A MULTI-CASE-BASED ASSEMBLY MANAGEMENT METHOD FOR THE SHIPBUILDING INDUSTRY

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ABSTRACT

This article describes a method for planning the assembly of ship hulls that focuses on a welding sequence, takes into account subassembly processes and makes use of a previously built database of structures. Different degrees of similarity between structures are taken into account. The described research led to the development of an intelligent hybrid sequencing method for structure assembly that uses fuzzy clustering, case-based reasoning and evolutionary optimization. The method is called 'Multi-case-Based Assembly Planning (MBAP)'. The method is developed to provide satisfactory solutions with low user effort. The analyses carried out show that the calculations are highly time-efficient. The developed evolutionary algorithm converges on sub-optimal solutions. The MBAP method can be directly implemented by any shipbuilder that assembles hulls. Apart from this, fuzzy clustering integrated with case-based reasoning can be applied in practice. The integration of fuzzy clustering and case-based reasoning has been taken to a level higher than previously described in the literature.

Keywords: assembly management,shipbuilding,case-based reasoning,fuzzy classification

INTRODUCTION

The introduction of welded joints in ship hulls a century ago brought about technological changes in shipyards around the world. Thanks to the thermal joining of steel, the modular hull building method was developed. These modules are called sections and blocks – the largest structures that a dockyard can move (Fig. 1). These subassemblies are also built from modules, so-called lower-stage subassemblies.

The shipbuilding industry is following the global trend toward the Fourth Industrial Revolution (Industry 4.0), which poses three main challenges:
- improvement of production efficiency,
- ensuring ship safety, and
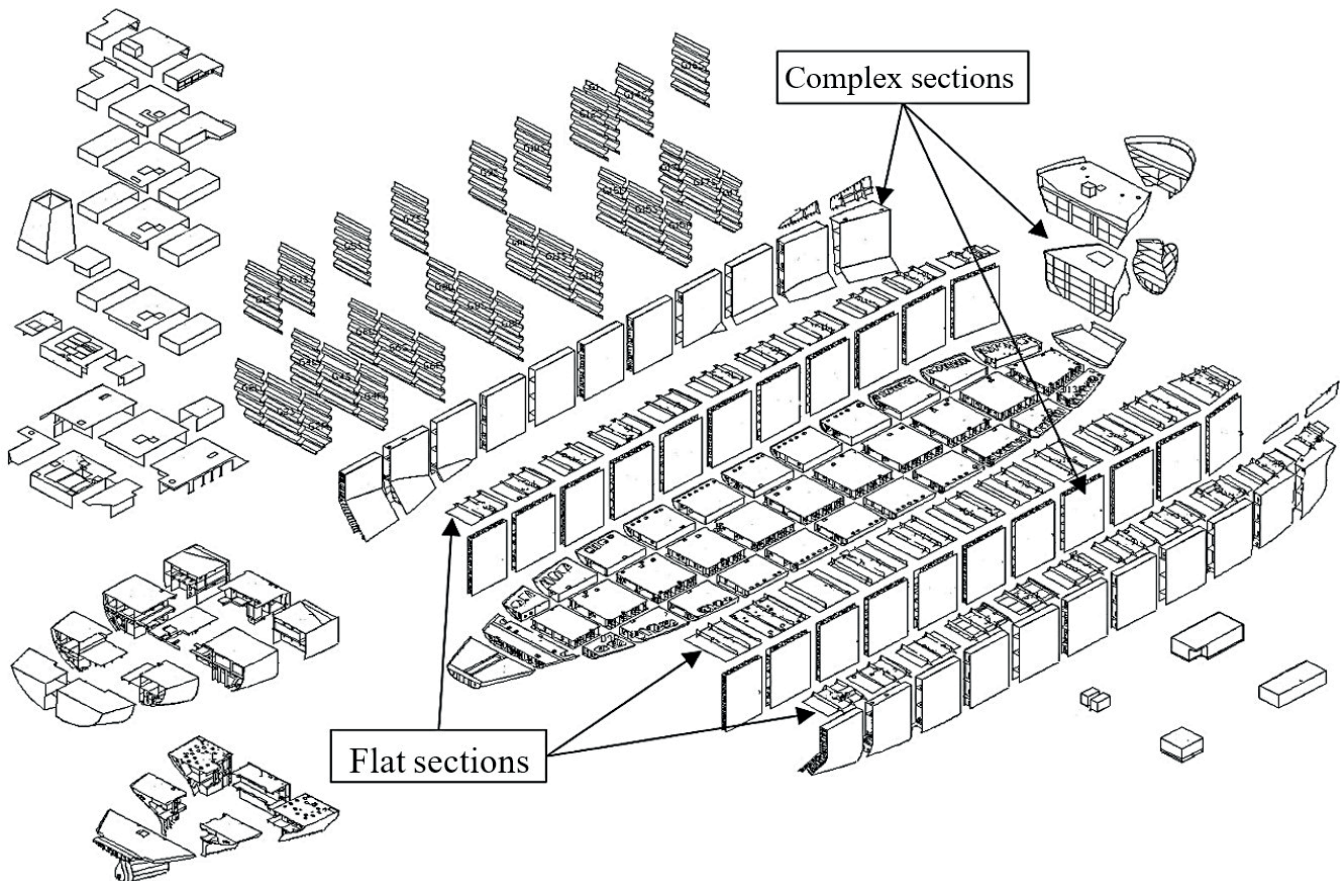- balancing economic efficiency with economic responsibility.

Fig. 1. Division of a chemical carrier hull into flat sections (open, single-shell structures) and complex sections (spatial, double-shell structures)

A shipyard in the age of Industry 4.0 should be a company that wisely adapts to changes in the environment, efficiently manages resources, is ergonomic and works closely with a ship owner and their suppliers. However, complete development toward automated shipbuilding requires balanced development of knowledge in key areas. There are several tasks that Computer Integrated Manufacturing (CIM) tools intended for this industry do not perform due to gaps in global knowledge such as in areas concerning the predictability of weld deformations, optimization of sheet metal cutting or modelling of the assembly of structures with complexity at least near to that of small vessels' hulls. This is mainly due to the size and complexity of the assembled structures. Individual shipyards are trying to solve these problems independently, but a comprehensive approach is needed to develop methods to control the processes of building large ship structures.

An important resource for each dockyard is the experience and knowledge being collected in production documents over decades. This knowledge is often stored in file cabinets, while experience passes away with retired employees. For a shipyard to become a knowledge-based company, it is necessary to seek solutions that will use databases for the management of key processes, including hull assembly. This article is intended to address this issue.

LITERATURE REVIEW

The methods of planning the assembly of mechanisms have been developed for decades [1]. In building a hull, unlike mechanisms, the assembly cannot be planned by focusing solely on structural elements. Adding successive elements is conditional upon having previously completed certain welding operations to reinforce the structure and provide access for welders and equipment. In addition, this work may affect the structure geometry, which requires permanent verification of key dimensions [2]. Except for welding processes, the shipbuilding industry employs a very extensive collection of various subtractive and additive technologies. Each of them may have an unpredictable influence on the geometry of the assembled structure [3][4].

Hull assembly planning with a focus on welded joints is described in [5]. It addresses the issues of sequencing and scheduling for joints to be completed. The described models are based on a so-called sequence matrix, which is a binary record of the workflow. The assembly sequence serves to draw up a schedule, which takes into account additional aspects related to balancing the production capacity. Other authors [6] took into account the issue of hull welding. They combined the element of assembly sequencing with the prediction of welding deformation. A major problem with this model is the time taken to analyse temperature, elasticity and plasticity, which increases exponentially with the complexity of the structure. The serial nature of the generated sequences is a significant limitation of the method.

A way to simplify the planning of the assembly of large structures is to use a framework called subassembly-based division. The hull assembly process is completed at special workstations equipped with automatic welding machines, horizontal and vertical means of transport, structure turntables, beds with extendible supports etc. The planning of the hull structure assembly is related to the organization of the entire production system. However, these two issues are considered separately in the literature. The models for optimizing the shipyard's assembly lines are based on a pre-established assembly plan [7][8].

Bonneville, et al. were the first to propose the use of genetic algorithms (GA) as a tool for finding optimal and semi-optimal assembly plans [9]. The idea of using GA in assembly planning processes was developed further in [10]. The authors distinguish two types of limitations, that is, physical limitations and structure geometry limitations. It was noted that, for the proposed assembly plan to be considered acceptable, it must comply with all geometrical limitations. The physical limitations concerning the available equipment, assembly difficulty and cost were used as optimization criteria for the proposed algorithm.

In addition to evolutionary methods, so-called case-based reasoning (CBR) is included among computational intelligence methods. CBR methods have been developed since the early 1980s and are based on considerations given to the possibilities of digitally storing, analysing and gaining knowledge useful in predicting future events from past experience [11]. The first formal CBR system, CYRUS, was developed at Yale University in 1983 [12].

The main elements of CBR systems were described in [13]. The authors point out that the cyclical procedure consists of four stages (the so-called 4R cycle): analysis of the degree to which the database cases are similar to the case under consideration (retrieve), generation of a solution modelled on similar cases (reuse), verification of the generated solution (revise) and addition of the new case to the database (retain). Attempts have been made to adapt CBR methods to hull assembly planning since the 1990s, but difficulties are faced due to the complexity of the problem and the need for labour-intensive input by experts to control the calculations.

Shipeng et al. proposed use of the CBR method to generate assembly sequences for small sections of the hull [14]. It is worth noting the two-level classification of joints, which is the basis for analysing similarities between structures. However, CBR is only a supporting module in the proposed method. Serial sequences of elements are being determined.

The search for similarities between structures based on the classification of joints and structural elements is also proposed in other papers [15]–[18]. Authors dealing with the assembly of hulls introduce the classification of welded joints by their geometry. There are butt joints, fillet joints and cruciform joints. This is a simplification of the hull's geometric complexity. This approach limits the application of the methods to selected areas of hulls with a typical, repeatable structure, for example, in the area of a middle body.

In hull structures, there is a considerable variety of solutions, and many structures contain very similar parts. In that situation, it is difficult to clearly distinguish a subset of similar structures. This problem can be solved by using an intelligent hybrid system with fuzzy clustering [19]. The fuzzy c-means (FCM) algorithm allows the inclusion of different degrees of similarity between structures and thereby improves the effectiveness of case-based reasoning. Khan and Khan described the method of fuzzy clustering of a database in order to reduce a set of potentially similar cases [20]. However, the method does not use the information about the fuzzy cluster membership in the reasoning phase.

THE CONCEPT OF ASSEMBLY PLANNING

The method described in this article involves the use of a database that stores the characteristics of multiple hull structures or their parts. In addition, every structure is linked to an assembly plan that has been previously implemented and verified for performance. The general scheme of the procedure in this method is modelled on the CBR method. However, it is necessary to adapt its basic components to solve the issues of hull assembly planning. *A case* is defined as any reference structure in a database. The architecture of the structure is the so-called *case problem*, and the assembly plan is *the solution to the case (problem)*. A progressively extended database is used as a *case library* (Fig. 2).

The proposed method will be referred to as 'Multi-case Based Assembly Planning' (MBAP). This method is distinctive due to the inclusion in the classic 4R cycle of fuzzy data clustering and the evolutionary search for the optimal solution. In addition, the author has described the unique architecture of the structure and its assembly plan.
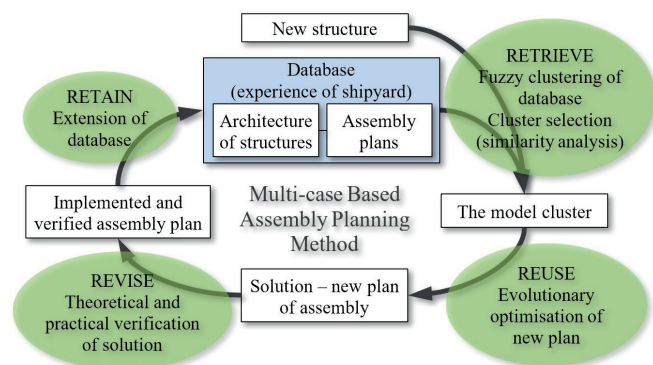

Fig. 2. The general MBAP scheme – the link between the 4R cycle, fuzzy clustering and evolutionary optimisation

The cyclical operation of the MBAP method allows the dockyard to perform the important role of learning from experience. To this end, the shipyard has to fulfil a number of additional functions associated with designing and manufacturing, namely to monitor the assembly of new structures in order to verify the planned subassembly-based

divisions and the order in which the elements are added, and to record all completed and corrected cases in the database.

FORMAL DESCRIPTION OF THE STRUCTURE'S ARCHITECTURE

The structure under analysis is composed of E elements and J welded joints. Each joint is located between two structural elements. Every element can be connected to multiple others.

For example, consider sample structure no. 1, consisting of eight elements and 13 welded joints. The architecture of the structure is presented in Fig. 3, with squares representing the elements and the lines between them representing the joints. Joint numbers are circled, for example, joint 1 is between elements 1 and 2, joint 5 is between elements 2 and 3, etc.
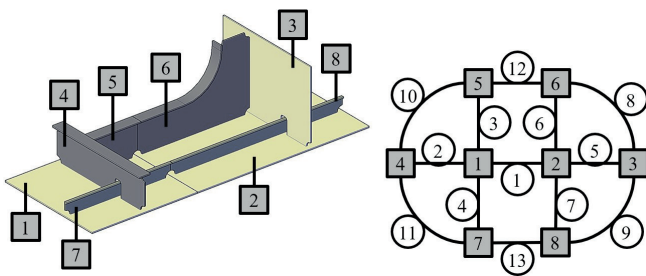

Fig. 3. Sample structure no. 1 and its architecture graph

The architecture of a structure can be described with a square matrix: $\mathbf{A} = (a_{e1,e2})_{E'E}$, where, for each pair of elements indexed with $e1$ and $e2$ ($e1, e2 = 1, 2, \ldots, E$):
$a_{e1,e2}$ is the number of a joint between the elements,
$a_{e1,e2} = 0$ indicates that there is no welded joint between the elements,
$a_{e1,e2} = a_{e2,e1}$.

For the structure shown in Fig. 3, we have an architecture matrix (zero values are skipped beyond the diagonal):

$$\mathbf{A}^1 = \begin{pmatrix} 0 & 1 & & 2 & 3 & & 4 & \\ 1 & 0 & 5 & & & 6 & & 7 \\ & 5 & 0 & & & 8 & & 9 \\ 2 & & & 0 & 10 & & 11 & \\ 3 & & & 10 & 0 & 12 & & \\ & 6 & 8 & & 12 & 0 & & \\ 4 & & & 11 & & & 0 & 13 \\ & 7 & 9 & & & & 13 & 0 \end{pmatrix} \quad \textbf{(1)}$$

One can determine the number of joints as follows:

$$J = \max(\mathbf{A}) \quad \textbf{(2)}$$

Another important feature of the structure is the classification of its welded joints. They can be divided into butt joints (no. 1), fillet joints (no. 2) and cross joints (no. 3), classes typically distinguished in shipbuilding. It is also worth considering the types of elements to be joined. It is easiest to

divide the elements into plates (no. 1), frames (no. 2), stiffeners (no. 3) and brackets (no. 4). As a result, each joint can be described with a three-digit class code: *abc*, where *a* and *c* are the types of elements being joined, while *b* is the joint type. For example, a joint classified as 221 is a fillet joint between a frame and a plate.

Not all joint classes can be found in real structures; for example, brackets are never joined, and there are no cross joints between stiffeners. For further analysis, 10 classes of welded joints are considered in Table 1.

Tab. 1. Classes of welds

Class number	Class code	Joined elements	Weld
1	111	plate + plate	butt
2	212	frame + frame	butt
3	313	stiffener + stiffener	butt
4	121	plate + plate	fillet
5	122	plate + frame	fillet
6	123	plate + stiffener	fillet
7	222	frame + frame	fillet
8	324	stiffener + bracket	fillet
9	133	plate + stiffener	cross
10	233	frame + stiffener	cross

It should be noted that this model does not impose a specific classification system. That system should be adapted to the individual needs of a user. A set of joint classes should not be so large as to make the analysis too complex. It is important to be able to clearly identify which joints are considered to be members of the same class and which joints are treated as essentially different.

Considering K joint classes, the classification using a binary matrix is defined: $\mathbf{C} = (c_{j,k})_{J \times K}$, where $c_{j,k} = 1$ if and only if the j-th joint is assigned to the k-th class. A classification matrix for sample structure no. 1 (Fig. 3) is presented in Table 2.

Tab. 2. Classification of welds of sample structure no. 1

$\mathbf{C_1}$		Classes									
		1	2	3	4	5	6	7	8	9	10
Welds	1	1									
	2					1					
	3					1					
	4						1				
	5				1						
	6						1				
	7							1			
	8						1				
	9									1	
	10							1			
	11										1
	12		1								
	13			1							

The matrix $\mathbf{C}_1$ indicates that class 8 is not represented in the structure. Fillet joints between plates and frames (class 5) are the most frequent.

CLUSTER ANALYSIS OF A DATABASE OF STRUCTURES

There is a very wide variety of structures in shipyard practice. In order to analyse the similarities between them, one needs to build a database of all structures described under a common classification system. Therefore, a universal set of joints can often go beyond a description of a single structure.

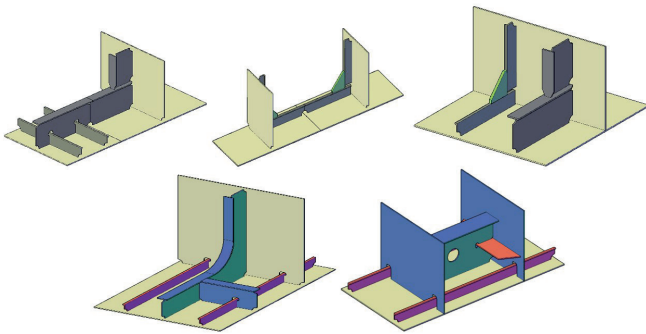The considered database includes structure number 1 and five other structures shown in Fig. 4.

Fig. 4. Sample structure nos. 2–6

For each structure in the database, the cumulative classification vector is determined:

$$\chi = (\chi_1, \chi_2, ..., \chi_K), \quad \forall k = 1, 2, ..., K : \chi_k = \sum_{j=1}^{J} c_{j,k} \qquad (3)$$

where χ_k is the number of the class k joints that are present in the structure.

Each structure is therefore represented by a point in K-dimensional space.

The database is a set of B elements $\{\chi_1, \chi_2, ..., c_B\}$ and is subject to cluster analysis in order to evaluate all structures for similarities and differences. Clustering is completed by the FCM method. This method determines the degree of each structure's membership in each of the N clusters, and the result is the following matrix: $\mathbf{U} = (u_{n,b})_{N'B}$, where $u_{n,b} \hat{I} [0,1]$ is a measure of the membership of structure b in cluster n.

In the FCM method, the solution depends on a control parameter $m > 1$. This parameter provides control over the degree of cluster overlap. Values close to 1 result in a sharp division. Increasing the parameter value results in equalisation of the structure's membership in different clusters. The calculation is performed according to the following algorithm:
1. filling in the initial membership matrix $\mathbf{U}$ by a draw,
2. determining cluster centres:

$$\boldsymbol{\alpha}_n = \frac{\sum_{b=1}^{B} u_{n,b}^m \boldsymbol{\chi}_b}{\sum_{b=1}^{B} u_{n,b}^m} \qquad (4)$$

3. updating the structure's membership in clusters:

$$u_{n,b} = \frac{1}{\sum_{\eta=1}^{N} \left(\frac{\|\boldsymbol{\chi}_b - \boldsymbol{\alpha}_n\|}{\|\boldsymbol{\chi}_b - \boldsymbol{\alpha}_\eta\|} \right)^{\frac{2}{m-1}}} \qquad (5)$$

4. calculation of the target function:

$$Q = \sum_{b=1}^{B} \sum_{n=1}^{N} u_{n,b}^m \|\boldsymbol{\chi}_b - \boldsymbol{\alpha}_n\|^2 \qquad (6)$$

5. repeat steps 2–4 until the target function improvement is not less than a set level or until the iteration limit is reached.

Fuzzy membership of each structure in three clusters is shown in Table 3. For example, structure no. 1 is assigned to the third cluster more than to the first or second. However, the parameters of membership in all clusters do not differ by much. In turn, structure no. 3 was definitely assigned to cluster 2.

Tab. 3. Clustering for 3 groups with parameter m = 4

$\mathbf{U}_4$		Structure					
		1	2	3	4	5	6
Cluster	1	0.2614	0.3012	0.0461	0.3584	0.7552	0.4447
	2	0.1301	0.1727	0.9085	0.2719	0.0801	0.2311
	3	0.6085	0.5261	0.0454	0.3697	0.1647	0.3242

Based on the membership matrix $\mathbf{U}$, a structure importance matrix is determined in clusters:

$$\forall n = 1, ..., N, b = 1, ..., B : w_{n,b} = \frac{u_{n,b}}{\sum_{\beta=1}^{B} u_{n,\beta}} \qquad (7)$$

The results of the calculations are presented in Table 4. As a result of the transformation of matrix $\mathbf{U}$ into matrix $\mathbf{W}$, the sum of the values in each row is equal to 1.

Tab. 4. Importance of structures in clusters for parameter m = 4

$\mathbf{W}_4$		Structure					
		1	2	3	4	5	6
Cluster	1	0.1206	0.139	0.0213	0.1654	0.3485	0.2052
	2	0.0725	0.0962	0.5063	0.1515	0.0446	0.1288
	3	0.2985	0.2581	0.0223	0.1813	0.0808	0.159

Matrix W characterizes each cluster by means of weights assigned to individual structures. The higher the weight of the structure in the cluster, the greater its impact on the characteristics of the cluster. The method of determining this characteristic is described below.

ASSEMBLY PROCESS MODELLING

The assembly process will be described into a sequence of stages. Each stage is a period on the process timeline. In other words, we divide the process timeline into successive intervals of some indefinite length. Welding of one or more joints starts in every stage. Welding of any joint may take more than one stage, but the welding start time must be at the beginning of one of the stages. The stages do not have to be of equal duration. A structure assembly plan is a vector:

$$\mathbf{p} = \left(p_1, p_2, ..., p_J \right) \tag{8}$$

where p_j is the number of the stage in which welding of the j-th joint starts.

For the database-stored structures shown in Fig. 3 and Fig. 4, assembly plans, which have been tested in practice and subjected to critical assessment, are defined. It is assumed that a plan stored in the database is a preferred solution for the given structure.

ASSEMBLY SEQUENCE KNOWLEDGE

Based on the assembly plan $\mathbf{p}$, one can define a sequence relationship between joints with a square matrix:

$$\mathbf{SW} = \left(sw_{j1,j2} \right)_{J \times J}, \quad \forall j1, j2 = 1, 2, ..., J : sw_{j1,j2} = \frac{p_{j2} - p_{j1}}{S - 1} \tag{9}$$

where S equals the maximum value in vector $\mathbf{p}$.

The sequence $\mathbf{SW}$ is determined for each structure stored in the database. For example, for structure no. 1, the matrix shown in Table 5 is obtained.

Tab. 5. Sequence of welding of example structure no. 1

SW₁		Welds												
		1	2	3	4	5	6	7	8	9	10	11	12	13
Welds	1	0	−0.7	−0.3	−1	−0.7	−1	−1	−0.3	−0.3	−0.3	−0.3		
	2	0.7	0	0.3	−0.3		−0.3	−0.3	0.3	0.3	0.3	0.3	0.7	0.7
	3	0.3	−0.3	0	−0.7	−0.3	−0.7	−0.7					0.3	0.3
	4	1	0.3	0.7	0	0.3			0.7	0.7	0.7	0.7	1	1
	5	0.7		0.3	−0.3	0	−0.3	−0.3	0.3	0.3	0.3	0.3	0.7	0.7
	6	1	0.3	0.7		0.3	0		0.7	0.7	0.7	0.7	1	1
	7	1	0.3	0.7		0.3		0	0.7	0.7	0.7	0.7	1	1
	8	0.3	−0.3		−0.7	−0.3	−0.7	−0.7	0				0.3	0.3
	9	0.3	−0.3		−0.7	−0.3	−0.7	−0.7		0			0.3	0.3
	10	0.3	−0.3		−0.7	−0.3	−0.7	−0.7			0		0.3	0.3
	11	0.3	−0.3		−0.7	−0.3	−0.7	−0.7				0	0.3	0.3
	12		−0.7	−0.3	−1	−0.7	−1	−1	−0.3	−0.3	−0.3	−0.3	0	
	13		−0.7	−0.3	−1	−0.7	−1	−1	−0.3	−0.3	−0.3	−0.3		0

The value of the component $sw_{j1,j2} < 0$ (negative) indicates that joint $j1$ is completed at a later stage than joint $j2$. The extreme value −1 means that joint $j1$ is completed in the last stage of the process and joint $j2$ in the first stage. The positive values of the component $sw_{j1,j2}$ indicate the opposite case. Of course, this equality holds: $sw_{j1,j2} = -sw_{j2,j1}$

We generalize our knowledge of the assembly processes of individual structures by using the classification of their joints. The joint class sequence matrix is found with the formula:

$$\mathbf{SC}^{un} = \mathbf{C}^T \cdot \mathbf{SW} \cdot \mathbf{C}$$
$$\mathbf{SC} = \frac{\mathbf{SC}^{un}}{\max \left(\mathbf{SC}^{un} \right)} \tag{10}$$

As with the matrix $\mathbf{SW}$, the class sequence also shows the direction and strength of the precedence relationship, but it applies to classes of joints. For structure number 1 discussed above, we obtain the matrix in Table 6.

Tab. 6. Sequence of welds classes for structure 1

SC₁		Classes									
		1	2	3	4	5	6	7	8	9	10
Classes	1	0			−0.2	−0.7	−0.6	−0.1		−0.1	−0.1
	2		0		−0.2	−0.7	−0.6	−0.1		−0.1	−0.1
	3			0	−0.2	−0.7	−0.6	−0.1		−0.1	−0.1
	4	0.2	0.2	0.2	0	0.1	−0.2	0.1		0.1	0.1
	5	0.7	0.7	0.7	−0.1	0	−1	0.3		0.3	0.3
	6	0.6	0.6	0.6	0.2	1	0	0.4		0.4	0.4
	7	0.1	0.1	0.1	−0.1	−0.3	−0.4	0			
	8								0		
	9	0.1	0.1	0.1	−0.1	−0.3	−0.4			0	
	10	0.1	0.1	0.1	−0.1	−0.3	−0.4				0

Class 5 is quite strongly indicated to precede classes 1, 2 and 3. Class 6 has a smaller tendency to precede classes 1, 2 and 3 but a greater tendency to precede classes 4, 7, 9 and 10. Class 8 welds (comprising a stiffener and a bracket), do not have a specific relationship with any class. This is understandable because this class is not represented in structure 1.

The class sequences are calculated for all structures in the database in order to obtain aggregate knowledge of preferred solutions within the previously determined clusters. In practice, we determine each cluster's sequence matrix as a weighted average:

$$\forall n = 1, 2, ..., N : \quad \mathbf{SCC}_n = \sum_{b=1}^{B} w_{n,b} \cdot \mathbf{SC}_b \tag{11}$$

Of course, there is still the parameter m, which controls the importance of structure in clusters. For example, with the value of $m = 4$ and for the division of the described database into three clusters, three sequence matrices are obtained.

A sample matrix for cluster number 3 is shown in Table 7. Values significantly different from zero are in bold type.

Tab. 7. Sequence for cluster 3 and parameter m = 4

$SCC_{4,2}$		Classes									
		1	2	3	4	5	6	7	8	9	10
Classes	1	0			−0.09	−0.34	−0.32	−0.03	−0.01	−0.03	−0.03
	2		0		−0.09	−0.34	−0.31	−0.03		−0.03	−0.03
	3			0	−0.06	−0.21	−0.19	−0.03	−0.01	−0.03	−0.03
	4	0.09	0.09	0.06	0	−0.07	−0.35	0.06		0.03	0.09
	5	**0.34**	**0.34**	0.21	0.07	0	−0.87	**0.33**	0.18	0.10	**0.36**
	6	**0.32**	**0.31**	0.19	**0.35**	**0.87**	0	**0.38**	0.20	**0.36**	**0.46**
	7	0.03	0.03	0.03	−0.06	−0.33	−0.38	0			
	8	0.01		0.01		−0.18	−0.20		0		
	9	0.03	0.03	0.03	−0.03	−0.10	**−0.36**			0	
	10	0.03	0.03	0.03	−0.09	**−0.36**	**−0.46**				0

The selection of the cluster and the related matrix **SCC** depends on the architecture of the new structure under analysis and for which we are planning the assembly. We select the cluster with a centroid **a** (see formula 4) that is closest to the new structure's aggregate classification vector.

OPTIMISATION OF THE NEW STRUCTURE'S ASSEMBLY

In order to use the developed mathematical models in shipbuilding, it is necessary to supplement the method with a module for generating new assembly plans. The computational algorithm expanded to include the optimisation of the new plan can be summarised in the following steps:

- setting the control parameter m, for which the database is clustered,
- determining the number of stages of the assembly process being planned S_{new}^{max},
- determining an aggregate classification vector χ_{new},
- selecting the cluster with its centroid at the smallest Euclidean distance from the vector χ_{new},
- determining the sequence matrix $SCC_{m,n}$ for the selected n-th cluster,
- searching for the plan vector p_n, which corresponds to a sequence of joint classes SC_{new} that minimizes the function:

$$f = \sum_{k1=1}^{K-1} \sum_{k2=k1+1}^{K} \chi_{new,k1} \cdot \chi_{new,k2} \cdot \alpha_{n,k1} \cdot \alpha_{n,k2} \cdot \left| sc_{new,k1,k2} - scc_{m,n,k1,k2} \right| \rightarrow \min \quad \textbf{(12)}$$

The plan can be optimised by an evolutionary method, using classic crossover and mutation operators. The draw of the first generation produces the assumed number of plan vectors. Each vector is a sequence of random numbers from the interval $[1, S_{new}^{max}]$. The crossover of plans contained in the population is relatively simple, as it is performed by exchanging some vectors **p** assigned to two parents. The intersection of the vectors is selected randomly. The crossover may cause a change in the number of assembly stages,

which is desirable as it increases the diversity of plans being analysed. The mutating operator is used with a predetermined probability. This operator replaces one of the components of the plan vector **p** with another random value from the range $[1, S_{new}^{max}]$. Fig. 5 shows the procedure for planning the assembly of a new structure.
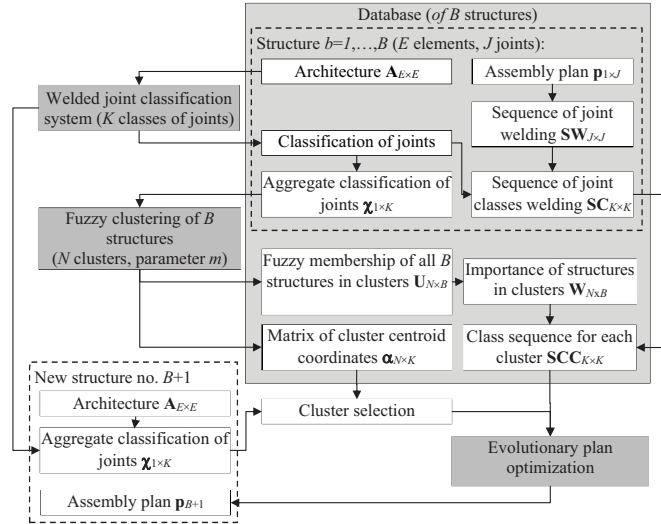

Fig. 5. Algorithm of the procedure for implementing the RETRIEVE and REUSE stages of the proposed MBAP method

EXAMPLE OF APPLICATION

Sample calculations were performed for the structure shown in Fig. 6. It consists of five plates (elements 1–5), two frames (elements 6 and 7), two stiffeners (elements 8 and 9) and a bracket (element 10). The complexity of structure no. 7 has been matched to the relatively non-complex structures in the database.
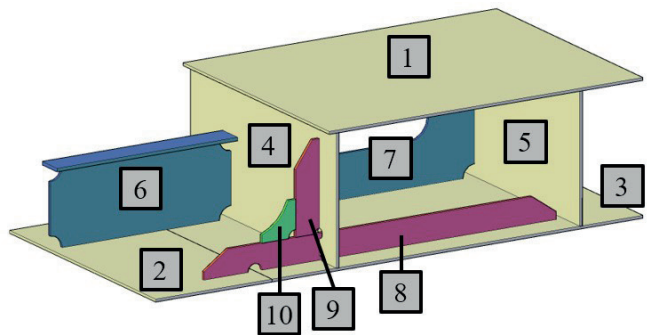

Fig. 6. Sample structure no. 7

The architecture of structure no. 7 is a simplified two-shell structure. There were 19 welded joints identified between the elements.

The analysis is aimed to verify whether the MBAP method can generate an assembly plan that is feasible and meets the sequence rules included in reference structure plans.

For 10 classes and the structure consisting of 19 joints, the optimization calculations were performed by a mid-range computer in 1 second. The evolutionary algorithm has reached a suboptimal solution after 200 cycles when there were 20 specimens in the population.

The calculation resulted in the following assembly plan:

$$\mathbf{p}_7 = \left(1,1,2,1,2,2,3,3,2,4,2,4,2,4,4,2,5,5,5\right) \quad \text{(13)}$$

The plan $\mathbf{p}^7$ is implemented in five stages (Fig. 7). In the first stage, plates no. 2 and 3 are butt-welded, and plate no. 1 is joined with plates no. 4 and 5. In this way, two subassembled units are created, which are further expanded in the next step. Subassemblies are joined in stage 3. In stage 4, stiffener no. 9 is added, and structure reinforcement welds are completed. The last element, or bracket no. 10, is added in stage 5.

The result of optimisation calculations can be considered satisfactory. The advantage of this solution is that most welds can be completed from underneath. One of the subassembled units in its final position is shown in Fig. 7, but in practice, it will be completed in the inverted position. It should be considered whether frame no. 6 should be added before the two subassemblies are joined. Adding this element in stage no. 3 or later will enable better control of the welding deformation and easier relative positioning of subassemblies.
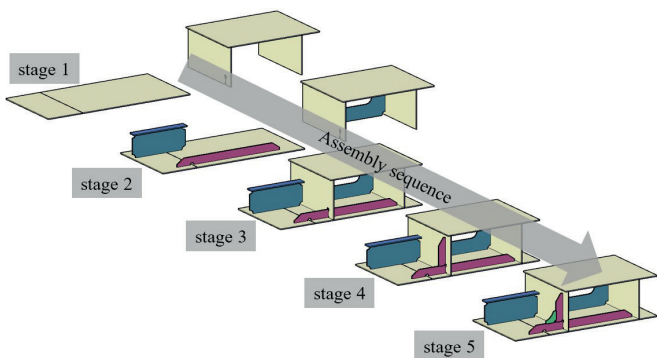

Fig. 7. Assembly sequence for structure no. 7 generated by the MBAP method

The major disadvantage of this solution is the addition of stiffener no. 9 only in stage no. 4. This operation requires welding vertically or rotating the entire structure when welding. It would be better to join this stiffener with plate no. 4 in the first stage of assembly and join plate no. 4 with plate no. 1 only in the next stage.

However, the obtained assembly plan confirms the ability of the MBAP to generate interesting solutions that can be a valuable support for production engineers.

CONCLUSIONS

This article has highlighted the complexity of planning problems in ship hull assembly. There are relatively few papers dealing with these issues, and they present a simplified approach with a strong focus on experts' involvement in the decision-making process. As a result, the published methods have a limited practical value. In this article, attempts have been made to develop a method for managing the shipyard database and generating assembly plans for structures of any size. The focus was on welding processes, as they are crucial to shipbuilding, which distinguishes this sector from the machinery industry.

The presented example of the application of the MBAP method shows that the general concept is correct. Successful reasoning based on the cases stored in the database can be traced. It has also been shown that the obtained results require independent evaluation. Like any method based on computational intelligence, MBAP also requires a large amount of data to function properly. The initial stages of its implementation require a learning process and the supervision of production engineers. During the implementation process, the values of the control parameters should be set.

The MBAP method requires a shipyard to archive and analyse the data on the processes completed in order to acquire knowledge useful for assembly planning. The article proposes a system that allows for flexible definition of element and weld classes. As a result, the method can be adapted to a specific production profile. The article proposes a two-step approach to classification. In the first step, structural elements are classified by their geometry and, at the same time, welded joints are classified by their geometry and the functions they perform. In the second stage, both element and weld classes are considered. As a result, a so-called class code is assigned to each weld. The classification is the basis for analysing the similarities between structures and clustering the database. The proposed method uses fuzzy clustering, but it is also possible to develop hierarchical links between structures. As a result, the shipyard is able to extend the CIM system to include further modules, for example, to assist in the planning of plate cutting during processing, planning of supplies, etc.

It is worth noting that the proposed approach to assembly planning is versatile and can be adapted to planning various processes, particularly, very complex, long-term and high capacity-intensive projects. The system should be further developed toward greater automation in data exchange between the computing module and the CAD software used in a shipyard's design office. Manual input of geometric data is too labour-intensive for hulls containing thousands of elements. Modern design software systems include functions for exporting necessary information, but the standardisation of data between different systems is currently being investigated. It is also important to stress the need to expand the capabilities of MBAP to include new optimization criteria. An important direction for development is, for example, to address the problem of job queuing at workstations. From a strategic planning point of view, it is important to examine more closely the links between production system performance and the assembly plans being implemented.

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