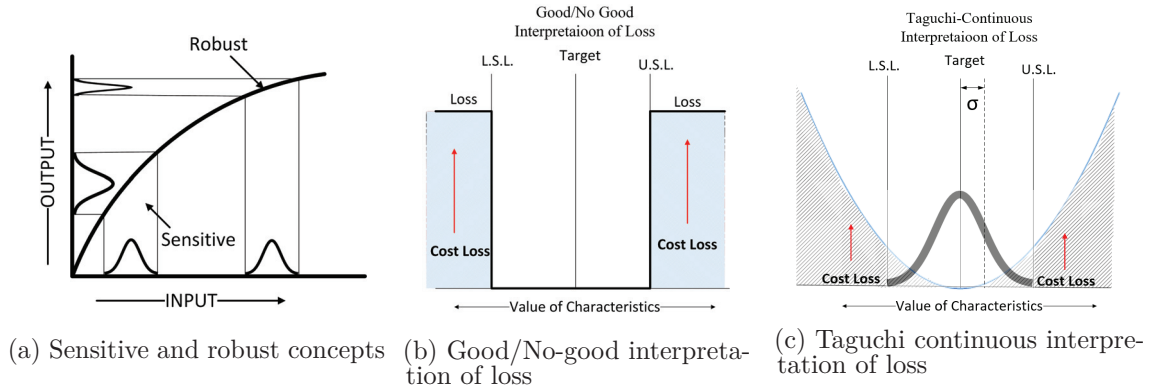


Figure 2.3: Principles of robust design. Adapted from (Söderberg et al., 2016; Taguchi, 1986)

Taguchi has introduced a way in which to interpret quality, considering quality loss (Taguchi, 1986). He proposes that the deviation of the performance characteristic and its effect on the cost due to quality loss follows the quadratic approximation:

$$L(Y) = f(Y - T)^2, \quad (2.1)$$

where $L(Y)$ is the cost loss, Y is the performance characteristic, and T is the target value. This interpretation of continuous loss function is shown in Figure 2.3c. This perspective has created a niche in quality control, compared to the previous good or no-good interpretation of quality loss, represented by a step function, Figure 2.3b. This interpretation has put the focus of quality control on considering the existing variation with respect to the standard deviation (σ) intervals.

Phadke has proposed a three-step approach to achieve a robust design (Phadke, 1995).

Concept design, where different technologies and tools are used to achieve a

specific function of a product.

Parameter design, where the best settings for the control factors are determined.

Tolerance design, where a trade-off between the quality loss and manufacturing cost is being made.

It has been argued that the dominant focus of the robust design approach is on parameter design. Thereby, the control factors in the geometry assurance context are discussed to achieve a geometrically robust assembly. The assembly system perspective in the geometry assurance process puts the focus on locating schemes, for rigid and non-rigid assemblies, and joining operation settings as the control factors, whereas the part variation is the noise factor (Söderberg & Lindkvist, 1999).

In this thesis, the joining operation setting, such as the joining sequence and number of the joining points, will be introduced as a controllable factor, to compensate for the assembly process noises. Achieving an assembly that is adaptable to the noises, results in a robust assembly insensitive to variations.

The parameter design of the joining sequences is the main focus in this thesis. The locating scheme in the assembly process plays a central role as a parameter, directly influencing the joining operation, and needs to be addressed, Section 2.2.

2.2 Locating Schemes

Locating schemes are positioning and supporting parts during the manufacturing processes and inspection activities. Moreover, they can also define how parts are assembled in the final product. An example of this type is when the locating system decides the position of the holes and screws. Locating schemes play a crucial role in a product's robustness and are the main focus of the geometry assurance process (Söderberg & Lindkvist, 1999).

Figure 2.4 visualizes the realization of a 3-2-1 locating scheme of a sheet metal part in a fixture. The three points A1-A3 are used to lock the translation in the X direction and the Y and Z axes rotation. The full steering pin and hole, point B1, and the one-direction steering pin and slot, point B2, lock the translation in the Y direction, and the X-axis rotation. Finally, the full steering hole and pin, point C1, locks the Z-direction translation. This way, all six degrees of freedom will be locked between the local part (sheet metal) and the target part (fixture) in a three-dimensional space. This system represents an orthogonal 3-2-1 locating scheme. In a non-orthogonal scheme, the directions of locking the DoF are not necessarily orthogonal to each other. Söderberg et al. have defined the various locating schemes, as 3-2-1 orthogonal, 3-point orthogonal, 3-directions non-orthogonal, 6-direction non-orthogonal, and N-2-1 orthogonal or non-orthogonal (Söderberg et al., 2006b).

In sheet metal assemblies, locating schemes are often over-constrained due to their non-rigid behavior. To compensate for additional forces, i.e., gravity, the locating scheme is expanded to N-2-1, where $N > 3$, enhancing the support in the planar

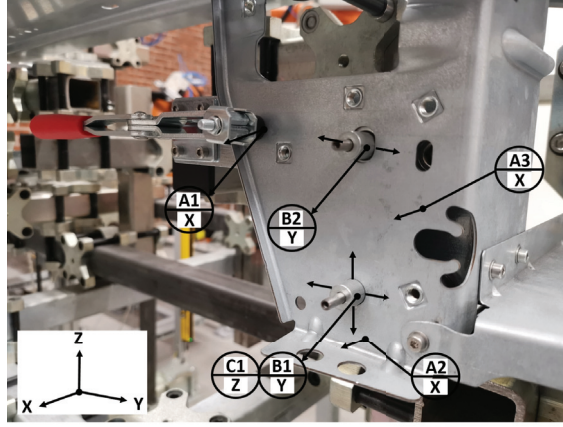
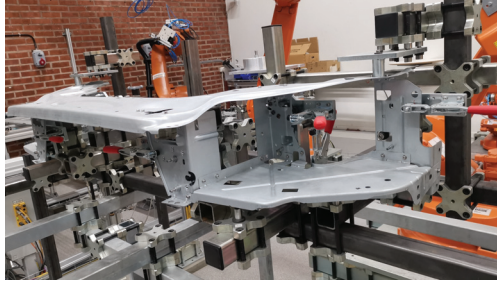
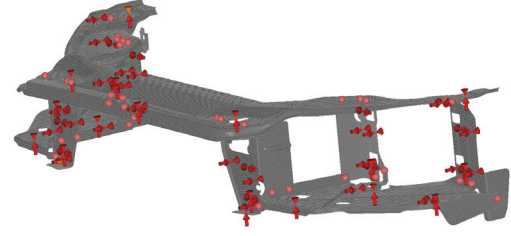


Figure 2.4: Realization of a locating scheme



(a) over-constrained positioning system in the assembly fixture



(b) Digital model of the assembly in the assembly fixture

Figure 2.5: Over-constrained positioning system

adjacencies (Cai et al., 1996). Figure 2.5a shows an over-constrained locating scheme of a non-rigid sheet metal part. In such a locating scheme, several support points, in the form of clamps or pushers in the fixture, are needed to assist the assembly process. Figure 2.5b shows a digital model of the assembly. The arrows show the positioning system in the digital model. The spot welds have also been shown with spheres.

The geometrical outcome of the assemblies is sensitive to the positions of these locating points. Any deviation in any of the locating points will result in a deviated assembly after joining (Söderberg & Lindkvist, 1999). To retrieve the sensitivity of a specific measure to the deviation in the locating scheme, the following linear relationship is built (Söderberg & Carlson, 1999):

$$d_m = A\delta_{lp}, \quad (2.2)$$

where d_m is the deviation of a defined measurement point in a specific direction, δ_{lp} is the deviation in the locating scheme, and A is a matrix in which each row connects the locating scheme matrix to the coordinate and direction in the specified measurement point (Söderberg & Carlson, 1999).

Exposing the assembly to multiple clamps increases the complexity of the deformation behavior due to the applied clamping forces and sequences applied during

the assembly (Xie & Hsieh, 2002).

The locating system's optimal position minimizes the geometrical variation during the assembly process allowing the tolerances to be relaxed; i.e., lower manufacturing costs are required to produce the assembly units. Extensive research over the years have been performed designing the optimal layout for fixtures, correspondingly the locating schemes (Cai et al., 1996; Camelio et al., 2004b; Chen et al., 2008; Franciosa et al., 2016; Pelinescu & Wang, 2002; Rezaei Aderiani et al., 2020).

As per tolerances, the joining process parameters are also interconnected with the positioning system. Joining operation with non-robust positioning and clamping conditions result in amplified variation in the final assembly. The joining operation parameters in the assembly cell, namely the number of the joining points and joining sequences studied in this thesis, are affected by the deformation state of the positioning and clamping conditions. Therefore, the industrial approach to determine the joining operation parameters is often defined by the locating schemes (Tabar et al., 2019a; Tabar et al., 2019b). In Section 2.3, the overview of the joining techniques and their governing parameters is presented.

2.3 Joining techniques

Joining processes play an essential role in the manufacturing industry. These processes strive to form a bond between components, constructing an assembly. These processes often create a joint of the mechanical (riveting), chemical (adhesives), or thermal (welding) forms (Martinsen et al., 2015). Since the non-rigid components are subject to bending and deformation, applied forces and reactions through such processes considerably impact geometrical quality. Therefore, controlling the joining operation parameters is a common challenge in the manufacturing industry (Söderberg et al., 2012). In this thesis, the joining sequences are evaluated based on the mechanistic behavior of the assembly connected with joining points.

The dominant joining methods for sheet metal assemblies are resistance spot welding (RSW), riveting, gas metal arc welding (GMAW), clinching, bonding, and laser brazing. While including all joining techniques into perspective is essential, time constraints allow the choice of dominant point-based methods for further investigation. Spot welding and riveting are among the most common point-based methods to join sheet metals.

RSW: In this operation, two electrodes push together two or multiple sheets to be welded on a specific point. When the parts are in contact, a large electric current bypasses the particular spot until the parts are melted and connected, forming a weld (Zhang & Senkara, 2011). Figure 2.6 is a schematic representation of the RSW process. Two different gun types are often used in this process. In the position gun, Figure 2.6b one electrode is fixed in a certain position, whereas the other electrode applies the force. In the balanced gun, Figure 2.6c, equal forces are applied by both electrodes. The balanced gun application is more challenging on the areas close to the curvatures, where

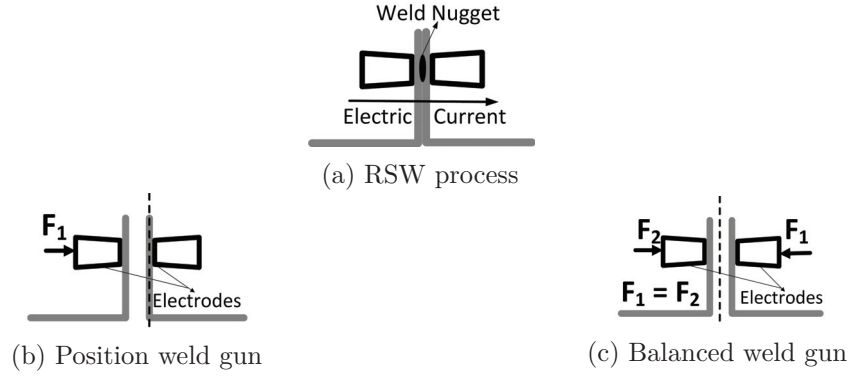


Figure 2.6: Schematic representation of the RSW process

tangential forces are acting, and force loss is expected (Dahlström, 2005). The changes in the RSW forces affect the local geometrical quality of the welds. Under-weld or expulsion conditions might also occur during the spot welding affecting the quality of the welding. Welding process parameters, such as applied current, squeeze time, clamping forces, welding time, electrode diameter, sheet thicknesses, and material properties, determine the quality of the weld and need to be accurately controlled (Zhang & Senkara, 2011). The joining points are welded one-by-one in a sequence. To model and evaluate such a complex process virtually, FEM is used (Nied et al., 1984). To evaluate the geometrical quality of the sheet metal assembly after spot welding, the mating conditions, kinematic relations, and non-rigid behavior of the sheets are taken into consideration (Söderberg et al., 2012). To reduce the complexity of the FEM model for evaluating the assembly deformations after welding, with infinitesimal strain assumption, stiff beams are introduced on the position of the weld, locking all degrees of freedom in the joining nodes (S. C. Liu & Hu, 1997; S. C. Liu & Hu, 1995). The modeling aspect is further described in Section 2.8.

Riveting: In this operation parts are forged together by means of a metal element, referred to as a rivet. The force is applied, and the metal element is passed through the sheets at the connection point, forming a joint on the adjacent parts' outer surfaces (He et al., 2008). Depending on the rivet type, pre-drilled holes in the sheets are used to position the rivet. Figure 2.7 shows the fundamental steps of the riveting process. The rivet is placed in its position, and the force is applied, Figure 2.7a. The joint is formed at both ends of the sheets and the metal element, also referred to as mandrel, is cut to finish the joining process, Figure 2.7b. Riveting process parameters, including the rivet, hole structure and squeeze forces, affect the quality of riveted joints, and must be controlled to satisfy the functionality of the joint (Cheraghi, 2008). For multiple joints, the riveting is performed in a sequence of operations. In this thesis, considering that the assembly deformations are studied, the riveting process, and any other point-based joining method, can be simulated using the same approach as spot welding, introducing stiff beams to the model



Figure 2.7: Schematic representation of the riveting process

and incorporating mechanistic behavior, sheet metal non-rigidity, and part deviations to the model (Söderberg et al., 2012; Wärmeffjord et al., 2016).

In this thesis, considering that functional joints are achievable through these processes, given that parts are positioned in the fixture, the effect of the joining sequences, the number of joints on the geometrical quality of the assembly is studied. Optimizing these parameters results in minimized geometrical variation, which leads to satisfying geometrical requirements, i.e., the set tolerances. As a consequence, the tolerance allocation aspects may get influenced, where relaxation of the limits are applicable. In Section 2.4 an overview of the tolerancing aspect in the assembly process is introduced.

2.4 Tolerancing

Tolerances are crucial for producibility and cost of manufactured products. Research within the tolerancing field has been developing and maturing during the years, mainly after the industrial revolution. Hong and Chang have performed a comprehensive review of the research within tolerancing (Hong & Chang, 2002). They have shown that extensive research has been conducted within tolerance definition, allocation, analysis, and evaluation. Several studies have divided the tolerancing research into the definition, application, and production (Hong & Chang, 2002; Shah et al., 2007).

The focus of tolerance definition is on accurate representation and categorization of the intended tolerances on products. The tolerance application field discusses the tolerance analysis aspects in terms of allocation, cost and losses. The tolerancing in production focuses on the process control parameters and root cause analysis of the failures to satisfy requirements. Tolerances are evaluated and adjusted based on the analysis of compliance of the assembly system with the manufacturing setup (Dahlström, 2005).

The context of the thesis presented leans towards the tolerance application field of research. Tolerances on a complete product are to be allocated and analyzed in a top-down or bottom-up perspective. The tolerances are broken down from the final requirements to the detailed tolerance specification on each component in the top-down perspective. The advantage of this approach is that the importance weights can be given to the critical areas in the final product; thereby, accurate tolerances will be assigned to the corresponding components. Comprehensive studies have been

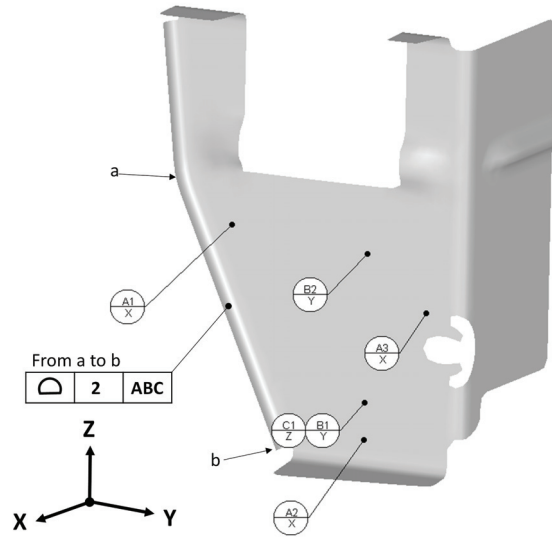


Figure 2.8: An example of a geometric tolerance

undertaken on this approach (Li et al., 2008; Lööf et al., 2007; Söderberg, 1995, 1993, 65). In the bottom-up perspective, the tolerances are assigned to the components, based on standard failure mode analysis methods and tacit manufacturing knowledge, and eventually build up the final tolerance specification of the product (Ghali et al., 2017).

The tolerance analysis methods for the rigid-bodies are divided into the worst-case stack-up analysis and statistical methods. Sampled methods have also been introduced in either of the approaches (Chase & Parkinson, 1991). In the next section, some of these methods are introduced. As mentioned previously in Section 2.2, the locating schemes are often used as reference points to evaluate geometrical tolerances. While verifying the defined geometrical tolerances, the parts should be positioned at the specified points. Figure 2.8 visualizes a definition of surface requirement of a sheet metal assembly. The specified surface can vary within two millimeters while the part is held in the locating scheme. The physical setup of a similar part while it is being held in the fixture with the specified locating scheme is shown in Figure 2.4. Any disturbances in the locating scheme will directly affect the variation achieved and may consequently result in a failure to satisfy the specified tolerance limits based on the relationship provided in Equation (2.2).

Given that the non-rigid assemblies can be analyzed with respect to the incoming part deviations, the optimal setup of the assembly parameters, namely joining sequences, can be used to minimize the effect of such disturbances. As a consequence, a more accurate tolerance specification is achievable in a top-down tolerance allocation perspective. The challenge is indeed to estimate the assembly variation after joining given the part tolerances. In Section 2.5, the evolution of the tolerance analysis methods are presented.

2.5 Statistical Tolerance Analysis

Previous reviews within the tolerance analysis field have identified a variety of statistical tolerance analysis methods (Kumar & Raman, 1992). In general, these approaches can be divided into analytical and sampled methods. The main challenge in tolerance analysis is to predict the moments of distribution of an assembly. The four moments of distribution have been introduced as the mean, variance, skewness, and kurtosis coefficients (Nigam & Turner, 1995). Most tolerance analysis methods express the assembly response t_f as a function of the tolerance of the n components in the assembly ($t_1, \dots, t_n$):

$$t_f = f(t_1, t_2, \dots, t_n) \quad (2.3)$$

Before introducing these techniques, the basic statistical terms and definitions are presented to facilitate understanding. The terms and definitions are based on (Montgomery & Hoboken, 1994).

First of all, the mean value of the sample $x_1, \dots, x_n$ is calculated as:

$$\bar{x} = \frac{1}{n} \sum_{k=1}^n x_k \quad (2.4)$$

The variance of the same sample can be calculated as:

$$s^2 = \frac{1}{n-1} \sum_{k=1}^n (x_k - \bar{x})^2 \quad (2.5)$$

The sample standard deviation based on the calculated variance is:

$$\hat{\sigma} = s = \sqrt{\frac{1}{n-1} \sum_{k=1}^n (x_k - \bar{x})^2} \quad (2.6)$$

The normal distribution is extensively used and referred to within the tolerancing research. The probability density function of the normal distribution is:

$$f(x|\mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \quad (2.7)$$

where μ is the population mean.

Most tolerances on parts are defined considering the normal distribution of the variation. According to the central limit theorem, even if parts are manufactured by processes not following the normal distribution, the stack-up function response will be approximately normal using a sufficient number of parts (Nigam & Turner, 1995).

In order to control the process variation, the six sigma tools have been introduced. Within these tools, the process capability index (C_p) is an indicator of process performance (Taguchi & Chowdhury, 2004). This index, where USL and LSL represent the upper and lower specification limits, is calculated as:

$$C_p = \frac{USL - LSL}{6\sigma} \quad (2.8)$$

To estimate the process capability, considering an un-centered mean process, the adjusted capability index C_{pk} is introduced. This index is a measure of both the process variation, similar to C_p , while also providing information on the mean shift of variation.

$$C_{pk} = \min \left\{ \frac{USL - \bar{x}}{3\sigma}, \frac{\bar{x} - LSL}{3\sigma} \right\} \quad (2.9)$$

Figure 2.9 illustrates the difference between varying values for C_p and C_{pk} . Figure 2.9a shows the same value for the two indices and the mean value is centered between the specification limits. In 2.9b, the process is off-centered and the mean is shifted. In this case, the C_{pk} index can provide this information. However, the C_p value is still constant, as it is only a measure of variation. In (c) and (d), the changes in variation are captured by both indices. At a value of 1.33 for the C_{pk} and C_p of the statistically stable processes, they are evaluated to be in control with a process yield of 99.99%. However, there are drawbacks associated with interpreting a process solely by means of these index values. Statistical quality control methods and capability indices need to be evaluated hand-in-hand. Other threats to the misinterpretation of these indices are non-normality of the process and tool wear management (Kane, 1986).

With the basic statistics provided, the tolerance analysis techniques are introduced as follows.

The most traditional approach is the worst-case 1-dimensional stack-up analysis. In this approach, the maximum tolerances (t_p) in one dimension for all parts ($p_1 \dots p_n$) are added together to reach the final tolerance on the assembly (t_f):

$$t_f = \sum_{p=1}^n t_p \quad (2.10)$$

The probability of occurrence of the worst case scenario for all parts is minor; therefore, such a technique is unrealistic and may result in cost loss.

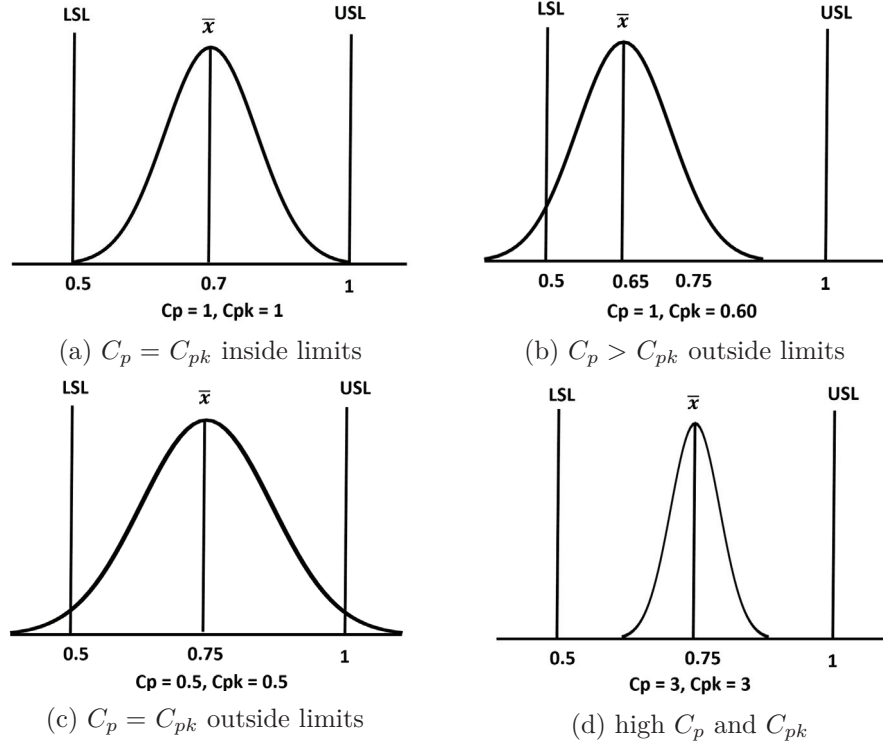
The root sum square (RSS) method and combinations of the worst-case and RSS have also been introduced in order not to solely consider the worst-case.

$$t_f = \sqrt{\sum_{p=1}^n t_p^2} \quad (2.11)$$

Spotts' modified model and modified statistical model are built upon the same principles (Kumar & Raman, 1992). The mean shift model is introduced to include the mean shift of the process into the tolerance analysis models (Chase & Parkinson, 1991). In this approach, an estimated mean shift factor (m_p) between zero and one is considered for each part of the assembly.

$$t_f = \sum_{p=1}^n m_p t_p + \sqrt{\sum_{p=1}^n ((1 - m_p) t_p)^2} \quad (2.12)$$

The Taguchi 6σ approach assumes a normal distribution for assembly tolerance (Nigam & Turner, 1995; Taguchi & Chowdhury, 2004). Defining the mean of

Figure 2.9: Interpreting C_p and C_{pk}

the process for each part as μ_p , and the final assembly mean deviation, μ_f , gives $\mu_f = \sum_{p=1}^n \mu_p$. The standard deviation of the final assembly, σ_f , can be calculated as $\sigma_f^2 = \sum_{p=1}^n \sigma_p^2$, and $\sigma_f = \sqrt{\sum \sigma_p^2}$. Now, if each part is produced in 6σ quality (corresponds to 99.73% acceptable parts at $C_p = 1$), the resulting assemblies will experience 2700 defects per million (Taguchi & Chowdhury, 2004).

More analytical Taylor series expansion of different orders of the assembly response function have also been addressed in the literature (Cai et al., 2005; Evans, 1975; Nigam & Turner, 1995). An extended Taylor expansion method is represented as (Nigam & Turner, 1995):

$$\begin{aligned}
 t_f = & f(\mu_1, \dots, \mu_n) + \sum_a (t_a - \mu_a) f_a \\
 & + \frac{1}{2!} \sum_{ab} (t_a - \mu_a)(t_b - \mu_b) f_{ab} + \dots \\
 & + \frac{1}{5!} \sum_{abcde} (t_a - \mu_a)(t_b - \mu_b)(t_c - \mu_c)(t_d - \mu_d) \\
 & \times (t_e - \mu_e) f_{abcde} + O[(t - \mu)^6],
 \end{aligned} \tag{2.13}$$

where f_a , f_{ab} , and so on, are the partial derivatives of f with respect to t_a , t_b , evaluated at $t_i = \mu_i$.

The above mentioned analytical methods are computationally inexpensive. However, the challenge of computing the derivative of the Taylor series may lead to complex algebraic manipulations. Moreover, it is uncertain whether analytical

methods accurately represent assembly behavior (Cai et al., 2005).

Other numerical approaches are involved with sampling strategies using Monte-Carlo simulations. In the Monte Carlo model, random numbers generate part tolerances based on specific part distributions. The assembly response is generated when a large number of iterations are performed. The accuracy of the approach is highly dependent on the number of iterations considered for the Monte Carlo simulations; therefore, the method is more computationally heavy (Nigam & Turner, 1995). The Monte Carlo model has been used within the CAT tools, to retrieve the assembly response.

In a more recent study, statistical tolerance analysis methods are reviewed and categorized into eight analysis methods (Cao et al., 2018). These methods include technologically and topologically related surfaces (Desrochers & Clément, 1994), the matrix model (Desrochers & Rivière, 1997), vector loop model (Chase et al., 1995), T-MAP model (Mansuy et al., 2013), deviation domain model (Giordano et al., 2007), jacobian-torsor model (Ghie, 2009), GapSpace model (Morse & You, 2005) and skin model (Anwer et al., 2013; Dantan et al., 2008; Schleich et al., 2014). Most methods presented are combined with the Monte Carlo simulation and are implemented in a computer-aided environment for evaluating assemblies of rigid bodies. A comprehensive analysis of advantages and disadvantages of each method is provided in (Cao et al., 2018)

Whereas most methods presented focus on assembly simulations based on the specified tolerances, the simulation accuracy depends on the existing physical deviation in parts before and during assembly. From the methods mentioned, the skin model is identified to have future application in digital twins incorporating the part deviation into the model. The fundamental idea in the skin models, is incorporating the part deviations, stemming from the operations into the Computer-Aided Design (CAD) geometry features, to represent the interface between the part and its physical environment (Schleich et al., 2014). The integration of the part deviation into the simulation models, in the context of this thesis, is further discussed in Section 2.8.

With the integration of the tolerance analysis methods in the algorithmic computer models, the CAT tools are developed enabling evaluation of the tolerances applied to CAD geometries. The next section provides an overview of the analyses performed in such tools.

2.6 Computer Aided Tolerancing

Several CAT tools and methods have been introduced for estimating the geometrical outcome, given the part tolerances, over the years (Prisco & Giorleo, 2002; Shen, 2003; Teissandier et al., 1999). The main characteristics of the evaluation process in such tools are summarized as (Mazur et al., 2011):

1. CAD definition
2. Tolerance specification

3. Definition of the mating conditions and assembly sequences
4. Specification of a measurement point to evaluate geometrical quality
5. Tolerance stack-up analysis using worst-case or statistical methods

In this thesis, the commercial software Robust Design and Tolerancing (RD&T) has been used to retrieve the geometrical outcome of the assemblies (RD&T Technology, 2019). This tool is based on Monte Carlo simulation combined with Finite Element Analysis (FEA) for non-rigid variation simulation, Section 2.8. The tool's functionalities, capabilities and the working order within the product realization loop have been introduced by Söderberg et al. (Söderberg et al., 2016). Figure 2.10 shows an overview of the three main functionalities in the CAT tool RD&T.

Starting with the concept phases, a stability analysis of the concept is performed. With this function, the part's locating schemes are disturbed, and the response to those disturbances is propagated in the part (Söderberg & Carlson, 1999). After identifying the sensitive areas, a locator optimization is performed to secure the geometry during the manufacturing and production phases. In this task, the location of the locating scheme is optimized for minimum part or assembly sensitivity.

Later in the concept phases, the variation simulation is performed (Söderberg et al., 2006a). In this analysis, the response of a critical measure in the assembly is estimated using the Monte Carlo simulation. Random numbers are assigned to part tolerances based on the specified distribution. The locating scheme is also subject to the process and part disturbances. Tolerances can also be assigned to these points. The assembly response to the assigned tolerances is calculated, and the distribution of the variation in the specified measure is achieved. Having the USL and LSL, the outcome can be analyzed for acceptance or adjustment of tolerances.

In an assembly outside the specified limits, a contribution analysis is performed to identify the critical tolerances. A High-Low-Mean analysis is performed and all model parameters are varied one at a time on the three levels. The maximum achieved output is registered for all critical measurement points. A list of tolerance contributions to the specified measure variation will be achieved through this function, calculating the difference in the specific parameter's registered output (Δp_i^2) in the measure over all the registered output in the included model parameters ($\sum_k \Delta p_k^2$)¹ (Söderberg et al., 2016). The designer can then decide on changing a specific tolerance or readjusting the limits given the optimal positions of the locators.

For non-rigid assemblies, parts are bent and deformed during assembly. To allow for non-rigid analysis the FEM is combined with the variation simulation to retrieve assembly geometrical outcome. Followed by an introduction to FEM in Section 2.7, this aspect is addressed in Section 2.8.

¹Contribution for tolerance i in measure $m = \Delta p_i^2 / \sum_k \Delta p_k^2$, where k is the number of the tolerances, and Δp is the maximum registered output of the High-Low-Mean analysis in measure m .

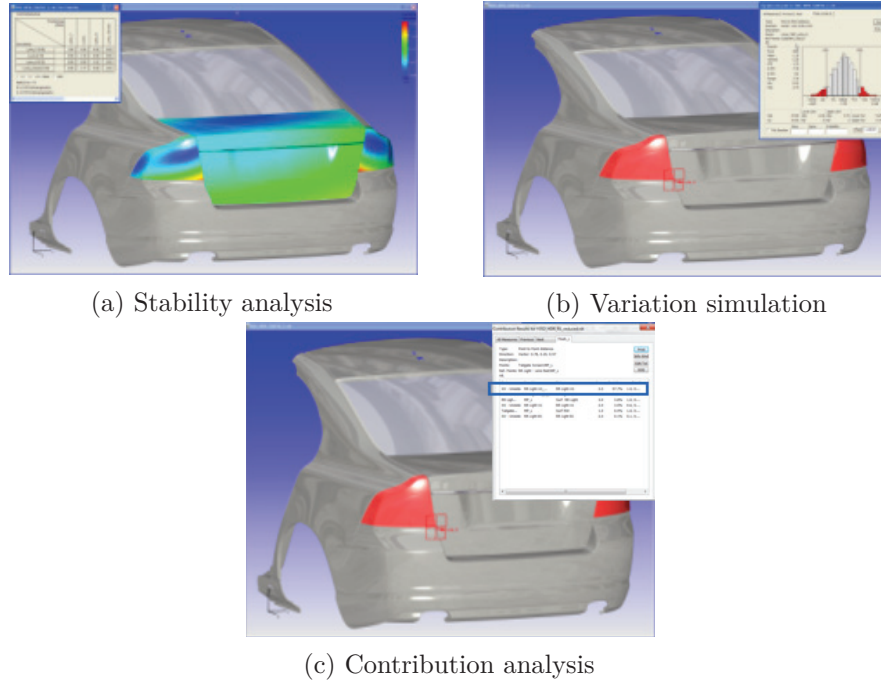


Figure 2.10: Different functionalities in the CAT tool. Adjusted from (Söderberg et al., 2006a).

2.7 Finite Element Method

FEM is a numerical method for solving partial differential equations. By discretizing the problem space, a domain is divided into smaller sub-domains, referred to as finite elements. The discretization is performed by transferring the geometry into a mesh. The governing equations for the boundary value problem are established for each element. The equations are then assembled, gathering all the elements together, and an approximation of the primary domain response is derived (J. N. Reddy, 2019). Figure 2.11 visualizes a three-dimensional domain that is discretized into a mesh. Nodes and vertices define each element. The applications of FEM are widespread in the fields of fluid mechanics, heat transfer, and structural mechanics (Larson & Bengzon, 2013). In this thesis, FEM is used to retrieve the displacements of the assemblies, given the boundary conditions, i.e., positioning points, support elements and joining points. FEM solvers and commercial tools have been introduced for efficient formulation and analysis of such problems. Although nominal geometries can be considered to estimate the displacements in engineering structure models, the analysis can be improved by combining statistical simulations for predicting the assembly variation (S. C. Liu & Hu, 1997). In the next section, the details of such an approach are introduced.

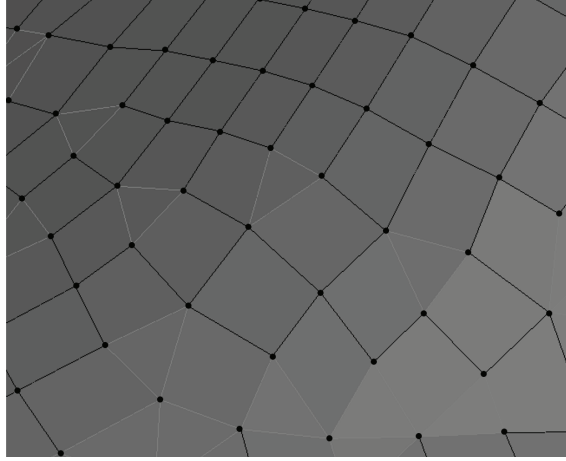


Figure 2.11: A three-dimensional surface meshed into elements

2.8 Non-rigid Variation Simulation

The review of the tolerance analysis methods presented in Section 2.6 and CAT in Section 2.6 have been applied to rigid body assemblies. However, in non-rigid parts, such as sheet metals, the parts are bent and deformed during assembly. Therefore, the locating scheme can be over-constrained, Section 2.2.

The response of the assembly to the applied forces including clamping, joining, gravity, fixture disturbances, and part variation for the non-rigid parts can be retrieved using FEM. A FEM solver is incorporated in the deployed CAT tool RD&T (RD&T Technology, 2019) to allow for non-rigid analysis.

A generic approach to get the assembly's response concerning part and process variations is the Direct Monte Carlo (DMC) simulation. However, since many iterations are required to achieve satisfactory accuracy in the Monte Carlo simulation, and the full FEM problem is solved consecutively in each iteration, the method is time consuming.

Compared to the DMC, the Method of Influence Coefficients (MIC) is more time-efficient (S. C. Liu & Hu, 1997). The method is based on the small part deviation assumption and is applicable when the material properties, namely the stress-strain relation, are linear. With these assumptions, the linear relationships between part deviations and assembly deviations are established. A sensitivity matrix is constructed describing this linear relationship. This sensitivity matrix is then used together with the Monte Carlo simulation iteratively, bypassing the full FEM problem calculation. The main steps for the point-based joining methods, like spot welding, are as follows:

Positioning and clamping: The parts are being positioned into a fixture, and the errors from the nominal geometry for all nodes in the assembly are calculated. The deformation of the assembly, (u_{def}), prior to joining, is being determined from the sensitivity matrix (S), $u_{def} = Sd$. Here, d represents the displacements of the weld points and clamps. From this information, the total displacements

of all nodes in the assembly can be calculated, adding up the positioning offset and the deformation of the parts.

Joining: On the position of the joints, a stiff beam is introduced into the joint pairs locking all degrees of freedom. The normal displacements on these points are forced to be zero. The sensitivity matrix is being updated after this operation. The choice of the welding gun affects the applied welding forces; see Figure 2.6.

Release and spring-back: To retrieve the spring-back of the assembly, on the position of the clamps, clamping forces in the opposite sign are introduced to the assembly. The response of the assembly to these forces are calculated, and the final displacements are derived.

One inaccuracy that can arise during this method is the penetration of the adjacent parts into each other. Forces that are applied from the interaction of the mated surfaces between each other are neglected. To avoid this problem and to retrieve more accurate assembly responses, contact modeling has been added to the non-rigid variation simulation (Dahlström & Lindkvist, 2007; Lindau et al., 2016; Wärmefjord et al., 2008). Through this method, the contact surfaces are being defined using contact nodes on each part. Similar to the first step in the MIC approach, the displacements in the contact nodes are calculated. In case of penetration, the corresponding forces are applied to the model pushing the parts away from each other, until surface-to-surface contact is achieved. Contact modeling is also performed after the parts are joined together. Since contact modeling is an iterative non-linear method, the MIC retrieves the assembly response using contact modeling and behaves non-linearly. Contact modeling also increases the computation-time requirement of the MIC approach. The state of the art in contact modeling with the MIC method is quadratic programming formulation of the contact problem (Lindau et al., 2016; Lupuleac et al., 2020). Studies have been made reducing the computation-time needed to retrieve the response of the assembly using MIC and contact modeling (Lorin et al., 2017). The extended MIC and contact modeling is integrated within the CAT tool RD&T utilized in this thesis.

With the combined MIC and contact modeling, the joints can be set simultaneously and the response can be retrieved at once. However, this approach is not realistic and besides it is physically infeasible. In a typical assembly station, multiple robot arms are performing the spot welding. However, the number of weld points are often greater than the number of guns available. Nevertheless, given the same number of guns and weld points, absolute simultaneity is complex to achieve. Therefore, the sequence of the joining operation becomes a critical parameter to achieve accurate responses (Cai et al., 1996; Gannon et al., 2010; S. C. Liu & Hu, 1997; Wärmefjord et al., 2010b). To include the sequence of joining in non-rigid variation simulation, Wärmefjord et al. have considered a recursive approach where the assembly is joined at each point and the MIC and contact modeling is performed (Wärmefjord et al., 2010b). They have shown that including the sequence of joining increases the accuracy of simulations. They have validated the simulation accuracy by comparing

the outcome with the physical inspection data. Although the introduced approach increased the accuracy, the intermediate spring-back calculations after each joining point increase the calculation time. To avoid these steps, Lorin et al. have formulated the extended MIC, where the intermediate spring-back steps are not performed (Lorin et al., 2019; Lorin et al., 2018).

An overview of the parameters influencing the simulation accuracy is given in Figure 2.12 (Söderberg et al., 2012). The focus in this thesis is on the joining sequence parameter, which has shown to impact the geometrical outcome of the assembly in the appended papers and the accuracy of the simulation (Wärmefjord, 2011; Wärmefjord et al., 2010b). Another important parameter which influences the simulation accuracy is the inspection data. As mentioned in Section 2.5, for accurate representation of the assembly process, part deviations need to be integrated into the model. In such an approach, the point cloud of the scanned part geometry can represent the input to the simulation accurately (Wärmefjord et al., 2017). Including the part deviation of the fabricated part geometries in the simulation enables application of the digital twins for real-time geometry assurance (Franciosa et al., 2020; Söderberg et al., 2017).

Other studies have intended to extend the MIC method from a single station to a multi-station strategy by the state-space representation of the assembly stations (Camelio et al., 2003), and using a two-stage FEA for calculating the coefficients and spring-back (Gerbino et al., 2008). Camelio et al. have considered analyzing variation using component geometric covariance. They utilized statistical methods to extract patterns in the deformations of the components. The effects of these patterns are evaluated using FEM. They have illustrated using a case study that the approach can significantly reduce the computational time for variation analysis of non-rigid components (Camelio et al., 2004a). A review of the methods used to retrieve the sensitivity matrices in MIC is presented by Polini et al. (Polini & Corrado, 2020b). They have identified negligible differences between unit force, unit deviation, and the super element method. However, the performance of the super-element method has been faster with respect to computation time. Franciosa et al. have considered modeling and simulation of the shape errors in a small number of control points by a morphing mesh procedure in order to evaluate geometrical variation. The approach is applied to a two-part assembly, and the results are compared to linear methods based on sensitivity matrices. It has been concluded that using contact modeling helps to achieve more realistic simulations with the trade-off of the simulation time, in combination with the MC simulations. The morphing approach helps to include cumulative part deviations into the simulation compared to linear models with independent part tolerances (Franciosa et al., 2011). In another study using a direct approach, displacements during the spot welding process are simulated considering material plasticity (Moos & Vezzetti, 2015, 1). Friction models for the clamps and welding gun, the thermal effects, and the welding sequence are considered in the analysis model. The variation analysis has been based on constant offsets from the CAD geometry. Contact iterations avoiding the penetration of parts are not reported. They have compared the simulation results to the experimental results and elastic material models. Based on the comparison presented, in some measurement

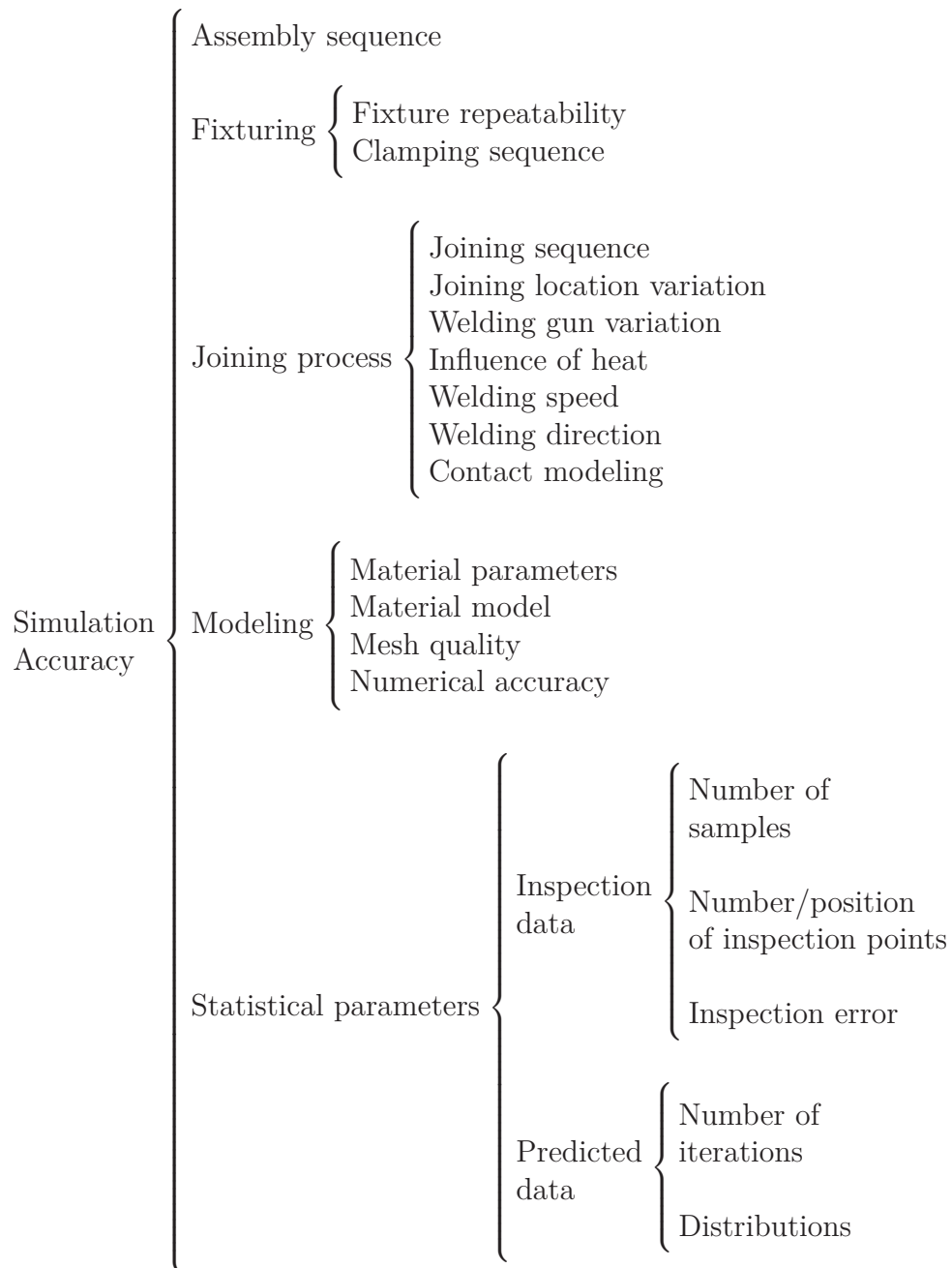


Figure 2.12: Parameters affecting the simulation accuracy in variation simulation

points, including plastic material and temperature fields, simulation accuracy has been improved, whereas in some other points, modeling without temperature effects has been more accurate.

Other studies can be found on non-rigid variation simulation of the assemblies, adapting the MIC of Direct methods to the specific needs of the assembly process problems. Du et al. have considered a modified direct stiffness method for optimal fixture lay-out design (Du et al., 2020, 6). Choi et al. have considered proposing a modified MIC approach to take into account sources of variation proposed in (Chase & Parkinson, 1991), to consider welding distortion (Choi & Chung, 2015). A nonlinear material model for part variation simulation has been incorporated with the MIC model (Camuz et al., 2019). Liu et al. propose a hybrid non-linear variation model to take into account welding angular distortion and shrinkage (C. Liu et al., 2020). Lorin et al. combines the thermal expansion with non-rigid variation simulation (Lorin et al., 2013). In another study, they incorporate the stress simulations with the MIC approach (Lorin et al., 2014) and thereafter, the variation simulation of non-nominal welded geometries are introduced (Lorin et al., 2015).

In this thesis, the effect of joining sequences are analyzed. For evaluating the assembly outcome, the extended MIC and contact modeling presented in (Lorin et al., 2019; Lorin et al., 2018; Tabar et al., 2021), incorporated in the RD&T CAT tool is utilized. The nature of the sequencing problem is combinatorial, where non-rigid variation simulation needs to be performed for different joining sequences. In Section 2.9, combinatorial optimization aspects are introduced.

2.9 Combinatorial Optimization

Optimization is about finding the "*best*" solution among all possible alternatives. The suitability of the best solution is measured against one or multiple criteria. The general mathematical optimization methods and algorithms can be divided into various categories of problems, i.e., stochastic, continuous and discrete (Boyd & Vandenberghe, 2004; Nocedal & Wright, 2006), and details of each method is not part of the scope of this thesis. The joining sequence problem is about identifying the best combination of joining points among available alternatives (Arora, 2012), which perfectly fits the definition of the combinatorial problems. The combinatorial optimization lies within the discrete optimization methods (Parker & Rardin, 2014).

Combinatorial optimization looks for a solution among a finite set of alternatives. The set of alternatives can be represented by a graph, including nodes and vertices, in their simplest form of representation. The set of alternatives grows exponentially by increasing the nodes in the graph. Consequently, examining all possible alternatives, also referred to as an exhaustive search, is infeasible (Schrijver, 2003). Combinatorial problems are purely non-differentiable and their function cannot be defined at non-discrete points (Arora, 2012). A typical problem within this type is the well-known traveling salesman problem (TSP). The TSP investigates the shortest path to visit a given number of cities and returns to the original city. A general formulation of this

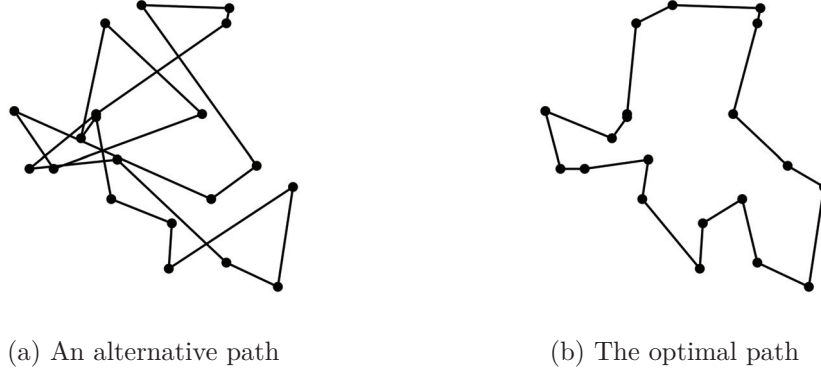


Figure 2.13: An alternative and the optimal path for a TSP with 19 cities

problem is (Dantzig, 2016):

$$\begin{aligned}
 \min \quad & \sum_{i=1}^n \sum_{j \neq i, j=1}^n c_{ij} x_{ij} \\
 \text{s.t.} \quad & x_{i,j} \in \{0, 1\} \quad i, j = 1, \dots, n; \\
 & \sum_{i=1, i \neq j}^n x_{ij} = 1 \quad j = 1, \dots, n; \\
 & \sum_{j=1, j \neq i}^n x_{i,j} = 1 \quad i = 1, \dots, n;
 \end{aligned} \tag{2.14}$$

where c_{ij} is the distance between nodes i and j , n is the number of the nodes to be visited, and x_{ij} is a variable that gets the value one, if the path goes from i to j , otherwise zero. Here, the first equality constraint defines each node is visited from exactly one other node. The second equality defines from each node, only one other node can be visited. Another critical constraint that should be considered for this problem is the limitation of the sub-tours. Starting from one node, all the nodes should be visited on a single tour. There are various formulations available for this constraint, and in general, the TSP problem (Schrijver, 2003). Figure 2.13 shows an alternative path and the optimal path for a two-dimensional TSP with 19 cities. The cities are represented by the nodes and the distance between the cities by the vertices. The optimal path results in total distance of 376 km, whereas the other alternative has 540 km total covered distance.

In general combinatorial problems are difficult to solve since the feasible solution space is large and the number of available alternative grows fast. For example, the TSP problem including 100 cities consists of $100!$ feasible solutions. The same problem including 101 cities, encompasses $101 \times 100!$ solutions. Therefore, evaluating all possible alternatives are often not in the realm of possibility. The problems in combinatorial optimization are formulated using binary decisions, which ultimately for problems like TSP, that requires polynomial time to be solved, exhibit non-deterministic behavior in the binary decisions. For this reason, the TSP is categorized in the non-deterministic polynomial-time (NP) hard class of problem complexity (Parker & Rardin, 2014).

For combinatorial problems, including TSP, integer programming algorithms (Parker & Rardin, 2014), search algorithms (Clausen, 1999), branch and bound (Arora, 2012) and meta-heuristic algorithms (Dorigo & Di Caro, 1999) are often used. Algorithms for solving these problems are deterministic, i.e., branch and bound and greedy approach (Parker & Rardin, 2014), or non-deterministic algorithms, i.e., evolutionary algorithms (EA), such as the Genetic Algorithms (GA) (Holland et al., 1992). Finding the global optimum using the meta-heuristics, e.g., GA, requires large population sizes and is not guaranteed. Deterministic algorithms to solve NP-hard problems are often based on evaluating several combinations of subsets of the problem. An example of the deterministic algorithms is Dynamic Programming. In this method, the complete set is divided into subsets, The cost of the subsets are evaluated and stored by means of look-up tables of subsets. The optimal solution is identified finding the minimum costs of the subsets (Held & Karp, 1962).

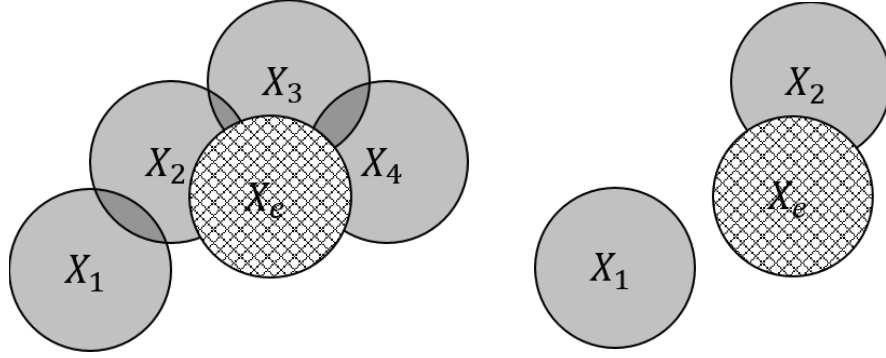
The issues of time consumption of the stochastic meta-heuristics, EA, apply to the joining sequence problem. For finding the sequence among all possible sequences that optimizes geometrical quality, a large number of sequences need to be evaluated. This aspect is further discussed in Section 2.12. The other challenge that hinders traditional integer and dynamic programming approaches for solving joining sequence optimization problems is the unknown behavior of the objective function. To further clarify this point, consider the formulation in Equation 2.14. The objective function is defined as a linear function of the sum of the distances (weights c_{ij}) of visited nodes. Now consider a sheet metal assembly with four joining points. A complete sequence is $1 \rightarrow 2 \rightarrow 3 \rightarrow 4$ and has a deformation u . The sum of the deformation of the sub-steps $[1 \rightarrow 2]$, u_s^1 , $[2 \rightarrow 3]$, u_s^2 , and so on, will result in larger deformations than the complete sequence, u . So the relation $u = \sum_{i=1}^3 u_s^i$ does not hold. The mapping function of the sub-steps to the final deformation exhibits a non-linear and non-convex behavior (Tabar et al., 2020a). Therefore, solving the problem with traditional formulations in integer programming depends on accurate weight assignment to each sub-step. This weight assignment problem *per se* is a complex problem with a non-linear function, and is not addressed in the existing literature for the joining sequence optimization problem. To better understand the behavior of the joining sub-steps, Section 2.10 introduces another aspect of the combinatorial optimization governing the subset selection problem.

2.10 Sub-Modular Set Functions

Sub-modular set functions are associated with various fields of discrete optimization and combinatorial optimization. The basic definition of this type of function and the connections to the joining sequence problem are given in the following.

Suppose that Ω is a finite set, for which f is a set function when $f : 2^\Omega \rightarrow \mathbb{R}$. This function is sub-modular if A and B are subsets of Ω and the following relation holds (Feige et al., 2011):

$$f(A) + f(B) \geq f(A \cup B) + f(A \cap B), \quad \forall A, B \subseteq \Omega \quad (2.15)$$



(a) Adding X_e to set $B = \{X_1, X_2, X_3, X_4\}$ (b) Adding X_e to set $A = \{X_1, X_2\}$

Figure 2.14: Diminishing returns of adding extra element to a sub-modular set function

Another property of such functions is diminishing returns. Consider $A \subseteq B$, now adding an extra element E to each set is resulting the following:

$$f(A \cup E) - f(A) \geq f(B \cup E) - f(B), \quad \forall A \subseteq B \quad (2.16)$$

The return of adding element E to A , which is a subset of B , is greater or equal to adding E to B . Optimization of such functions is considered a subset selection problem, where the goal is to find a subset that optimizes the function f . A typical example of the application of such an optimization problem is the maximum area coverage (Krause & Golovin, 2014). Each element of the set covers an area; for simplicity, a constant area for all elements is considered in Figure 2.14. In (a), the return of the area covered by adding element X_e to the superset is smaller than (b), where the same element is added to the subset.

The function f is either monotone or non-monotone. The sub-modular function is monotone if:

$$f(B) \geq f(A), \quad \forall A \subseteq B \quad (2.17)$$

The maximization of such functions is NP-hard, and greedy algorithms are often used to approximate the optimum subset that maximizes a monotone f (Nemhauser et al., 1978). For non-monotone functions, local search methods and modified greedy approaches are used (Barbosa et al., 2016).

The application of such functions in the context of joining sequence optimization is related to the geometry point selection or pre-joining processes, which will be described in Section 2.12. This problem is defined as selecting a subset S of joints from a set of available alternatives so that the objective is optimized. The function f is treated as a value oracle or black-box that provides the value of $f(S)$. The function of sub-steps of the joining sequence is non-monotone. Such perspectives have not been taken into consideration for joining sequence optimization problems, or geometry point selection problems in existing literature. In this thesis, the sub-modular behavior of this problem is introduced and discussed further in Section 4.5.

To be able to provide the value oracle or black-box evaluator of the joining sequences, non-linear models need to be built mapping the sequence of joining to their deformation state. In Section 2.11, the overview of this aspect is introduced.

2.11 Non-linear Modeling

In non-linear functions, the changes in output are not proportionate to the changes in input. Including exponents or inversions of variables causes non-linear behavior. Quadratic problems are of this kind. Representing the behavior of such functions using a mathematical model is referred to as non-linear modeling. By fitting a model to empirical data, and describing the physical relations between the variables, i.e., equations, non-linear models are established (Murray-Smith & Johansen, 1997). Parametric and non-parametric statistical models (Stone, 1985), non-linear regression models, e.g., neural networks (NN) (Hagan et al., 1997), kernel regressions, and support vector machines (SVM) (Vapnik, 2000), are among the methods used for this purpose. Going into the theory of the broad field of non-linear modeling is outside the scope of this thesis. Therefore, only the references to the theory of applied methods are provided.

In this thesis, non-linear models are built to represent the behavior between joining sequences and geometrical deformation in the assembly. The details of the attributes of the models are used in this thesis are provided in the appended papers. The modeling method that has been introduced and applied to the problem is Neural Networks. In Paper C, a radial basis function network has been formulated to approximate the sequences' input-output function to the assembly response. This network has proven to be a universal approximator (Park & Sandberg, 1991); therefore, the application of this network is widespread. The details of this network can be found in (Hagan et al., 1997; Lippmann, 1989). In Papers E and F, SVM models are used to build such input-output models (Vapnik, 2000). The SVM models are among non-parametric statistical learning methods and their applications are associated with various fields of classification and non-linear function approximation (Chorowski et al., 2014).

With the background provided around combinatorial optimization and non-linear modeling aspects, Section 2.12 introduces the joining sequence optimization related literature, applied formulations and proposed methods.

2.12 Joining Sequence Optimization

Joining sequence optimization strives for finding the best sequence among all possible sequences so that a specific objective becomes optimal. Different formulations and methods have been considered for this optimization problem. Due to the combinatorial nature of the problem, simulation-based optimizations and experimentation are dominant among existing literature. Heuristic approaches derived from industrial

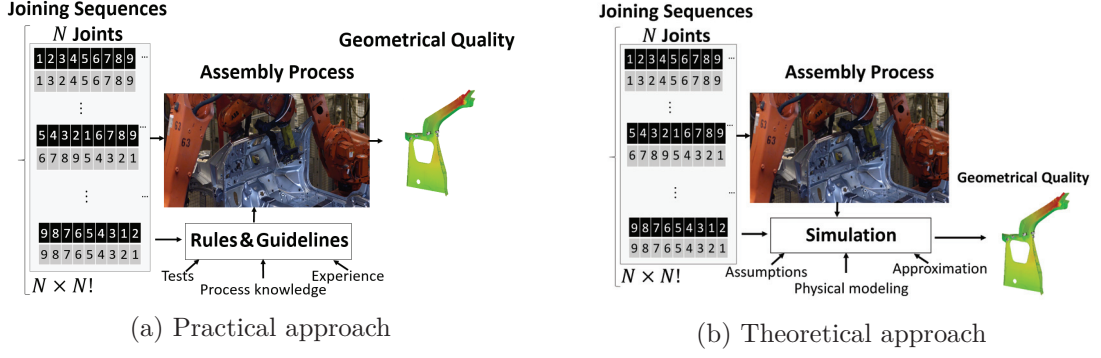


Figure 2.15: Joining sequence problem

practice are partially introduced and evaluated. The overview of such formulations, industrial and theoretical reference models, is presented in Figure 2.15. The problem formulations and applied methods in the previous research are categorized and presented in the following sections.

2.12.1 Problem formulations

There are several objectives considered for joining sequence optimization. These objectives include distortion and local shrinkage in the joining point due to melting and cooling (Fukuda & Yoshikawa, 1990), cycle time (Carlson et al., 2014), as well as stresses (Mochizuki et al., 2000). A review of applied objectives for weld sequence optimization is provided in (B. Wang et al., 2020) and (Beik et al., 2019). These studies have, among other optimization objectives, summarized torch movement, welding time, symmetry, distortion, displacement and residual stresses.

The joining sequence problem is mainly studied for spot welding, riveting, and continuous welding operations. Early in the 90s, Fukuda and Yoshikawa have introduced a discrete method for continuous problems, where the welding path is divided into several smaller paths. They have formulated a NN for this problem and have shown the potential of the method (Fukuda & Yoshikawa, 1990). In this discretized formulation, a continuous path is divided into smaller segments. Each segment is considered to be welded in the optimal direction and order to minimize the local shrinkage in the weld path. This discretized method has also been implemented to minimize the travel distance of the welding gun. In this study, nominal geometries are considered for local weld distortion evaluation. The described discretized approach has been implemented in several other studies for optimal weld path identification (Asadi & Goldak, 2011; Kadivar et al., 2000; Kim et al., 2002; Tsai et al., 1999).

Tsai et al. have evaluated the welding distortion of a thin-plate panel with respect to different sequences by means of FEM simulations for weld paths (Tsai et al., 1999). The objective is to identify the complete optimal path in order to reduce welding distortions. Mochizuki et al. have approximated the residual stress outcome in a butt-welded pipe with respect to different welding sequences (Mochizuki et al.,

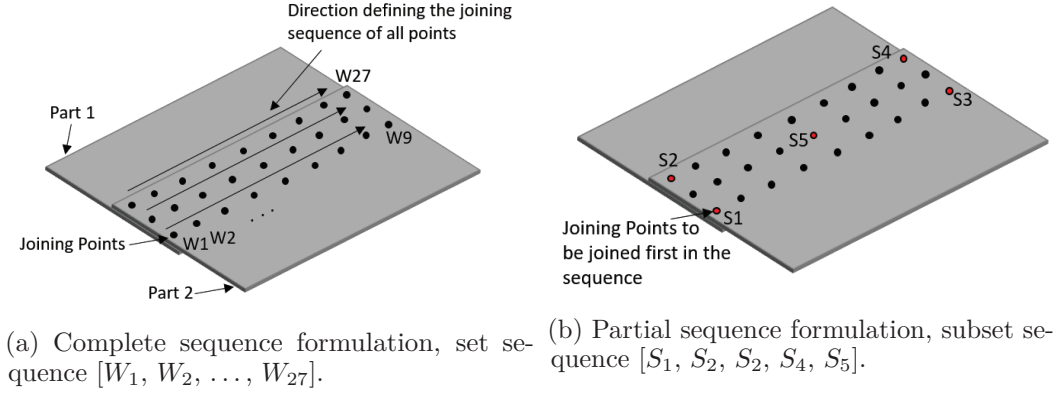


Figure 2.16: Joining sequence problem formulations

2000). They have built a simple approximation model by performing six different welding sequence cases. Using the approximation model, they identified the optimal sequence to avoid cracking. Since the approximation models have been built based on the results of welding cases, the optimal sequence is biased towards the outcome of the performed cases. Moreover, the effect of contacts and part deviations are not considered in the analysis. Kadivar et al. have stated that welding sequences are determined by the experience of the welder and therefore, simulation-based optimization needs to be performed to determine the optimal welding path (Kadivar et al., 2000). They establish a thermo-mechanical model of nominal geometry to determine the optimal weld path. The studies in (Voutchkov et al., 2005), (Asadi & Goldak, 2011), (Romero-Hdz et al., 2020) also strive to propose efficient simulation-based methods with which to determine the optimal welding path. The studies presented have developed methods suited to defining the path in the continuous welding application with a given approximation method for evaluating the effect of the heat on nominal geometries. With this approximation, a complete sequence is introduced, minimizing an objective. Stating that joining sequence is evaluated on the point-based joining methods of non-nominal parts in this thesis, the above studies are categorized as complete weld path formulations. Figure 2.16a shows an overview of the complete sequence formulation in an assembly of two parts with 27 joining points. Starting from the first point, W_1 , the joining operation is performed until all 27 points have been joined with the specified sequence, to minimize the deformations after joining.

Considering the point-based joining methods, Huang et al. have considered finding the optimal sequence with the minimum deformations after spot welding (Huang et al., 1997), using FEM. The modeling details are not further described, as the principal contribution has been on introducing a GA to solve combinatorial problems. Cycle time has also been introduced to the objective of this problem solved using GA (Xie & Hsieh, 2002). Other applications have also considered the simulations-based optimization with GA for minimized geometrical variation (Y. G. Liao, 2005; Segeborn et al., 2011). Although the studies introduce a method to find the optimal sequence for improved quality, the efficiency of the approaches have not been compared to one another with respect to time and accuracy. Heuristic

search algorithms and a branch and bound method have been considered to optimize the geometrical quality and the welding gun robot traveling path at the same time (Carlson et al., 2014). These studies are categorized as problems with complete sequence formulations. In these studies, the problem is formulated to achieve a complete sequence of spot welding minimizing the objective.

The other category of formulations where joining sequence is addressed is the partial sequence formulation. In this category, the problem is formulated as selecting a subset of joining points from a set of available alternatives, considering their sequence to minimize the objective. Figure 2.16b visualizes an example of an assembly of two parts and 27 joining points, where a subset of five points is chosen to be set in a sequence. The industrial application of this formulation can be related to the pre-joining processes in the aerospace, and the geometry point identification in the automotive sectors; Section 1.1.1. To address this problem, Aman et al. have designed an experimental setup with FEM to evaluate the riveting process parameters, including sequence (Aman et al., 2013). However, the experimental setup is performed on three rivets, where the optimal sequence can be identified by trying all combinations. Furthermore, Liu et al. have considered an approach based on MIC to evaluate the initial clearances between sheets as an objective to identify the optimal number, sequence, and location of the pre-joining points with a neighborhood search and GA (G. Liu et al., 2014). The method has been further expanded to a statistical analysis of the batch of assemblies (G. Liu et al., 2015). Although the approach has been argued to be computationally efficient, the application of the method is limited to the measure of the maximum residual clearance. Yang et al. have introduced a more comprehensive approach using MIC to propose an equivalent gap assembly model approximating residual clearances (Yang et al., 2016). Lupuleac et al. have considered identifying optimal fastener pattern with respect to the residual gap between parts, number of fasteners and defects using MIC and contact modeling (Lupuleac et al., 2020). They have included a comparison of different optimization algorithms, local variation, simulated annealing² (SA), and mesh adaptive direct search³ (MADS). They have identified that SA is time-consuming for solving this problem, whereas the local variation and MADS are suitable for identifying the riveting pattern. However, the different objectives are not considered simultaneously, and the effect of the sequence is not explicitly reported. Wärmefjord et al. have also evaluated the number of geometry points in several cases with two sheet metal parts. They have utilized MIC and contact modeling for deformation evaluation. They identified that for an assembly with two parts, two weld points are determining the geometrical quality of the assembly (Wärmefjord et al., 2010b). The overview of the literature review is presented in Table 2.1. In the following section, the applied methods are addressed.

²Optimization method presented in (Van Laarhoven & Aarts, 1987)

³Optimization method presented in (Audet & Dennis Jr, 2006)

2.12.2 Applied optimization methods

Based on the analysis of the proposed problem formulations 2.1, the applied methods have been divided into, *Meta-Heuristics* including EAs and SA, *Surrogate modeling*, *Experiments*, *Networks and Machine Learning*, and *Heuristics*. In the following, the literature has been categorized into these methods.

Meta-Heuristics: The most widely applied optimization method for this problem has been the GA. The GA is in the category of meta-heuristic optimization algorithms and is inspired by natural selection (Holland et al., 1992). Several other EAs, such as Ant Colony (ACO) (Dorigo & Di Caro, 1999) and Particle Swarm Optimization (PSO) (Kennedy & Eberhart, 1995), have also been introduced and applied to the sequencing problems. The typical steps in the EAs are:

1. Generate an initial random population of solutions.
2. Evaluate the fitness or cost of each solution.
3. If the ending condition is not satisfied, apply the algorithm-specific operators.
4. Create new generations of the population.
5. Evaluate the fitness or cost of each solution.
6. Repeat steps 3-5 until the ending condition has been satisfied.

The GA-specific operators are crossover and mutation. In the crossover operator, two solutions (encoded as chromosomes with genes as elements) are selected by different strategies. For example, in a single point crossover, chromosomes swap genes with each other from a single cutting point. A single solution is being chosen in the mutation operator, and the genes change position within the same solution.

By applying the traditional GA operators to the sequencing problems, repeated and infeasible solutions may also be generated, which is not desired. The random-key encoding approach is introduced to avoid the generation of repeated solutions (Bean, 1994). In this approach, the solutions are encoded as real numbers between zero and one. After crossover, these random-keys are decoded back to the integer numbers representing the sequence. Huang et al. have also introduced an approach with which to overcome the issues for solving sequencing problems utilizing GA (Huang et al., 1997). In this approach, the redundant elements are identified, algorithmically, and swapped with feasible elements. More information on the efficient application of these methods on the sequencing problems is given in Paper A. The applications of these meta-heuristics in both formulations for joining sequence optimization are widespread, at a 50% rate, in which 39% of the evaluated studies have utilized GA; Table 2.1.

Surrogate modeling: An issue associated with welding sequences is the combinatorial nature of the problem. The objective function to retrieve an evaluation of displacements, stresses, or heat effect includes a FEM. Evaluating all combinations using FEM is time-consuming. Therefore, a model of the outcome with respect to different sequences is built, specifically in ARC welding applications. These models are referred to as surrogate models. Mochizuki et al. have established simple approximation models, evaluating six welding scenarios, where the weld path starts in different directions, i.e., left to right, middle and outwards (Mochizuki et al., 2000). The approximation model is then built by a linear stack-up of the bending and axial shrinkage stresses. Such approximation models are case-specific and the accuracy of the model may be biased towards the results achieved in the welding scenarios. Kim et al. consider finding the optimal weld path for the minimized path and cooling time to avoid crack generation (Kim et al., 2002). They have proposed heuristic algorithms for this purpose. A more comprehensive surrogate modeling approach based on the experimental design of the welding paths is proposed by Voutchkov et al. (Voutchkov et al., 2005). In this study, the surrogate model is built based on the linear combination of sub-problems. Initially, 27 sequence experiments are performed. The given sequence is broken down into combinations the sequence elements, and the displacements after welding with a given sequence are approximated. Utilizing the look-up tables of the available sub-combination of the sequence, the approximation of the displacements with respect to each sub-element is identified and linearly stacked-up to build the deformation. An approximation model for the effect of heat is also included in the surrogate model. An aspect that may result in inaccuracy in this surrogate model is neglecting the part variation and contact modeling. With the successive non-linear contact modeling at each welding step, it is expected the sub-problems' deformations cannot be linearly stacked-up to build the final deformation. Asadi & Goldak, using the same approach as in (Voutchkov et al., 2005), proposed a surrogate modeling approach of 48 sequence experiments of three weld segments (Asadi & Goldak, 2011). The applicability of such models for point-based joining methods, is not self-evident. However the issue of neglecting part deviations and contact interactions hold in this study as well.

Experiments: In this category, the methods are based on simulation experiments. The sequence is determined by observing the best sequence among the performed experiments. These experiments often include case-specific rules and industrial practice as an approach by which to perform the experiments. Aman et al. have considered a simple three joint case and performed the simulation experiments on all sequences (Aman et al., 2013). Wärmefjord et al. have also performed simulation experiments on eight different cases with four weld points and identified the optimal sequence. They also considered the measure of inertia tolerancing to identify the number of geometry points with the optimal sequences. (Wärmefjord et al., 2010b).

Networks and Machine Learning: Fukuda and Yoshikawa have applied the Hop-

field neural networks on the continuous welding problem (Fukuda & Yoshikawa, 1990), to identify the optimal weld path. Other studies on the application of this type of network have shown the efficiency of the method for combinatorial optimization problems (Aiyer et al., 1990; Salcedo-Sanz & Yao, 2004; Talaván & Yáñez, 2002; L. Wang et al., 2004). The details of this type of network on point-based joining methods is presented in Additional Publication (AP) 2. Reinforcement learning is also applied to the problem incorporating the domain knowledge in a Q-learning algorithm (Romero-Hdz et al., 2020). Based on the simulations and predefined rules, the algorithm is initiated and the exploration and exploitation dilemma of the problem space is solved. They have included a comparison of different artificial intelligence methods on the continuous problem and concluded that reinforcement learning enhanced with domain knowledge result in less computation complexity. Such an approach can potentially be applied to point-based joining problems, whereas the domain knowledge required depends on fabricated part deviations.

Heuristics: Tsai et al. have proposed a joint rigidity method to identify the optimal sequence. In the joint rigidity method, the joint is disturbed by a unit moment, and the stiffness is calculated. They state that the sequence starting with more rigid joints and moving towards the less rigid joints will result in less bending after welding. The application of such an approach can be seen in (Wärmefjord et al., 2010a), where the relative sensitivities of the joint gaps are considered for sequence determination. Kim et al. consider a nearest neighborhood search, and a local search to minimize the weld paths and consequently improve cooling in ARC welding (Kim et al., 2002). Since the formulation of the objective function is a modified traveling salesman, a comparison of greedy search, tabu search is also provided. Such algorithms cannot be directly applied to FEM methods as the objective function cannot be evaluated with the summation of deformations at each joining sub-step, Section 2.9. Wärmefjord et al. have considered several strategies for sequence optimization. Among the strategies evaluated, relative weld gap sensitivity has been shown to be more accurate. Carlson et al. have applied a branch and bound algorithm to determine the optimal joining sequence with respect to geometrical variation. An issue in the formulation of the problem with the branch and bound method, is defining the upper and lower bounds. Generally, in point-based joining methods, after each joining step, the assembly displacement changes and may not correlate with the previous joining step. To overcome this issue, Carlson et al. have considered the outcome of the simultaneous weld as the lower bound of the problem (Carlson et al., 2014). However, the simultaneous welding result is not always in the problem bounds and might result in sub-optimal convergence. Lupuleac et al. have considered a local variation model and a mesh adaptive direct search method to identify the optimal riveting pattern (Lupuleac et al., 2020). These algorithms are suited to identify the ideal location of the joining points among a set of alternatives; however, the sequence of the joining cannot be directly determined with the given algorithms. Further studies are needed to investigate the applicability of

the MADS for sequence determination.

The overview of the utilized methods is presented in Table 2.1.

2.13 Frame of Reference Summary

In this chapter, the frame of reference is outlined, based on the areas of relevance and contribution illustrated in Figure 2.1. Starting from the design perspective, the concept of the robust design, Section 2.1 and locating schemes, Section 2.2 are presented. From a manufacturing perspective, the point-based joining techniques are introduced, Section 2.3. on the intersection of these two paradigms, the tolerancing field, Section 2.4, and the statistical tolerance analysis and simulations are presented, Section 2.5. Built on top of statistical analysis models CAT tools for evaluating assemblies with respect to part tolerances are introduced, Section 2.6. To allow for non-rigid analysis, FEM, Section 2.7, is included in the CAT tools for non-rigid variation simulation, Section 2.8. To introduce the joining sequence optimization problem and its associated challenges, combinatorial optimization aspects, Sections 2.9 and 2.10 are introduced. This is followed up by an introduction to the non-linear modeling approaches utilized in this thesis, Section 2.11. Finally, the literature on the joining sequence optimization methods and formulations are presented, Section 2.12.

Based on the literature review presented, it is identified that the joining sequence analysis and optimization problem is not reviewed and discussed from different formulations perspective. The presented literature does not converge into generic solutions to the problem, and is heavily case-specific. Real-time optimization perspectives are not considered comprehensively and consequently, the methods presented are often time-consuming. Generic and accurate methods for identification of the number, location⁴, and sequence of the critical joining points for geometrical quality are not rigorously addressed. For this purpose, the research questions (RQ), Section 1.4, have been formulated to address these research gaps in this thesis.

⁴In this thesis, the location of joining points is discussed with a given set of available alternatives; see Figure 2.16b. The exact positions (coordinates) of the joining points and their optimality are not discussed.

Table 2.1: Literature review of joining sequence optimization

Literature	Joining method	Formulation	Objective	Method
(Fukuda & Yoshikawa, 1990)	ARC Welding	Complete Path	Local Shrinkage & Gun Travel	Hopfield Neural Network
(Tsai et al., 1999)	ARC Welding	Complete Path	Welding Distortion	Joint Rigidity Method
(Kadiivar et al., 2000)	ARC Welding	Complete Path	Residual Stress & Distortion	GA
(Mochizuki et al., 2000)	ARC Welding	Complete Path	Residual Stress	Approximation model
(Kim et al., 2002)	ARC Welding	Complete Path	Weld time & Cooling Time	Heuristic search
(Voutchkov et al., 2005)	ARC Welding	Complete Path	Displacements	Surrogate model
(Asadi & Goldak, 2011)	ARC Welding	Complete Path	Distortion	Surrogate model
(Romero-Hdz et al., 2020)	ARC Welding	Complete Path	Deformation	Reinforcement Learning
(Huang et al., 1997)	Spot Welding	Complete Sequence	Deformation	GA
(Xie & Hsieh, 2002)	Spot Welding	Complete Sequence	Deformation & Cycle Time	GA
(Y. G. Liao, 2005)	Spot Welding	Complete Sequence	Deformation Variation	GA
(Segeborn et al., 2011)	Spot Welding	Complete Sequence	Geometrical Variation & Cycle Time	GA
(Wärnefjord et al., 2010a)	Spot Welding	Complete Sequence	Geometrical Variation	Rules
(Carlson et al., 2014)	Spot Welding	Complete Sequence	Geometrical Variation & Cycle Time	Branch and Bound
(Wärnefjord et al., 2010b)	Spot Welding	Complete Sequence	Geometrical Variation	Simulation Experiments
(Aman et al., 2013)	Riveting	Partial Sequence	Residual Stress & Sheet Gap	Neighborhood Search & GA
(G. Liu et al., 2014)	Riveting	Partial Sequence	Initial Sheet Clearance	GA
(G. Liu et al., 2015)	Riveting	Partial Sequence	Initial & Residual Clearance	GA
(Yang et al., 2016)	Riveting	Partial Sequence	Residual Clearance	GA
(Lupuleac et al., 2020)	Riveting	Partial Sequence	Sheet Gap	Mesh Adaptive Direct Search
In this thesis:				
(Tabar et al., 2018)	Spot Welding & Riveting	Complete Sequence	Geometrical Variation	GA, PSO, ACO
(Tabar et al., 2019b)	Spot Welding & Riveting	Complete Sequence	Geometrical Deviation	Rule-Based GA
(Tabar et al., 2020d)	Spot Welding & Riveting	Complete Sequence	Geometrical Deviation	Rule-Based Modified GA
(Tabar et al., 2020a)	Spot Welding & Riveting	Complete Sequence	Geometrical Deviation	Surrogate Modeling
(Tabar et al., 2020b)	Spot Welding & Riveting	Complete Sequence	Geometrical Deviation	Stepwise search algorithm
(Tabar et al., 2019a)	Spot Welding & Riveting	Partial Sequence	Geometrical Variation	Rules, Local Search & GA
(Tabar et al., 2020c)	Spot Welding & Riveting	Partial Sequence	Geometrical Deviation	Surrogate model and PCA
(Tabar et al., 2021)	Spot Welding & Riveting	Partial & Complete Sequence	Relative Displacements & Geometrical Deviation	Stepwise search algorithm

RESEARCH APPROACH

In this chapter, the description and justification of the research approach are presented. A reflection on the structures and methods and their inter-connectivity is presented to justify the results in this thesis. The approach to answering the research questions using the applied research methodology is also provided.

3.1 Background

The focus field of this thesis is within the area of geometry assurance and robust design. This field can be considered to be a subcategory of the design research field.

Design is a set of activities that develop a product from a need to the full realization of fulfillment of this need. This development process is to satisfy users' perceived needs (social or economic) (Blessing & Chakrabarti, 2009). Using this definition of design, product development, which includes the area of geometry assurance, could be merged into the design sciences. Figure 3.1 shows an integrated product and production development platform. The details of the product design, including the geometry assurance elements, such as tolerances and adjusting the operation parameters virtually, are developed simultaneously as the corresponding production system is developed. With the introduction of digital twins for the development processes, design activities can be performed in real-time, improving product and production quality (Franciosa et al., 2020; Polini & Corrado, 2020a; Rosen et al., 2015; Schleich et al., 2017; Söderberg et al., 2017). In such an environment, the development of a product and the realization needs of such product are developed hand-in-hand. This thesis is performed within the Wingquist Laboratory, in which the research process involves parallel development of the research challenge and industrial needs. Eventually, the research idea is generated and a demonstrator is developed. This demonstrator acts as a prototype, and defines the working procedure also used for industrial evaluation. Ultimately, this prototype leads to a product in use. The product is in the form of design specification, product development, consulting, or training services.

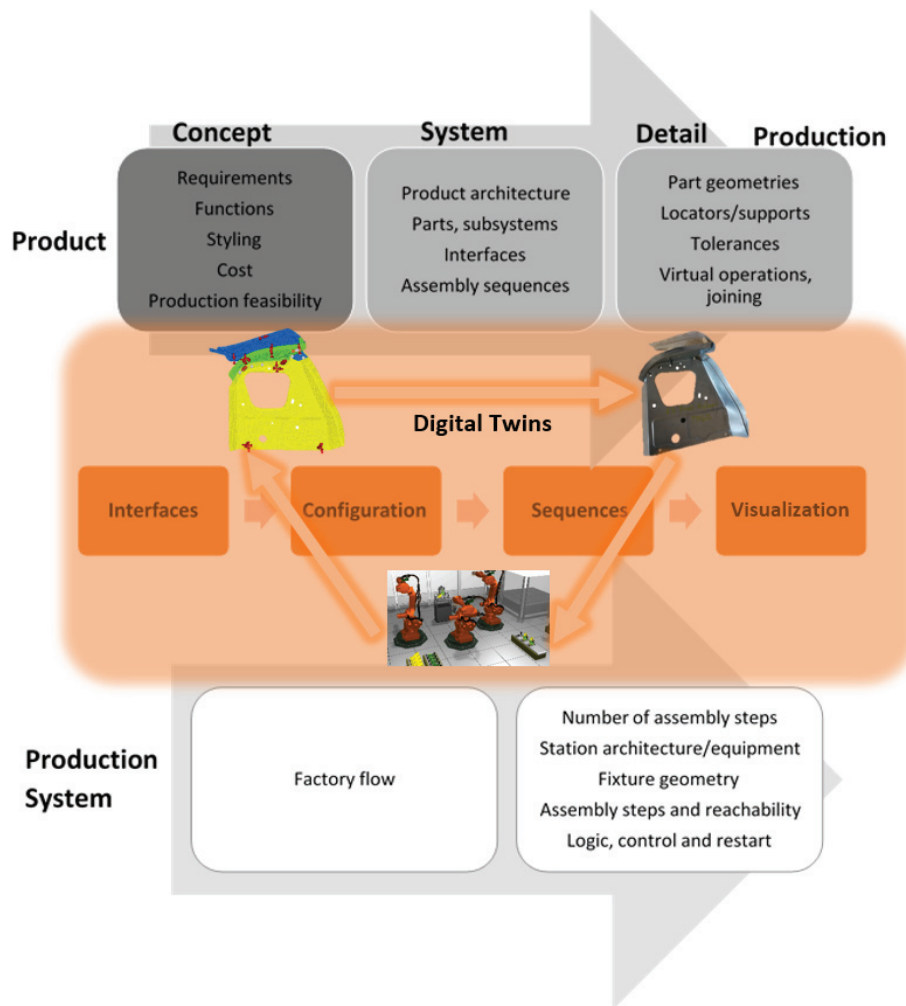


Figure 3.1: An integrated product and production development platform

According to Blessing and Chakrabarti (Blessing & Chakrabarti, 2009), research in the area of design involves the development of understanding and support. For arriving at a more efficient and effective product, which can be defined as the design research goal, understanding and providing support to that product should be tightly coupled. Figure 3.2 is a representation of the design research describing this inter-connectivity.

Different methodologies have been introduced within the design research field. Antonsson has introduced a six-step path to perform successful research in engineering design (Antonsson et al., 1987). These steps are: elucidating the design process by crafting design rule proposals, developing rules, applying the rules, measuring design productivity, evaluating results, and finally refining proposals. Although the process is perceived as straight-forward, it raises uncertainties. The fundamental uncertainties of the rule selection criteria, and the reliability of the sources based on which such rules are generated, are unclear (Reich, 1995).

Hubka and Eder have introduced a more generic two-dimensional perspective of the design science. They introduce design science as deriving information from

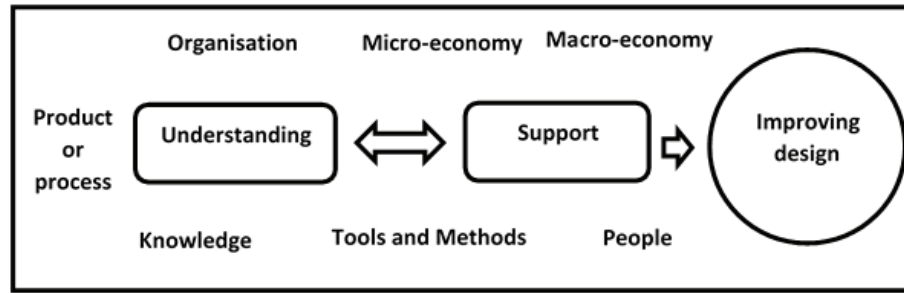


Figure 3.2: Design research: aim objectives and facets of design. Adapted from (Blessing & Chakrabarti, 2009)

natural sciences for utilization by the designers. Design science determines and categorizes the elements of a system. The statements within design science are descriptive or prescriptive, focusing on technical systems or design processes (Hubka & Eder, 1988). They have categorized four basic classes of statements in design science. (1) Theory of the technical systems (descriptive), (2) the know-how of fulfilling requirements in a technical system (prescriptive), (3) descriptive design process statements, and finally, (4) methodology of the design process (prescriptive).

Although different methodologies have been introduced to be applied within design engineering, following a strict set of steps and methods is not practiced. In most of the methodologies proposed, the descriptive and prescriptive design research stages are iterated and evolved during the design process.

3.2 Design Research Methodology

Blessing and Chakrabarti (Blessing & Chakrabarti, 2009) have introduced Design Research Methodology (DRM) as a framework within which to perform design research. According to their definition, a methodology is defined as “*an approach and a set of supporting methods and guidelines to be used as a framework for doing design research*” (Blessing & Chakrabarti, 2009). This framework is intended to provide understanding and support to help to improve the design. The design improvements proposals by DRM is achieved based on the applications of different research methods. The design method is defined as “*sequences of activities to be followed in order to improve particular stages of the design process (task clarification, conceptual design, detail design, etc.), and specific tasks within these stages (e.g., generation, evaluation, etc.)*” (Blessing & Chakrabarti, 2009).

Figure 3.3 is an overview of the DRM. The main stages are research clarification, descriptive study I, prescriptive study, and descriptive study II. At each stage, different methods can be used. Each stage has specific outcomes, from which different deliverables are generated.

As mentioned in the previous section, the DRM stages are connected and are not to be followed necessarily in a specific sequence. Different loops can be applied to different research projects. Since each design research is unique, going through the

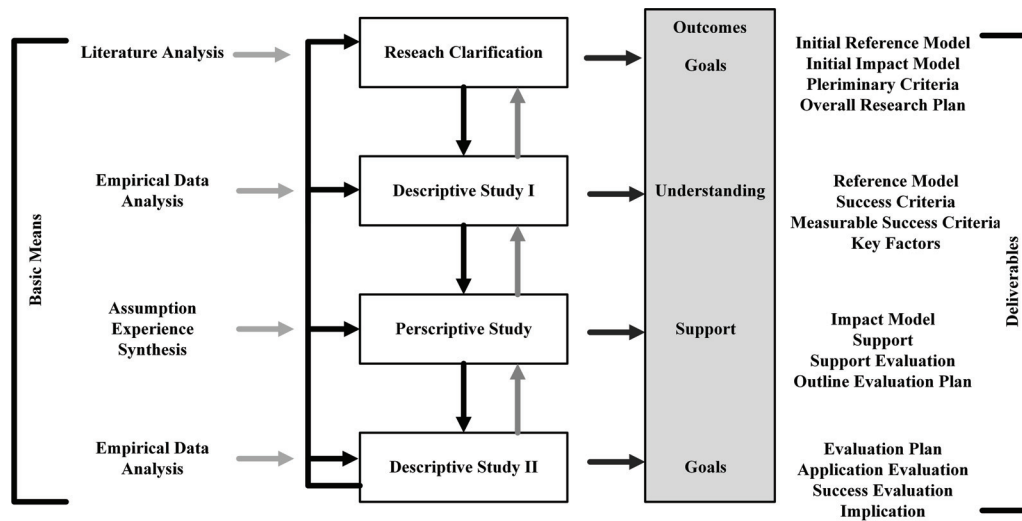


Figure 3.3: Design Research Methodology. Adapted from (Blessing & Chakrabarti, 2009).

stages back and forth will enhance understanding of the product or process under research.

In the research clarification stage (RC), the area of research contribution will be introduced, and the measurable success criteria are being preliminary defined. In the second stage, descriptive study I (DS I), the design's reference model is being developed. Moreover, the key design characteristics, defining the current state of design, are being established. The third stage, prescriptive study (PS), is where the actual support is being developed. From a design development aspect, this stage is where the actual development or improvements for making the products (or processes) more efficient are introduced. This efficiency can be evaluated using the previously defined, measurable success criteria. In the descriptive study II (DS II), the impact model (the improved model) is being implemented into the process and is evaluated with respect to the success criteria.

3.3 Applied Research Methodology

To describe how DRM is used in this thesis, the appended papers are considered to be the overall result of the presented research. Therefore, the following is about the inter-connectivity of each of these publications to the different DRM stages. Moreover, how these results are connected to the individual research questions are also described.

Figure 3.4 is a schematic view of the application of DRM in this thesis. The rounded rectangles are where the comprehensive studies have been conducted, whereas the leaf-shapes are where review-based studies are performed during the specific stage.

This research focuses on designing accurate and time-efficient methods for ana-

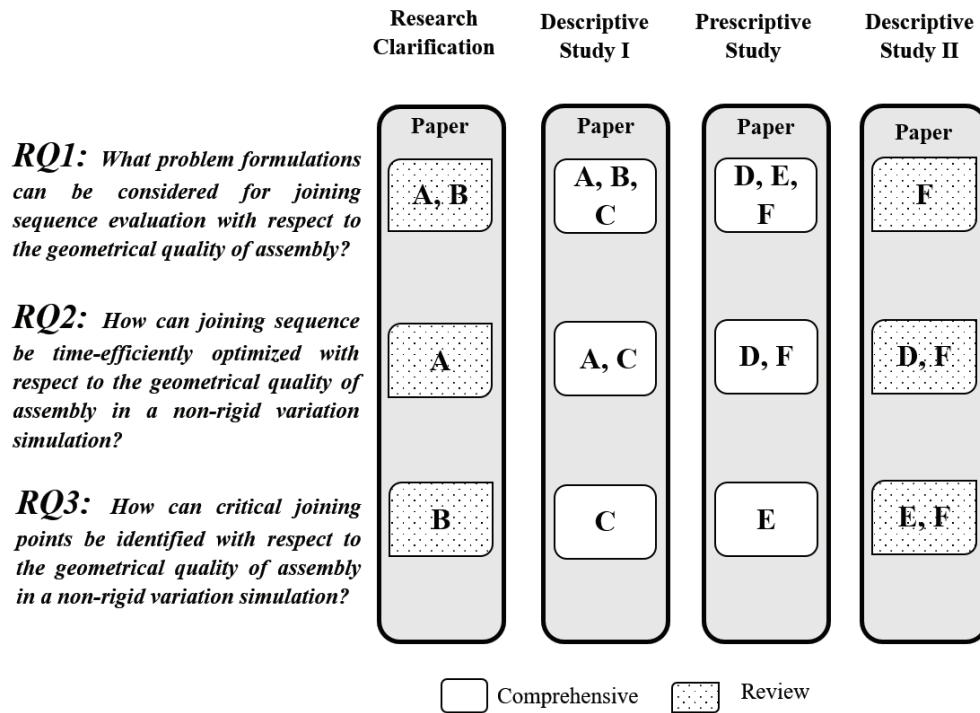


Figure 3.4: Applied Design Research Methodology

lyzing and optimizing the joining sequences for improved geometrical quality. The *accuracy* and *time-efficiency* of the evaluated and proposed methods have been the success criteria of the research. An aspect is developing support to analyze and optimize the joining sequences accurately early in the product development phases and evaluate the improvement potential of the geometrical quality concerning joining sequences. Another aspect of the research is to improve the efficiency of the existing evaluation and verification tools (non-rigid variation simulation) with respect to time, for evaluating and optimizing the joining sequences. The implementation of improvements in an industrial environment within a geometry assurance digital twin context is also considered in this thesis.

The results of this thesis are supporting decision making during the early design and realization (production) phases. The improvements in the optimization and evaluation tools should reduce the time required for decision-making, and reduce the needs for expensive physical testing. Additionally, the support presented (analysis and optimization methods) can be presented as enablers for future implementation. In case of failure in the real-time physical implementation of the supports presented, due to resource limitations, the results are put forward as scientific knowledge for future implementation.

This research has resulted in nine publications, seven of which are published in scientific journals in the area of Mechanical Design and Engineering, Manufacturing Science and Engineering, and Engineering Optimization. Two of the publications are presented at scientifically recognized conferences in the areas of computer aided tolerancing, and advanced manufacturing. From these publications, six have been

chosen to be included in the thesis, contributing to the major results presented in Chapter 4, referred to as Papers A-F. Three of the publications are considered to be supportive elements, yet they are not necessary for following the structure of the thesis, and are referred to as additional publications (AP) 1-3. In the following sections, the association of the results mentioned to different stages of the DRM is presented.

3.3.1 DRM on RQ 1

The first research question, RQ 1, is about identifying the key characteristics of the problem formulation. The pragmatical and the theoretical aspect of the problem, is sought in this question. This study will help formulating the success criteria, required to be achieved for answering RQ 2 and RQ 3. A comprehensive pre-study on the joining sequence optimization is performed in Chapter 2, Section 2.12, and the key assembly process parameters are studied in the research clarification phase. The initial reference models of the previously applied sequence analysis and optimization methods in the literature and industrial practice are established. The outcomes of the RC phase have been the preliminary success criteria, and the research goals of improving the efficiency of the methods used for joining sequence analysis and optimization. A summary of this phase is provided in a literature review of the topic studied in the papers presented.

A field study is also conducted for understanding the industrial application of the joining process used for sheet metal assemblies in the automotive industries. A process map of the experiential approaches for identifying geometry problems in the welding process is also achieved. The outcome of this study resulted in comparing the simulation approaches performed in the industry in Paper A and B.

The theoretical approach for formulating the sequence optimization problem using the EAs is achieved. Through data analysis, the reference model of the industrial and theoretical sequence analysis and optimization methods are analyzed for different assemblies and presented in Paper A, Paper B and AP 1. These studies identified that the need for improved sequence analysis and optimization methods is defined by presenting an *accurate* and *time-efficient* method.

Paper A, and AP 1-2, describe the application of the GA to joining sequence optimization, which has been the theoretical reference model, and evaluates it against the success criteria. Paper B evaluates the industrial approach by which the problem is formulated (the industrial reference model) descriptively. Paper C describes both the theoretical and industrial reference models in the same formulation, understanding the reason for the division between the reference models. This paper helps understanding why a set of joining points is considered to greatly affect the assembly's geometrical quality more in industrial practice.

The prescriptive element in Paper A is the introduction of the rule-based GA as a more time-efficient and accurate method for joining sequence optimization. Paper B compares different industrial approaches and integrates the results of Paper A, application of the GA on the theoretical problem formulation (theoretical

reference model), proposing a method for the accurate and time-efficient analysis and optimization of the sequences, prescriptively. In Paper C, a surrogate modeling approach is proposed evaluating the joining sequences measured against the success criteria and the reference model. Although there are prescriptive elements in Papers A-C, they are not presented as prescriptive outcomes in Figure 3.4. The reason behind this choice is that through interaction between the descriptive and prescriptive phases, the main contributions of the prescriptive elements in Papers A-C are reassessed in Papers D-F.

Paper D presents a new problem formulation (theoretical model) for *accurate* and *time-efficient* joining sequence optimization. This is considered as the impact model of the research, where the actual support (method for joining sequence optimization) is introduced. Papers E and F present a formulation for joining sequence analysis to achieve a reduced problem.

With a review-based study, Paper F demonstrates application of an *accurate* and *time-efficient* non-rigid variation simulation for joining sequence analysis and optimization. This study evaluated the application of the proposed method and formulation concerning the success criteria and compared them to the previously prescribed methods by means of data analysis for two assemblies.

3.3.2 DRM on RQ 2

The second research question, RQ 2, intends to propose a generic method for a complete sequence problem with the formulation identified in the reference model. Given a number of joining points on the assembly, how can the sequence be optimized *accurately* and *time-efficiently*?

From the literature analysis for identifying the optimal joining sequence in the RC stage, the theoretical reference model (GA for joining sequence optimization) is established in the DS I phase. Different algorithms are studied given this formulation of the problem, and the accuracy and time-efficiency of each are analyzed in the AP 1-2 and Paper A. Through these studies, the initial understanding of the behavior of the phenomenon under study was established. From data analysis and simulation experimentation in DS I, Paper C describes how the reference models generated (theoretical complete optimization formulation and the pragmatical reduced problem formulation) vary.

New methods have been prescribed for complete sequence optimization. In the initial PS study, these methods include a rule-based approach using GA in Paper A, and a surrogate modeling approach in Paper C. In Paper D, to achieve an *accurate* and *time-efficient* optimization algorithm, a new step-wise algorithm is proposed. Paper F prescribes a variation simulation method for sequence optimization and has been evaluated according to the success criteria. The result achieved in Paper F is used to perform the sequence optimization. These methods and algorithms are established from the findings in all the previous papers and have created the support and impact model of the research in the secondary PS phase.

The DS II stage requires integrating the optimization and simulation methods presented in Papers D and F, impact models, into a digital twin for geometry assurance. The methods are tested in a digital twin prototype steering the sheet metal assembly process virtually. This stage of the DRM is completed in the future, where the implication of the outcome of the physical applications of this concept is achieved.

3.3.3 DRM on RQ 3

The RQ 3 also requires the RC stage to initiate the study for retrieving an answer. This question intends to answer how reduced problem formulation of the joining sequencing can be achieved. In other words, how can the critical joining points with respect to geometrical quality be identified? This aspect is related to the industrial reference model achieved for RQ 1, where the critical weld points, geometry points, are identified to be set in a specific sequence. Details of the industrial approach by which to identify critical weld points, industrial reference model, is established in the DS I stage, built on the literature and field studies in the RC stage. This approach is evaluated according to the success criteria in Paper B. The theoretical foundation for identifying the critical joining points is also pinpointed in Paper C.

Built on the findings of Paper C, Paper E prescribes a generic method to identify the number and location of the critical weld points. The method is evaluated to comply with the success criteria. This method has been the provided support and the impact model in the PS stage.

With the results presented in Paper F, for efficient non-rigid variation simulation of joining sequences, the results provided in Paper E can be further enhanced for the success criteria *accuracy* and *time-efficiency*. In the initial stages of DS II, the functionalities of the support provided are established. The support provided needs to be further implemented in the Computer-Aided Tolerancing tool, and the feedback from potential users need to be retrieved to complete the DS II stage.

3.4 Methods

The research methodology, DRM, is a logic, connecting all research methods. In other words, it can be defined as a framework for the including methods and research elements. In this section, the methods utilized in the applied DRM are introduced. The methods are connected to the methodology in the order presented in Figure 3.4 in the previous section.

3.4.1 Literature studies

An imperative aspect of the research is clarifying and developing an understanding of the phenomenon under study. In this research, a fraction of the understanding is gained in all the DRM phases through literature studies. All papers presented

include a literature study to introduce the applied tools and further describe the different approaches in previous research.

3.4.2 Field studies

A field study is a method for data collection. In this method, the phenomenon is studied by direct or indirect observation or interview. The data gathered is in the form of notes, videos or images (Karlsson, 2010). This method is mainly used during the research clarification stage. The automotive industry has been studied. Sheet metal forming factories have been observed, and interviews with field experts were performed. The understanding of the physical sheet metal joining parameters and needs has been established. The information regarding the industrial sheet metal assembly simulation approach has been gathered. Industry best practice approaches and tacit manufacturing knowledge for spot weld sequencing have been studied in Papers A and B.

3.4.3 Hypothetico-deductive method

The Hypothetico-deductive method has been considered to guide scientific research (Lawson, 2000). According to Lawson, the method consists of the following six fundamental elements;

1. Raising questions.
2. Generating a hypothesis.
3. Assuming that the hypothesis is correct.
4. Using the process of deduction (if,..., and..., then, ...) to generate the expected results.
5. Conducting experiments and gathering evidence.
6. Concluding

The general hypotheses in the papers presented are;

Paper A states that if the complete optimization problem is formulated with EAs, then the manufacturing knowledge about the assembly can help to initiate the algorithms to achieve accurate results time-efficiently.

Paper B expects to retrieve accurate results by reducing the optimization problem while time is being saved.

Paper C proposes that in every assembly, a small fraction of the complete sequence has significant contribution to the geometrical quality of the assembly. Therefore the sequence of these points should be considered in the sequence analysis.

Paper D hypothesize that identification of the minimum assembly deviation of the fractions of the sequence problem leads to a near-optimal solution minimizing the assembly deviation in the complete problem.

Paper E states that given the information of the sensitivity of the assembly to joining sequences, the accurate number and location of the joints can be identified.

Paper F proposes that given the weld relative displacements in the assembly fixture for a specific sequence, the deformations in the inspection fixture can be estimated accurately and time-efficiently.

3.4.4 Experiment

In accordance with the description of the hypothetico-deductive method, experimenting is part of proving that a hypothesis is accepted or not.

Experiments have been used using numerical simulation to evaluate the hypotheses generated in all the presented papers. The experiment results have been presented in the method evaluation section of the papers presented .

RESULTS

This chapter presents a summary of the results presented in the appended papers. The inter-connectivity between the different results is also discussed in the presented summary.

Before introducing the details of the results, the terminologies used in the content of the results are recollected in Figure 4.1. A complete joining sequence is an enumerated collection of N joining points, in which repetition is not allowed. An assembly with N joining points has, N sequence element associated to it. Each sequence element can include any value from one to N , without repetition. A partial sequence¹ is a collection of sequence elements smaller than N .

The distribution of the results, each paper, over the applied formulation, approach, and methods is provided in Table 4.1. The formulations considered have been the complete sequence optimization, and partial sequence optimization for critical joint identification with respect to geometrical quality. The approaches are divided into black-box, where the objective function details are treated as unknown, and grey-box, where some properties of the simulation model are evaluated. The white-box

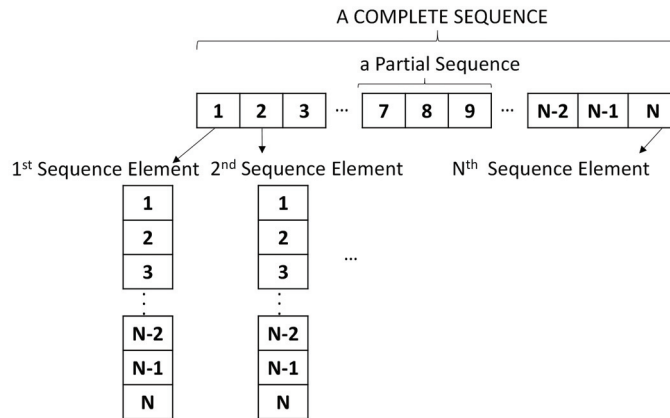


Figure 4.1: Sequence Construct

¹See also Figure 2.16b and 2.16a.

Table 4.1: Distribution of the results based on formulation, approach and method domains

Paper	A	B	C	D	E	F
Sequence Formulation	Complete Optimization	Partial Optimization	Complete Optimization	Complete Optimization	Partial Optimization	Complete & Partial Simulation
Approach	Grey-Box	Grey-Box	Black-Box	Black-box	Black-box	White-Box
Method	Rule-Based	Rule-Based	Surrogate Model	Search Alg.	Surrogate Model & Search Alg.	Surrogate Model & Search Alg.

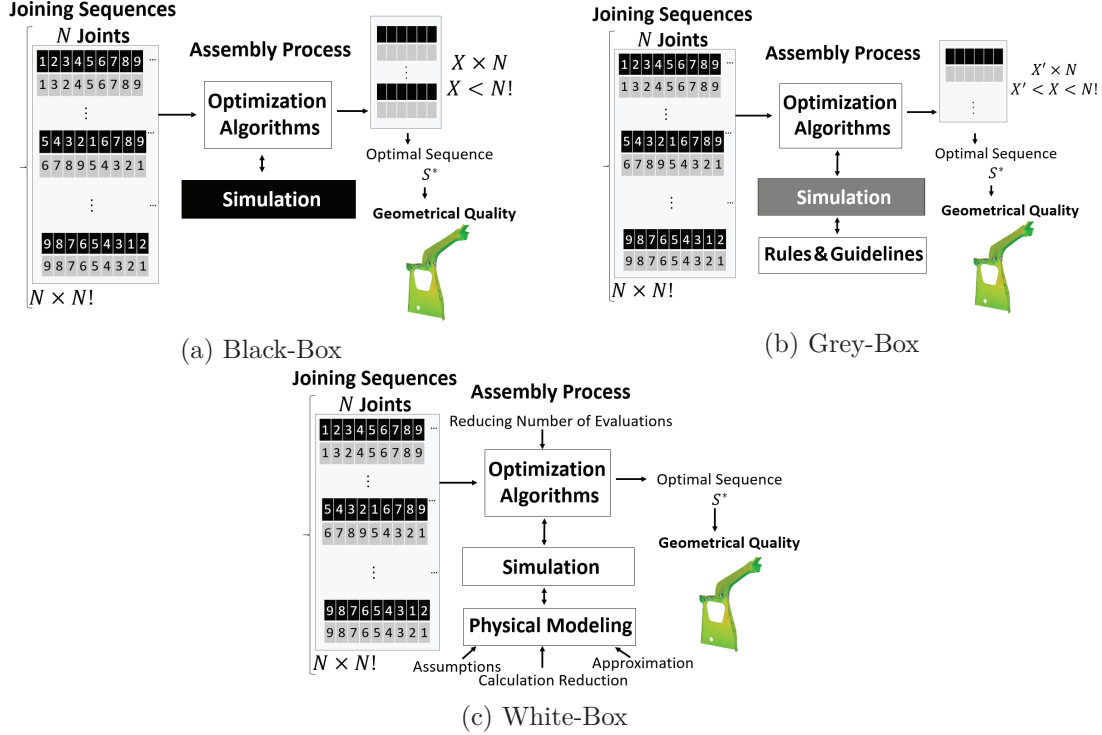


Figure 4.2: Proposed approaches

approach is where the simulation model is targeted directly to reduce simulation time. The overview of the proposed approaches is presented in Figure 4.2. The proposed methods are categorized into rule-based, surrogate model and search algorithm methods. A summary based on the proposed methods and formulation shown in Table 4.1 is provided as follows.

4.1 Rule-Based Joining Sequence Optimization

The joining sequence has shown to have a considerable impact on the final geometrical outcome (Fukuda & Yoshikawa, 1990; Segeborn et al., 2011; Xie & Hsieh, 2002). For solving this problem, previous studies have been focusing on simulation-based optimization using the GA. Several other EAs are also introduced and are shown to perform faster for different problem categories. For research clarification, to investigate the applicability of other EAs on the joining sequence optimization, the

well-known ACO, which is efficient for combinatorial problems (Dorigo & Gambardella, 1997), has been chosen. Moreover, the competitor of the GA for the continuous and combinatorial problems, PSO (Kennedy & Eberhart, 1995; Y. F. Liao et al., 2012), is selected for evaluation and comparison to GA on joining sequence optimization concerning geometrical quality. These algorithms are evaluated on three sheet metal assemblies. Based on the comparisons, it is realized that ACO and PSO can perform faster and more accurate compared to the previously applied GA, depending on the assembly complexity. It is concluded that the advantages of the stand-alone EAs compared to each other are not sufficient for real-time applications in a digital twin. The stand-alone EA algorithms are highly dependent on the quality of the randomly generated initial population. The details of this study are presented in additional publication (AP) 1.

From this study and previous research, Section 2.12, it is identified that simulation-based optimization using EAs and the MIC and contact modeling is time-consuming. Previous research has optimized the sequence, not considering the time aspect. Therefore, a consensus on the GA can be seen in the previous and more recent studies (Huang et al., 1997; Y. G. Liao, 2005; Segeborn et al., 2011; Xie & Hsieh, 2002). All of the studies mentioned have considered a stand-alone GA, in which the initial population is generated by random initiation of feasible sequences. The problem is formulated as finding a complete sequence of N joints, minimizing the objective, which in this thesis is geometrical deviation or variation. From optimization approach perspective, the function of the sequence evaluation with respect to the geometrical quality is considered as a black-box, Figure 4.2a. Ultimately, after generation, and evaluation of a number of sequences, shown with X in Figure 4.2a, the optimal solution is identified. With this approach the population size, and Number of the Function² Evaluations (NFE), X in Figure 4.2a, and, consequently, the optimization time are the critical factors influencing the accuracy of the optimal solution.

Rules and strategies for the selection of the joining points and sequence determination have also been studied separately, Section 2.12. In Paper A, these two approaches have been combined to propose a rule-based algorithm for time-efficient joining sequence optimization of each assembly. Three generic rules for assigning the initial population of the EAs have been introduced as follows:

- Distance to the positioning system
- Initial weld gap
- Recursive weld gap. In this rule, the initial weld gaps are evaluated, and a single weld point is being selected. The selected weld points are welded recursively, and the weld gaps are evaluated.

The details of each rule are presented in Paper A. The EAs can be initiated utilizing the rules presented. Due to the generality and GA's previous applications, this

²The cost function of the optimization, which here is the simulation using MIC and contact modeling.

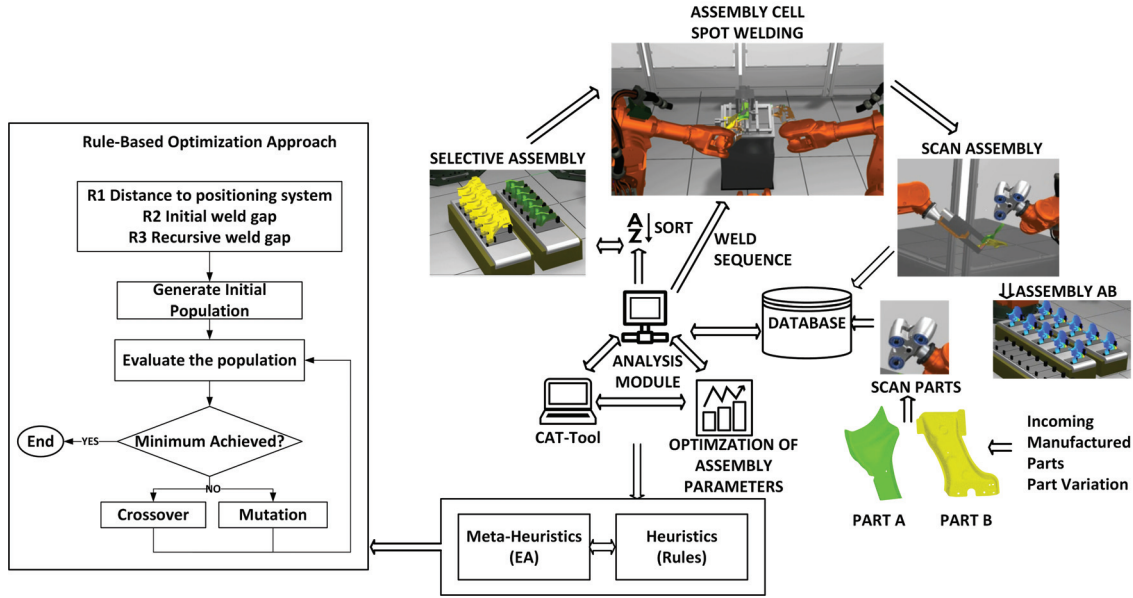


Figure 4.3: The overview of the rule-based joining sequence optimization with the GA

algorithm has been considered for integration with the rules. The sequences derived from the rules are assigned to the initial generation according to population size. For population sizes larger than the number of rules, the best rule mutations are considered for initialization. If the population size is less than the assigned rules, this is compensated by adding the required solutions to the initial population. The overview of the applied approach in the context of the geometry assurance digital twin is shown in Figure 4.3.

The rule-based genetic algorithm (RBGA) is applied to three automotive sheet metal assemblies, and a time comparison has been made with a stand-alone GA. Population sizes 2-100 have been tested, in which for each population size, 1000 trials have been performed. The improvements achieved by the RBGA compared to the stand-alone GA on the three assemblies were analyzed.

In most population sizes, the RBGA has performed faster to reach the global optimum. In population sizes 10 to 11, a considerable improvement of 10 to 80 percent is achieved.

The study has shown that applying the rules to the EAs improves the efficiency of the algorithms with regard to the number of evaluations required to converge to the global optimum. In other words, less optimization time is needed. The rule-based algorithm is further expanded by creating time-efficient model-based rules in AP 2. For utilizing the EAs, it is suggested that a parallel rule-based algorithm is implemented in the concept of the self-compensating assembly line, presented in (Söderberg et al., 2017), for further time reduction.

Main outcome: Introduction of a rule-based evolutionary algorithm for a more time-efficient and accurate joining sequence optimization.

4.2 Rule-Based Critical Joint Identification

Joining sequence optimization is a computationally heavy task. Previous studies have considered solving the complete sequence problem. In the automotive industry, the joining operation is divided into two steps, the geometry cell and the re-spot cell. The most critical points for the geometrical outcome of the assembly are being joined first in the geometry cell. The selection of the geometry joining points has not been rigorously addressed in the relevant literature. In Paper B, by introducing the methods for the geometry joining point selection, a reduced sequencing problem is achieved, and a significant amount of time to optimize the sequence is reduced. Three strategies for choosing geometry points have been introduced and used to reduce the optimization problem size.

In the proposed geometry point identification approach, the location of a pre-defined number of geometry points are initially identified with the support of the three proposed selection methods; the sequence of these points is optimized using the GA. The number of the geometry points is decided by industrial experience. The sequence of the rest of the joining points can be set in any arbitrary sequence. In this case, simultaneous joining simulation has been considered for the rest of the points.

Three strategies for geometry point selection are presented for integration into the above method:

- Distance to the positioning system
- Weld gap
- Weld point relative sensitivity

These selection methods are similar to rules for sequence determination, presented in Section 4.1, with the exception of the weld point relative sensitivity. In this rule, a unit disturbance is applied to each joining point, and an indicator for joint sensitivity is achieved. The details of each method are presented in Paper B. The optimization problem is formulated for finding the optimal sequence of geometry points with respect to Root Mean Square (RMS) of the 6σ variation of all nodes in the assembly. GA is considered for integration in the proposed method, whereas any other evolutionary algorithm can also be used.

The method has been applied to three automotive sheet metal assemblies, and the mean NFE and RMS are reported in 1000 trials. The results are also compared to simultaneous joining. The time comparison is made between a GA on the complete and the reduced problem.

The results show that the selection of geometry points based on the relative sensitivity of the points is superior to other methods, resulting in a set of points with lower impact from re-spots and the lowest error compared to simultaneous welding results. The time comparison also shows that with the method presented, the relative sensitivity geometry point selection, 36% to 93% of the NFE required to optimize the complete problem, can be saved.

Based on the results achieved, it is concluded that the approach of geometry point selection followed by sequence optimization is both efficient in time by reducing the sequence problem size, and accurate achieving marginal errors from simultaneous joining. Generic and numerical approaches to select geometry points can help to reduce the sequence problem size and facilitate reducing the calculation complexity of the joining sequence optimization.

Main outcome: Introducing rule-based methods for identifying the location of a predefined number of critical joining points concerning the geometrical quality, from a set of available alternatives.

4.3 Surrogate Assisted Joining Sequence Optimization

Joining sequence optimization belongs to the category of combinatorial problems, where for each sequence, a non-rigid variation simulation is required to retrieve the assembly deviation, considering part deviations. The standard GA has been applied to the problem in previous research (Huang et al., 1997; Segeborn et al., 2011; Tabar et al., 2018). Rule-based algorithms have been introduced in this thesis to increase the efficiency of the algorithm (Tabar et al., 2019b, 2020d). Moreover, reducing the problem size by selecting the geometry points is shown to be an effective approach for this purpose (Tabar et al., 2019a). In Paper C, an effective approach to map the sequence input to the assembly deviation output is presented. Based on the approach proposed, a black-box function is approximated, and a surrogate model is built to retrieve the assembly deviation of each sequence. The time comparison between the method presented and the standard GA for sequence optimization is highlighted.

The outline of the proposed method is as follows (Tabar et al., 2020a):

1. Generate a sample including all possible combinations of the first s number of sequence elements, $\binom{N_w}{s}!$, (N_w stands for the number of the joining points in the assembly and s represents the initial sequence elements). The rest of the sequence can be established with any feasible alternatives³.
2. Evaluate the sample in parallel, based on available evaluators, to capture geometrical quality.
3. Approximate the input-output function of the sample using an RBF network, and build a surrogate model.
4. Evaluate all sequences using the surrogate model⁴.
5. Retrieve the sequence corresponding to the minimum geometrical deviation.

³For details of how the sample is being selected see Paper C

⁴The surrogate model can be used in combination with any optimization algorithm, in assemblies where all sequences cannot be evaluated.

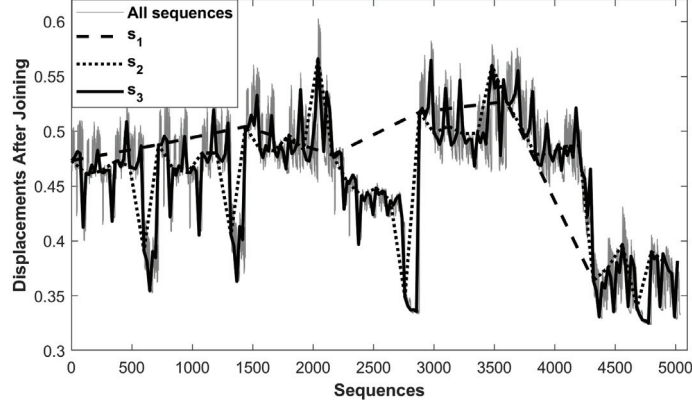


Figure 4.4: The displacement behavior after joining for all the combinations of initial sequence elements s .

6. Evaluate the proposed sequence, using non-rigid variation simulation, to verify the outcome.
7. Refine the surrogate model with more sample points, and repeat steps 2-6.

For increased accuracy of the models, the number of sample points can be increased. The method has been applied to three automotive sheet metal assemblies, and accuracy and time comparisons to the GA have been performed.

The results provide that the sequence of the initial sequence elements are defining the geometrical outcome of the assemblies. Figure 4.4 depicts the displacements after joining for different number of initial sequence elements, in an assembly with seven weld points. In s_1 all the combinations of the first sequence elements are evaluated. In s_2 and s_3 , all the combinations of the first two, and three sequence elements are evaluated, respectively. Increasing the number of the initial sequence elements, and evaluating all of their combinations, enhances the accuracy of the approximation. The surrogate models are then built, based on such samples. This evaluation provides the sensitivity of the assembly with respect to the joining sequences.

It has been shown that the proposed surrogate assisted approach is capable of providing sequences with marginal errors from the global optimum. For time comparison, the surrogate-assisted method is advantageous compared to the standard GA, due to its ability to parallelize the method. It has been shown through the application of the proposed method, depending on the number of evaluators used, that a considerable time improvement can be achieved compared to a standard GA. The method has established a niche for future studies on sequence optimization and identifying the critical joining points time-efficiently based on simulations. The results achieved in Paper C established the foundations for the results presented in Papers D and E.

Main outcome: Describing the behavior of the joining sequences with respect to the geometrical quality of the assembly. Proposing a surrogate assisted approach to optimize the joining sequences, time-efficiently and accurately.

4.4 Rapid Joining Sequence Optimization

Previous research has evaluated the applications of the GA on the joining sequence optimization problem. In Paper A, it has been shown that the GA is dependent on a large number of evaluations using a non-rigid variation simulation, depending on the internal parameter setting. These parameter settings require extensive evaluation time for solution space exploration (Tabar et al., 2019b). In Paper C, it has been shown that the initial sequence elements, set in the sequence, are defining the behavior of the displacements with respect to the joining sequences in a sheet metal assembly (Tabar et al., 2020a). The optimal choices of the initial sequence elements position a solution in a near-optimal space. In Paper D, a state-space search algorithm is proposed with which to explore the sequence elements stepwise and to accurately and time-efficiently minimize the assembly deviation. The outline of the presented algorithm is as follows (Tabar et al., 2020b):

1. Generate all possible complete sequences, Figure 4.5, Step 1.
2. Evaluate all possible alternatives of the primary element(s) in the sequence to capture assembly deviations. In Figure 4.5 Step 1, the sequences shown by thick lines are evaluated.
3. Find the sequence with minimum assembly deviation.
4. Set the primary element(s) of the sequence accordingly. The element illustrated with double circles represents the determined sequence element, Figure 4.5 Step 2.
5. Generate the updated set of sequences with the determined element(s) and all combinations of the next sequence element(s), Figure 4.5 Step 2.
6. Evaluate the new sequences to find the minimum assembly deviation.
7. Set the next sequence element(s), Figure 4.5 Step 3 .
8. Iterate until the complete sequence has been established, Figure 4.5 Step 4.

The overview of the state-space search approach for an example with 4 joints is shown in Figure 4.5. In this example, all possible alternatives of the sequence elements are evaluated one-by-one, at each step, until the complete sequence has been determined.

The overall approach is creating the sequences and calling the non-rigid variation simulation to evaluate the sequences generated. The proposed algorithm is evaluated on three sheet metal assemblies. The optimization steps using the one and two primary elements for the three assemblies are shown in Figure 4.6. The algorithms' time-efficiency and accuracy are compared to the standard GA, the rule-based GA presented in Paper A, and the PSO, previously applied in AP 1. The combined GA and PSO hybrid algorithm and the exhaustive search have also been included in the comparison. The comparisons show that the stepwise approach proposed

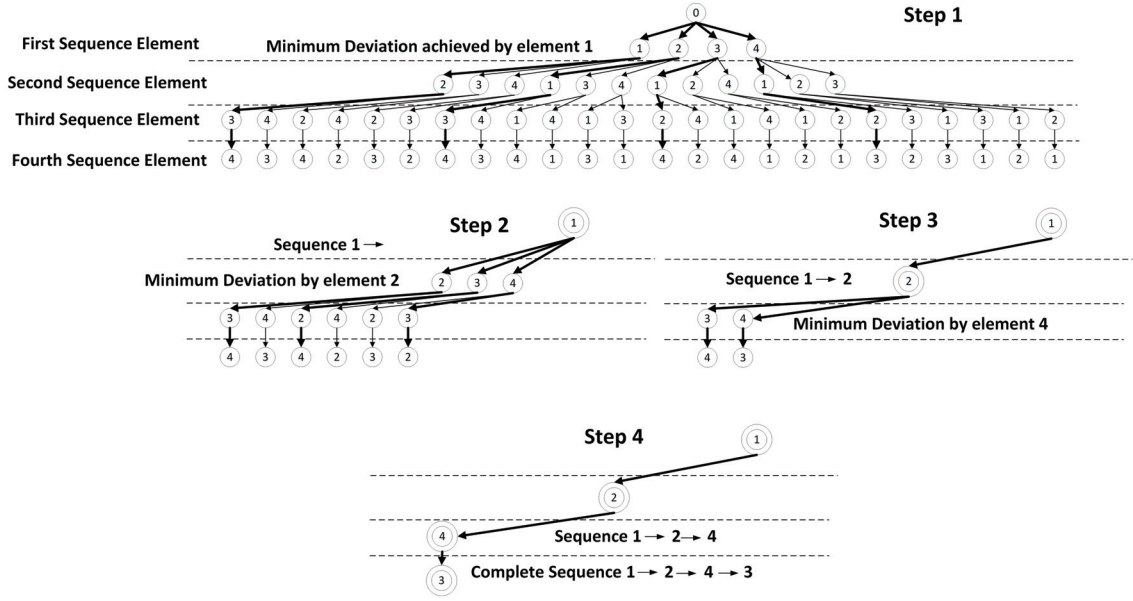


Figure 4.5: The state-space search approach on an example with four joints

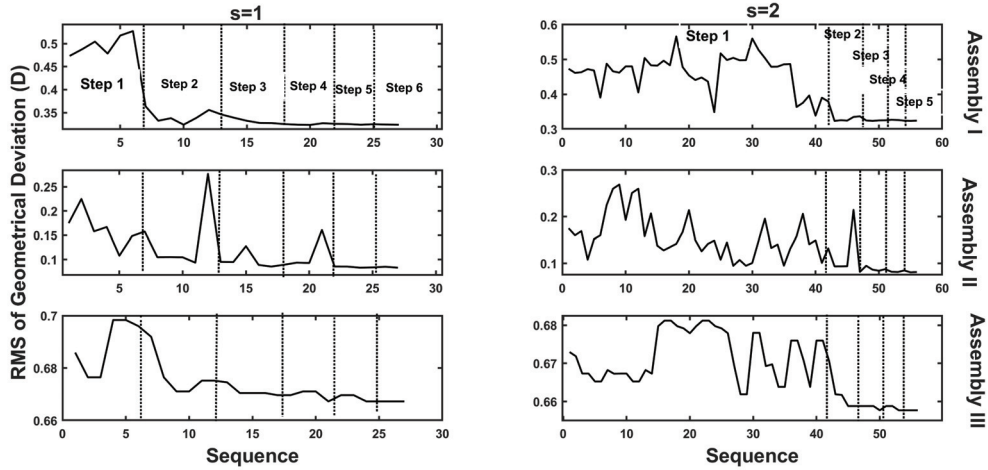


Figure 4.6: The optimization steps using the proposed stepwise algorithm (Tabar et al., 2020b)

reduces the optimization time drastically compared to the previously introduced population-based algorithms while reaching the global optimum in all three sheet metal assemblies. A comparison of the sensitivity of the population-based algorithms to the internal parameters, as opposed to the stepwise algorithm in 100 trials, is provided in Figure 4.7. The proposed algorithm does not require any additional parameter setting, leading to time savings. Therefore, the proposed algorithm is well-suited for being integrated to the concept of the self-compensating assembly lines (Söderberg et al., 2017), thereby minimizing assembly deviation by rapidly providing the optimal joining sequence.

Main Outcome: Proposing a deterministic state-space search algorithms for

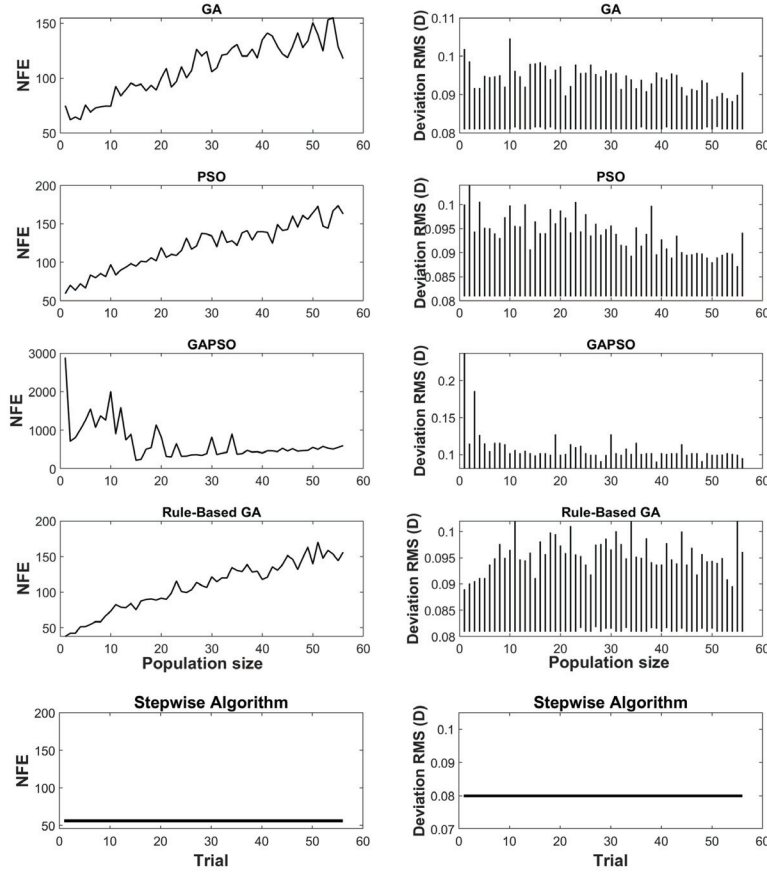


Figure 4.7: Sensitivity of the applied algorithms to interval parameters. Adapted from (Tabar et al., 2020b)

rapid and accurate joining sequence optimization.

4.5 Accurate Critical Joint Identification

Paper B presented a rule-based approach for the identification of a predefined number of the geometry joining points. The location of these points is discussed, and their sequence is optimized successively (Tabar et al., 2019a). In Paper C, it is identified that the initial sequence elements assigned to the sequence are critical to sequence optimization. Based on the definition of the geometry points, these points determine the geometrical quality of the assembly. The need for a generic approach to identifying the accurate number, location, and their sequence is evident. In Paper E, a method for identifying the number and location of the critical joining points, and their sequence is identified (Tabar et al., 2020c). The method describes the contribution of sequence elements to the geometrical variation among joining sequences.

Initially, a black-box surrogate model presented in Paper C is built to model sequence responses. Based on the surrogate model response, sequence data is divided into intervals. Each interval's sequence elements are analyzed to identify the common

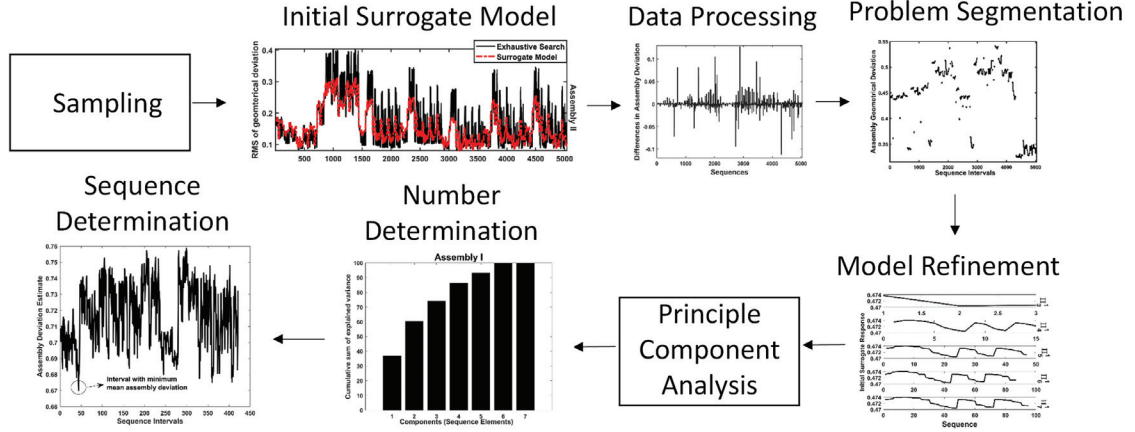


Figure 4.8: The overall approach of identifying number and sequence of critical joints

trends in the sequence elements' appearance. New data sets are generated, evaluating additional sequences at each interval. Updated black-box SVM models are built with new data sets for each interval. These models are used to estimate the geometrical deviation of the sequences situated in each interval. Apart from accuracy, the other advantage of this data division is that each interval's input data is much smaller than all sequences where the data have grown factorially. Therefore, the models can be built in a shorter time and parallel to one another.

An explanatory data set is needed to identify the number of the sequence elements contributing the most to the geometrical variation among the sequences. In Paper C, it has been shown that the initial triplets of the sequence ($s = 3$) approximately reveal the range of assembly deviation for all sequences. This triplet's position in the sequence can be cycled to cover all sequence element positions. Now having accurate surrogate models for each sequence interval, the data set is evaluated and the geometrical deviation after joining is approximated.

Such a data set can capture the significant differences between the sequences and the minor changes in the deviation. To identify which elements of this data set contribute the most to the geometrical deviation, a PCA analysis is performed. With the help of this analysis, the number of critical joining points that satisfy the arbitrary geometrical requirements specified on the assembly can be identified. The overview of the proposed approach is presented in Figure 4.8.

The method is applied to three sheet metal assemblies. The number of critical points, their location, and their sequence are determined. A comparison to the previous weld gap sensitivity approach presented in Paper B, (Tabar et al., 2019a), is made. The results indicate that a small fraction of the sequence elements, critical weld points, determine more than 60% of the variation caused by joining sequences (Tabar et al., 2020c). The accuracy comparison performed with the previous approach indicates that the proposed SVM and PCA approach can identify the number, location, and sequence accurately. The previous gap sensitivity approach is based on a predefined number of joining points and has larger error ranges than the approach

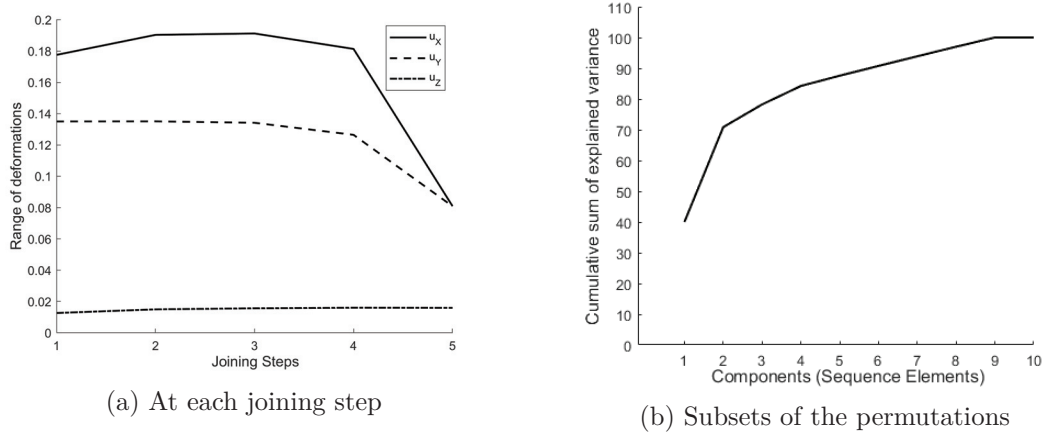


Figure 4.9: Diminishing returns at each joining step

proposed.

As pointed out in Section 2.10, the differences in the range of the displacements at each joining steps are non-monotone. In Figure 4.9 (a), this aspect is visualized. The ranges of the deformations in three directions u_x , u_y , u_z , for all the joining steps, in an assembly of five joining points, are observed. In u_x , this aspect is visually apparent, where at joining step 2, the range increases, and after that, the range decreases. This behavior can also be related to the diminishing returns of increasing the number of sequence elements at the latter joining elements in the permutations. In Figure 4.9 (b), this aspect is visualized. The sum of the explained variances of the deformation after joining by adding sequence elements to the permutations decreases. Therefore, the gain from including more sequences using the combinations of the ending joining sequence elements is smaller.

Consider all permutations of joining points 1 to n , Ω , where $n = 5$. The sets⁵ X_1 to X_4 are subsets of Ω , including all possible combinations for first to fourth elements, respectively. The set function is the range of the deformations after joining in an assembly. This function is shown by means of the area around each subset X_1 to X_4 , in Figure 4.10 (a)⁶. With the definition of sub-modularity provided in Section 2.10, the following holds for the presented example:

$$f(X_1 \cup X_3) - f(X_1) \geq f(X_2 \cup X_3) - f(X_2), \quad X_1 \subseteq X_2 \quad (4.1)$$

The left hand side of the non-equality statement is visualized in 4.10 (b), and the right hand side in (c). The problem of finding a subset of the joining points set in a sequence that maximizes the range of the deformations is an NP-hard optimization exhibiting sub-modularity with a non-monotone function. As presented in Paper D, the local search approach with a greedy formulation shown to be efficient for solving this problem. This formulation of the problem complements the findings in Paper E

⁵In the context of order of the joining points multisets are applicable.

⁶The area for each sequence subset is only considered to visualize the function, as it can be more tangible compared to scalar deformation range output of the set function.

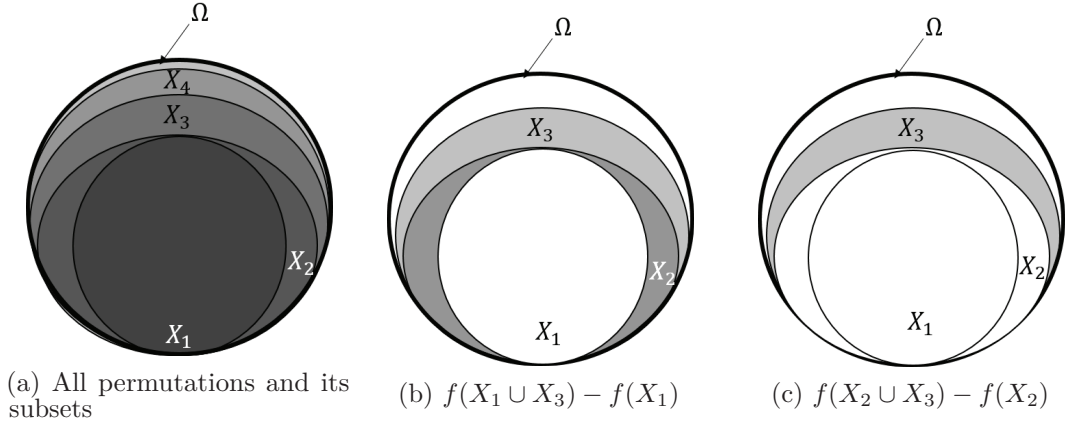


Figure 4.10: Sequence subset sub-modularity

with respect to scientific rigor, describing the essence of the subset selection problem, and its application to joining sequence analysis and optimization.

Main Outcome: Introducing the joining sequence optimization as a subset selection problem. Proposing a generic approach for identifying the number, location, and the sequence of the critical joining points with respect to geometrical quality.

4.6 Efficient Joining Sequence Simulation

Joining sequence optimization concerning the geometrical quality is a combinatorial problem with an expensive objective function. The MIC and contact modeling method are used to retrieve the assembly geometrical outcome after joining considering the part variation in non-rigid variation simulation. In Papers A, C, and D, methods to identify the optimal sequence with a reduced number of evaluations using the complete non-rigid variation simulation are introduced. Joining sequence optimization is depending on the evaluation of each sequence input to the simulation method. Faster simulation methods for evaluating each sequence outcome are desired for further time reduction in sequence analysis and optimization. In Figure 4.2 (c), this approach has been visualized. The details of the physical modeling necessary for simulation is explored.

The MIC and contact modeling simulation method is based on successive sensitivity matrix updates after each assembly step. After the assembly has been joined, it is typically released from the assembly fixture and placed in an inspection fixture. In the non-rigid variation simulation using MIC and contact modeling, the spring-back calculation in the inspection fixture is a time-consuming step. In Paper F, an efficient joining sequence simulation in non-rigid variation simulation is proposed.

The simulation method proposed is based on joining relative displacement evaluation in the assembly fixture. Through correlation analysis, it is identified that the outcome of the assembly in the inspection fixture is significantly correlated to

the relative displacements of the joints. To identify the optimal sequence for the whole assembly in the inspection fixture, the RSS of the relative displacements in the assembly fixture only needs to be evaluated. Using this approach, the spring-back calculation in the inspection fixture has been bypassed (Tabar et al., 2021).

The RSS of the relative displacements describes the whole assembly's behavior with respect to the sequences. However, such a measure cannot describe the behavior of each assembly node. Evaluating each inspection point (node) requires a model fit to the direction and magnitude of the joining points relative displacements. Based on the findings in Papers C-E, the SVM models are built to map the relative displacement of the joints to the deviation in the inspection point, and the sequence optimization is performed stepwise.

The proposed simulation method is applied to two sheet metal assemblies, and the sequence optimization is performed for the whole assembly and the inspection point. The accuracy and time comparisons are performed to the complete non-rigid variation simulation. The results show the optimization for the given measure of joint relative displacement results in identical sequences with the RMS of the magnitude of the displacements of all the assembly nodes in the inspection fixture, whereas 30% less simulation time is required. The comparison of the inspection point deviation optimization indicates that results achieved with the proposed method have marginal errors compared to complete simulations whereas the simulation time is reduced by 23%. The results indicate that the joining sequence can be simulated accurately and time-efficiently in the assembly fixture, enabling real-time evaluations and optimization of the joining sequences in the concept of the self compensating assembly lines presented in Section 1.1.4.

Main Outcome: Proposing a time-efficient and accurate non-rigid variation simulation for analyzing the geometrical quality with respect to the joining sequences.

4.7 Results in the Geometry Assurance Context

Based on the summary of the papers, the results can be positioned in the geometry assurance context.

Figure 4.11 locates the results based on the geometry assurance activities performed during the product development phases. In the concept development phases, for identifying the hot-zones of the assembly, which is influenced the most by the joining sequences, a sensitivity analysis can be performed, based on the findings in Paper C. This analysis can be followed up by determining a suitable objective for sequence optimization. Methods for joining sequence optimization for improved geometrical quality are proposed and can be performed based on historical data on the fabricated components, Paper A, C, and D. The critical joining points with respect to the geometrical quality can be identified, facilitating the assembly process balancing, Paper B, E. Finally, in the production phase, the findings in Paper D

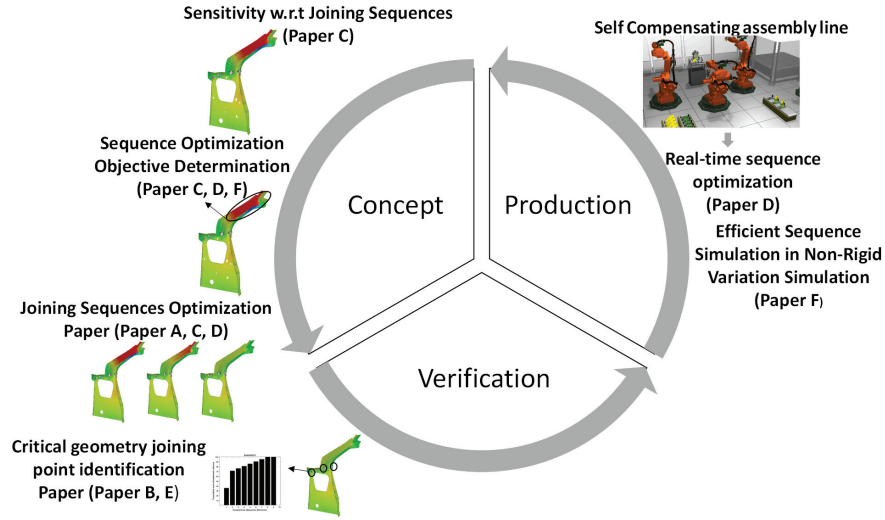


Figure 4.11: Results in the Geometry Assurance Context

and F enable real-time analysis and optimization of the joining sequences within the geometry assurance digital twin, for a self compensating sheet metal assembly line.

4.8 Thesis Results Summary

The results presented are categorized into time-efficient and accurate joining sequence optimization, identifying the critical joining points concerning geometrical quality, and non-rigid variation simulation time reduction. In the following, a summary of the findings in each category is provided.

- A more time-efficient joining sequence optimization using a rule-based method and a grey-box approach, Figure 4.2b, Paper A. Using surrogate models to approximate the deformation of the assemblies accurately with respect to the sequences, reducing the number of evaluations, using a black-box approach, Figure 4.2a, Paper C. Rapid sequence optimization for implementation in a digital twin for geometry assurance, using a black-box approach, Paper D.
- Rule-based methods for identifying the location of the predefined number of critical joining points in the assembly with respect to geometrical quality, using a grey-box approach, Figure 4.2b, Paper B. Accurate identification of the number, location, and sequence of the critical joining points concerning the geometrical quality, using a black-box approach, Figure 4.2a, Paper E.
- Reducing the evaluation time needed for non-rigid variation simulation of joining sequences, using a white-box approach, Figure 4.2c, Paper F. This time-reduction reduces the analysis and optimization time in a digital twin for real-time geometry assurance of sheet metal assemblies.

Real-time optimization and analysis of the joining sequences in a digital twin for geometry assurance of the sheet metal assemblies is achievable by, firstly, reducing the number of the performed simulations, and parallel evaluations, addressed in Papers A-E. Secondly, by reducing the simulation time required for each evaluation of the geometrical quality addressed in Paper F.

DISCUSSION

This chapter answers the research questions based on the results presented and the papers appended. The scientific and industrial contribution of this research is outlined. The validation and verification discussion are also provided.

5.1 Answers to the research questions

The answer to each research question is presented in the following sections.

5.1.1 Answer to RQ 1

What problem formulations can be considered for joining sequence evaluation with respect to the geometrical quality of assembly?

Geometry dependent rule-based approaches for spot welding sequence evaluation and assembly process planning have been studied in the previous research. Example of these approaches are direction based approaches and heuristics outlined in Section 2.12. Guidelines for identifying the critical weld points have also been addressed; spreading the points and distance to the locator are among these guidelines. Extensive physical experiments and tacit assembly process knowledge are needed to determine the joining sequence in an assembly from this perspective. Based on the literature review, Section 2.12, the majority of the studies have considered complete sequence optimization for the assembly geometrical deviation, using FEM, search methods and EAs.

Based on the results, two primary formulations of the problem are identified.

1. Complete sequence optimization with respect to geometrical quality:

There are two main approaches considered in this formulation. First, the objective function of the optimization is considered to be a black-box, and meta-heuristics are applied to find the optimal solution. The optimization time and accuracy aspects are often not addressed. Second, the grey-box

approach, in which, experiments are performed based on the FEM simulation, and heuristic methods are developed. In the black-box approach, the EAs are used to optimize the sequence of all the included joining points in the assembly. This formulation has been evaluated using a black-box approach in Papers C, D, AP 1, and with the help of a grey-box approach in Paper A and AP 2. Papers A, C, D, and AP 1-2 evaluate the EAs and compare them to the proposed methods. In Paper D and AP 1, the comparisons between different EAs using this formulation are provided. Papers C-D compares this formulation solved with EAs against other optimization techniques, namely surrogate modeling and a search algorithm. Paper F presents another approach, in which the objective function is considered as a white-box, and the physical-modeling aspect is manipulated to evaluate the assembly geometrical deviation for complete sequence optimization time-efficiently.

2. Identification of the critical joining points on the assembly with respect to geometrical quality:

Identification of the most critical joining points leads to a reduced sequencing problem. In this formulation, a subset of the available joining points is chosen to be joined first. This implies a sequence between the subsets and a sequence inside each subset. The same black-box and grey-box approaches are considered in this formulation, similar to the previous formulation. Meta-heuristics and heuristics are among the applied methods. Paper B, using a grey-box approach, evaluates the rule-based approaches and heuristics for critical joint identification, i.e., subset selection. This is followed by sequence optimization using a black-box approach inside each subset. Paper E studies the identification of the number, location, and the sequence of the critical joining points in the assembly. The subsets are selected considering their internal sequence using a black-box approach by means of the surrogate-assisted and the PCA methods outlined. The white-box approach proposed in Paper F can be used to evaluate the geometrical quality of the assemblies using any of the formulations above.

5.1.2 Answer to RQ 2

How can joining sequence be time-efficiently optimized with respect to the geometrical quality of assembly in a non-rigid variation simulation?

EAs are proposed in the literature, yet time requirement and the accuracy are not discussed. Combining the heuristics methods and meta-heuristics improves the efficiency of the population-based algorithms dealing with this problem. This interaction helps to shift the randomness of the algorithms to near-optimal solutions in the initialization stage. Moreover, the pure black-box approach of using meta-heuristics on this problem changes to a grey-box approach, in which model-dependent solutions are introduced to the algorithms. The time-efficiency and accuracy of the results achieved increase, as a consequence of this interaction, on the joining sequence optimization problem. Paper A presents a new rule-based genetic algorithm using this approach. The algorithm showed to provide the optimal sequence time-efficiently

compared to the previously applied standard GAs. This approach is further enhanced by introducing a method to generate rule-based sequences corresponding to minimum contact displacements in AP 2. The performances of different EAs on the problem are also compared in Paper D.

Although the rule-based approaches proposed are time-efficient compared to standard EAs, a considerable fraction of sequences must be evaluated with the non-rigid variation simulation approach to identify the optimal sequence. The reason is that these algorithms rely on a population of solutions to converge. These populations are randomly assigned in standard EAs. Therefore, in Paper C, a surrogate-assisted approach is introduced, reducing the evaluation time required to propose a sequence resulting in the assembly's minimum geometrical deviation. Paper C using a black-box approach shows that the initial elements of the joining sequence define the sensitivity of the assembly with respect to geometrical quality. The understanding of this property enabled proposing the efficient sampling approach of evaluating all the combinations of the initial sequence elements. This perspective is further developed in Paper D. From Paper C, it is known that the objective function is evaluated for initial elements, with a complete sequence set on the solution. Given this knowledge, in Paper D, the sequence problem space is explored stepwise for different sequence elements using a greedy method. The stepwise method proposed has shown to be deterministic and time-efficient compared to the previously proposed EAs, requiring a minimum number of evaluations by the non-rigid variation simulation. Furthermore, the stepwise method has shown to be accurate, identifying the optimal sequence improving geometrical quality.

In all above papers, for time-efficiency, a method is sought to reduce the number of evaluations with non-rigid variation simulation. In Paper F, the simulation is considered to be a white-box where all inputs, outputs and internal processes are observed. It is identified that the main cause of retrieving different geometrical quality by joining sequences is the relative displacements in the joining point, before and during the assembly process. Calculating these relative displacements in the assembly fixture is less time-consuming compared to the complete simulation. Typically, to evaluate the outcome of a joining sequence, the spring-back of the assembly is calculated in an inspection fixture. However, the relative displacements of the joining points only need the assembly fixture. With this evaluation, a considerable fraction of the simulation time can be bypassed. Using this simulation in combination with the proposed algorithms leads to time-efficiency while maintaining the accuracy criteria for the retrieved optimal results.

5.1.3 Answer to RQ 3

How can critical joining points be identified with respect to the geometrical quality of assembly in a non-rigid variation simulation?

A subset of joining points need to be chosen from a set of available alternatives, acting as the assembly's critical joining point with respect to geometrical quality. Therefore, a partial sequence problem needs to be identified and solved to capture the

major effect of the joining sequences on the geometrical quality. This partial sequence problem formulation is achieved by the rule-based selection methods proposed in Paper B. Among the rules investigated, the joining gap sensitivity has shown to be a consistent rule among the tested reference assemblies. Three rules are proposed for selecting the geometry points, the subset, and the sequence of these points is optimized using the GA.

Although the rule-based selection approach presented in Paper B is consistent, the number of critical points is predefined. Given that joining sequences can be evaluated time-efficiently, the variance of the geometrical deviation with respect to each sequence element needs to be evaluated to determine the size of the subset. In Paper E, the accurate number of critical joints is identified using the PCA approach proposed. The approach is based on the findings in Paper C, where a surrogate-assisted approach is used to evaluate the sequence outcomes accurately. Moreover, from the findings in Paper E, it is identified that the joining sequence subset selection to maximize the range of the covered deformation by each sequence element exhibits the properties of a sub-modular set problem with a non-monotone set function. In other words, this problem can be solved with the stepwise algorithm presented to time-efficiently determine a subset that maximizes the range of the deviations covered among the sequences in each subset. Such an approach can complement the critical joining point identification problem formulation providing the sensitivity of each sequence element, helping to define the threshold needed to set the number of the critical points.

Paper F unveils the potential of the simulation approach for identifying the initial sequences to be considered for partial sequence evaluation. Knowing that the cause of geometrical variation concerning the sequences is the relative displacements in the joining points before and during the assembly, the proposed optimization methods, can be performed with respect to this objective. This approach enables a time-efficient critical joining point identification.

5.2 Research Contribution

The research presented holds both scientific and industrial relevance. These two levels of relevance correspond to the characteristics of applied sciences, i.e. design and engineering, where a tangible application of the scientific approach is developed. These two aspects are discussed below.

5.2.1 Scientific contribution

The scientific contribution of this thesis involves increased knowledge about the joining sequence parameter and its effect on the geometrical outcome and computational efficiency to find an optimal solution. This contributed knowledge is as follows:

- Evaluation of different optimization algorithms on the joining sequence problem with respect to the success criteria addressed in Papers A, B, D, AP 1-2.

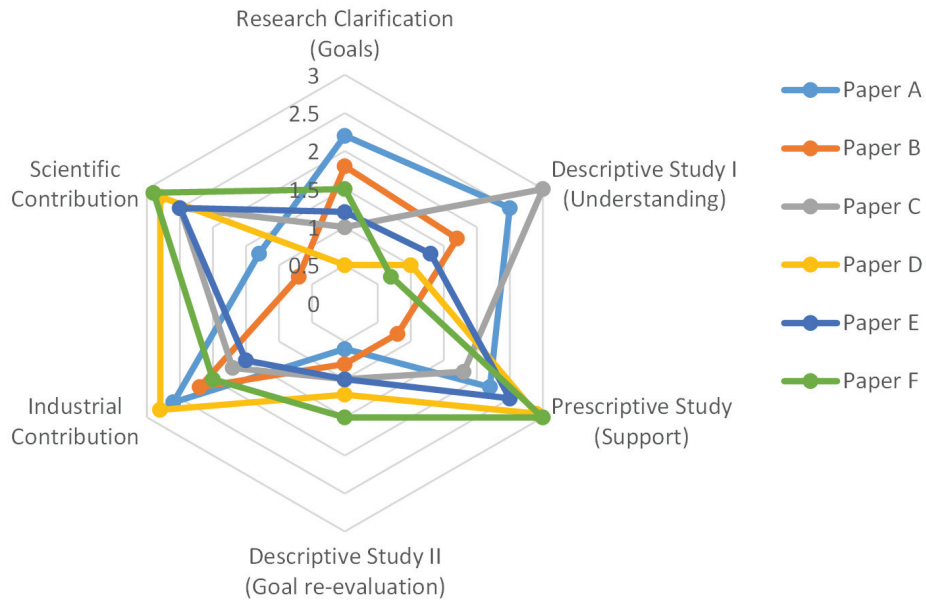


Figure 5.1: Overview of the impact of the research presented with regard to methodology and contribution

- A rule-based optimization approach for increasing the efficiency of the reference model algorithms, population-based algorithms, to solve the joining sequence optimization problem is developed, Papers A, AP 2 and B.
- The essence of the behavior of the joining sequences are derived, Paper C.
- The ultimate formulation of the joining sequence optimization problem is provided, Paper D.
- Efficient methods with respect to the success criteria are introduced, solving the joining sequence problem with proposed formulations, Papers D, E.
- Based on the problem formulation properties, the categorization of the partial sequence optimization problem is introduced, Paper E.
- The cause of the geometrical variation with respect to joining sequences are identified, Paper F.

The body of the contributed knowledge lies inside the scientific field of geometry assurance and robust design in the engineering and technology scientific field. Figure 5.1 aims to provide an overview of the impact of the results, i.e., each paper, in the context of design research methodology and scientific and industrial relevance. The impact of the results is on descriptive and prescriptive stages, whereas the results that are in the secondary descriptive studies have a larger scientific contribution impact.

5.2.2 Industrial contribution

The industrial contribution of this thesis corresponds to the application of the proposed scientific methods into the product development cycle of any industry dealing with joining sequence evaluation. This proposed method can be implemented in different perspectives:

- Providing support to evaluate the sensitivity of the assembly to joining sequences, Paper C.
- Providing support to identifying the critical points affected by joining sequences, Papers B and E.
- Proposing an optimal joining sequence with respect to the geometrical quality objective. This is achieved by integrating the proposed optimization methods into CAT tools, Papers A, D.
- The proposed scientific approaches help to integrate joining sequence parameter into the geometry assurance digital twin concept to improve the geometrical quality, Papers A, D, E.
- A time-efficient non-rigid variation simulation to evaluate joining sequences, Paper F.

Papers A and B are derived from the established heuristics in industry for dealing with joining operations or assembly processes; therefore, the industrial contribution impacts of these results are relatively large compared to their scientific contribution, Figure 5.1. Papers C-F are in the initial phases of the second descriptive study stage; therefore, their industrial contribution impact is relatively minor compared to the scientific contribution. However, the results in Papers D and F in the prescriptive study have shown the potential for the straight-forward applications in the CAT tools used in industry for geometrical quality evaluation. Thus, these results hold larger industrial impact compared to Papers C and E.

5.3 Evaluating Research Quality

This thesis is based on the research conducted within the DRM framework, including research clarification, descriptive and prescriptive studies. The research aims to build knowledge and understanding of the effect of the joining sequences on geometrical quality and provide support for controlling the geometrical quality of the joined structures.

The quality of the research can be evaluated concerning the validity and verification of the outlined results. The definition of validation and verification are put forward in the following to establish a common ground.

According to Boehm, verification of a product involves determining whether the product satisfies requirements. Validation is the process of ensuring the compliance of

the product with requirements (Boehm, 1984). To put it simply, these statements can be translated into verification, i.e., if the product is being built right, and validation, i.e., if the right product is being built.

5.3.1 Verification of the results

To verify if the methods are proposed and built right, *logical verification* and *verification by acceptance* are followed (Buur & Andreassen, 1990). *Logical verification* entails consistent, coherent and complete research elements.

Consistency is achieved when there are no conflicts between individual axioms of the research theory. The consistency of the research has been verified by crosschecking that no contrary results are obtained. From a DRM perspective, the consistency of the results is achieved by re-evaluating the descriptive and prescriptive studies and clarifying research goals. The results presented in this thesis are distributed at different stages of this framework, and the consistency is checked during the evolution of results.

Coherency is the agreement of established methods with theories. The coherency of the established methods is verified by constructing each element from the previously applied research within the research scope. From the DRM perspective, the coherency of the results is achieved following the bottom-up research development, from research clarification to descriptive and prescriptive studies. The results outlined in this research is initiated by research clarification followed by descriptive and prescriptive studies.

Completeness is achieved when the theories established can describe all relevant observations or findings. The completeness of the research elements is verified by following the guidelines of the applied research methodology. A complete research involves the completion of the secondary descriptive study. The research results have reached the initial stages of DS II, in which the needs and platforms for implementation are investigated. The complete implementation of the proposed methods is realized in the second descriptive study of the methodology, where the methods within the self-compensating assembly cells are implemented in a physical setup. The outcome of such implementation needs to be evaluated to finalize the research outcome. As stated in (Blessing & Chakrabarti, 2009), achieving complete design research is outside the scope and time frame of a degree research project.

Verification by acceptance involves accepting the research by experts within the field of the subject. With the definition of the validation provided, this aspect can be interpreted as a validation process over the verified research elements. In this thesis, the results are put forth in the form of scientific papers. The process of publishing the results in international journals involves extensive peer-review process. Experts and experienced fellows in the scientific community review the results and raise concerns and issues. Based on the rationality of the scientific statements, acceptance

or rejection for publication is achieved. Moreover, in order to apply the proposed methods in an industrial context, acceptance by the industrial community is required. The research problem is raised and conducted in close collaboration with industry, ensuring the acceptance of the results.

5.3.2 Validation of the results

The validity of the research conducted can be discussed from three different viewpoints, internal, external, and construct validity (Winter, 2000).

Internal validity: Concerns about the validity of the results within the study, i.e., identifying whether the meaningful causes of the outcome are studied. This aspect was ensured in the studies by performing numerical simulation and experiments analyzing the involved parameters in the model. Statistical methods have been implemented in the studies, analyzing the mean and variance of the results achieved. For statistical significance, the simulations have been performed with more than 100 trials in the studies A, B, and D. Statistical model validation techniques have been performed in Papers C, E, and F. *Degenerate tests* (Sargent, 2010) have been performed in Papers A-D in the form of screening and in Papers E-F in the form of hyper-parameter optimization and k-folds technique for meta-model validation, identifying the algorithm behavior and optimal parameters setting. As Sargent categorizes, graphical representations of the results, *operational graphics* is a technique utilized for validation of the simulation models (Sargent, 2010). Using CAT tools, the deformation propagation and stochastic results are visualized to further validate the results achieved.

External validity: Concerns about the generalizability of the results outside the environment of the study. The studies have been designed for analyzing the sequence of the joints. The joining process is modeled in all studies with the joining points being entirely functional, assuming small local deformation. With this assumption, it can be claimed that any other point-based joining method, locking all DoF in the joining nodes, could be analyzed with the proposed formulation. *Comparison to other models* is another validity technique (Sargent, 2010). The results of all the outlined studies have been compared with different models to ensure the generalizability of the results to other assemblies with different parameters.

Construct validity: Concerns the validity of the study measuring the outcomes claimed. In other words, construct validity measures the appropriateness of the inferences made based on the studies performed. The studies in Papers A-F intend to increase the efficiency of the optimization methods while being accurate. Exhaustive searches have been performed on all studies, and it has been ensured that the global optimum is achieved, where applicable, while the optimization time is reduced. Given the knowledge of the global optimum from the exhaustive search, the accuracy of the prescribed methods is validated,

comparing the retrieved optimum by the proposed method and the global optimum. The time-efficiency of the methods proposed is compared to the existing methods prescribed. In Paper F for non-rigid variation simulation, correlation and causality analyses are performed, ensuring the validation of the measure of deformation introduced. As Sargent defines, *face validity* is when system experts are asked for reasonable outcomes for simulation validation (Sargent, 2010). The simulation outcomes have been checked by industrial partners knowledgeable in the assembly process of sheet metals. In addition, the variation simulation results are compared to the physical measurements (Wärmefjord et al., 2010b). This aspect validated the simulation by means of *historical data validation*. The *face validity* technique (Sargent, 2010), can also be interpreted as *verification by acceptance*, in which the research results are accepted by the scientific community through the journal publication medium.

CONCLUSION

In this section, conclusions are drawn based on the analysis of the results. Future research plans are also proposed.

6.1 Conclusions

To ensure the future competitiveness of the manufacturing industry and reach global sustainability goals, optimization, and simulation-based approaches are becoming prominent. With recent breakthroughs in the digitalization arena and availability of big data in the vision of the cyber-physical manufacturing systems, the concept of the geometry assurance digital twin and self-compensating assembly line has been introduced. Real-time optimization of the assembly parameters for individualized assemblies is within the scope of this concept.

The joining sequence has shown to have a significant impact on the geometrical outcome of the assembly. This parameter has been considered hard to control, specifically in industry. The function of the input sequences to the displacements after joining has been unknown. The previous research has explored geometry dependent heuristic approaches and EAs. The heuristic approaches may not result in optimal outcome. The computational expenses of the proposed EA approaches have been infeasible for real-time applications. In this thesis, a detailed explanation of the applied formulations on the joining sequence optimization has been provided. Two formulations and three approaches have been proposed and discussed in the presented results. The complete and partial sequence optimization problem, with black-box, grey-box, and white-box approaches have been considered. Based on the results outlined, it can be concluded that:

- Standard evolutionary and heuristics have mainly been applied in the previous research, without considering the computation time aspect, which makes the methods heavily time-dependent.
- Partial sequence formulation of the joining sequence is achieved through efficient

geometry point selection and pre-joining processes and can help to improve geometrical quality, while a considerable amount of computation time is being saved. The number, location, and sequence of the points selected are critical to determine geometrical quality.

- Combining heuristic and meta-heuristics for joining sequence optimization reduces the meta-heuristics computational time complexion to ensure that the optimal sequence is achieved.
- Heuristic approaches, based on rules, help to identify the location of the geometry points, whereas the number and their sequence needs to be determined separately. Such an approach is shown to have considerable errors from the global optimum.
- Joining sequence optimization is a combinatorial problem, and solving such problems in real-time requires parallelization of the optimization process. To parallelize the process, the surrogate-assisted approach, together with the proposed sampling strategy, is introduced. The approach is fully parallelizable; by increasing the number of evaluators, computational time will be reduced drastically.
- The proposed approach of evaluating all combinations of initial elements provides a sensitivity of the assembly to joining sequences.
- To solve the joining sequence problem rapidly, sequence elements need to be evaluated stepwise, while all joining points are included in the sequence solutions.
- Determining the accurate number, sequence, and location of the partial sequence problem is dependent on the evaluation of sequence subsets. This problem is shown to exhibit a sub-modular set behavior with a non-monotone set function. To solve the problem, accurate surrogate models are needed for sequence determination. The PCA method can be used identifying the accurate number of elements in the subset.
- The cause of the assembly deviation after joining in a sequence is the relative displacements in the joining points during assembly.
- Large assemblies, with a large number of joining points, require a sensitivity analysis, objective selection, problem segmentation, and local sequence optimization.

6.2 Future Research

Future research, based on the findings highlighted and scope of the research project, includes:

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- Applying the methods proposed to other assembly steps, i.e., clamping sequences.
 - Proposing a framework for optimization of the other joining parameters, such as the position variation using a multi-disciplinary approach.
 - Proposing an optimization framework for assemblies with a large number of joining points.
 - Evaluating the effect of heat in the joining sequence determination.
 - Evaluating the effect of non-linear material models in the joining sequence behavior.

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