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GENETIC ALGORITHM-BASED MULTI-CRITERIA APPROACH TO PRODUCT MODULARIZATION

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ABSTRACT

Modularization is one of the key strategies for increasing responsiveness to customers. In modular product architecture a wide variety of product configurations can be generated by altering a limited number of modules and components. Product modules are identified by grouping highly coupled components in the same module. A Design Structure Matrix (DSM) is a compact presentation of the interaction between the components. In this paper, Analytical Hierarchy Process (AHP) and Genetic Algorithm (GA)-based methodology is proposed for the clustering of highly coupled DSM components in modules. Multi-criteria DSMs are proposed, which are aggregated by using weights generated by AHP. A genetic algorithm is designed to change the order of components in DSM and to bring highly coupled interactions near the diagonal. An illustrative case study is also made to validate the proposed algorithm. Two large sized and two small size modules are identified by selecting high density clusters around the diagonal. The clustered DSM also shows independent components and loose coupling between the two modules.

Keywords: Analytical hierarchy process; Clustering; DSM; Genetic algorithm; Modularization

1. INTRODUCTION

In the current competitive and volatile market, the challenges of managing a variety of products is increasing exponentially. Consequently, companies are looking for strategies to improve their competitiveness in terms of cost of production and lead time in the demand uncertainty environment. One of such concept, which satisfies customer needs by providing a range of products at optimal cost, without delay and without sacrificing the value of the product, is "Product Modularity" (Partanen & Haapasalo, 2004). This can be defined as a basic building block of a product, which performs a specific task. Modules are physical structures that have a one-to-one correspondence with functional structures (Ulrich & Tung, 1991). A product is usually made of two or more building blocks or modules, which interact through conversion or transmission of energy, and physically interface with one or more physical components.

Many researchers have proposed different methods for the modularization of products. Pimmler and Eppinger (1994) developed a system engineering technique by using design decomposition for complex interaction between design components. Stone (1997) proposed a new method for component clustering for the development of new products using modular design.

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Salhieh and Kamrani (1999) constructed a framework for the integration of components by using matching modular strategies, while Dahmus et al. (2001) presented a new approach for the development of modular product families, in which the modules are interchangeable. Kusiak and Huang (1996) developed a model and solution for modularity-based systems. Chen et al. (2011) proposed GA based panning system that employs building information model (BIM), object sequencing matrix (OSM), to obtain an optimal crew assignment under resource and workspace constraints. Nasruddin et al. (2018) applied a GA based optimization technique for optimizing total energy destruction and total annual cost of a geothermal power plant.

Kreng and Lee (2004) used a grouping genetic algorithm to create modular product design, while Nepal (2005) presented a fuzzy logic-based approach to product modularization. Lee (2010) proposed an NSGA-based methodology for the formation of modules using strategic factors; however, they did not consider important factors which define physical proximity, energy and information, and material-based interactions. Rogers et al. (2006) proposed a genetic algorithm-based method for the clustering of a DSM square matrix. However, their model only addresses a single matrix and does not consider the clustering of multiple matrices for mapping the interactions between components with respect to different factors. As the number of components increases, the complexity of the problem of identification of appropriate modules increases. In such a scenario, many of the existing methods either become very time consuming or inefficient. A genetic algorithm is a proven method for quickly finding near optimal solutions to complex problems.

This paper aims to develop an AHP, genetic algorithm and DSM-based methodology for developing product modules. The overall methodology is divided into three parts. In the first, DSM is used to populate the product architecture and identify the degree of interaction between the various components of the product. The component interactions are quantified in terms of factors such as spatiality, energy, information and material, depending upon the degree of interaction between factors. In the second part, the importance of each of the factors with respect to the formation of the product module is enumerated using the analytical hierarchy process (AHP). The weights of the factors are used to aggregate all the matrices into one matrix. Finally, a genetic algorithm (GA)-based method is proposed for the clustering of the DSM. The proposed method partitions the product into a set of modules, in which interactions within individual modules are maximized, and those outside them are minimized. The proposed method for developing product modules is then verified using an example of a real product.

2. THEORETICAL BACKGROUND

2.1. Design Structure Matrix

The design structure matrix (DSM) (Steward, 1981) is a square matrix with identical rows and column labels. It represents the relationships between elements in a system using the binary value of numbers. In the DSM, an off-diagonal element signifies the dependency of one element on another. A component-based DSM is used for product analysis and design based on interactions between various components of the product. It is constructed by identifying the interactions between product components and representing them as cells in the matrix. Documenting interactions between components is important, because it allows us to understand the degree of association between them for the identification of modules.

Manipulation of the matrix can be performed to obtain clusters of highly interacting components, while attempting to minimize inter-cluster interactions. The obtained clusters represent modules or chunks, which simplify the process of product design.

Pimmler and Eppinger (1994) classified component-based DSMs in four categories, i.e. Spatial, Energy, Information and Material, as depicted in Table 1. The explanation of the interactions between the components basically represents the current level of knowledge about the design. Furthermore, the interactions may be revised and updated with the emergence of new component knowledge. Table 2 shows the quantification arrangement proposed by Pimmler and Eppinger (1994) for mapping the degree of interaction.

Table 1 Simple classification of system element interactions

Spatial	**requirements for orientation or adjacency between two elements**
Energy	requirements for exchange/transfer of energy between two elements
Information	requirements for signal or data exchange between two elements
Material	requirements for exchange of material between two elements

Table 2 Example of an interaction quantification arrangement

Required	**04**	**Physical adjacency is necessary for functionality**
Desired	03	Physical adjacency is necessary for functionality
Preferred	02	Physical adjacency less effect functionality
Not preferred	01	Physical adjacency is beneficial and not necessary for functionality
Undesired	00	Physical adjacency does not affect functionality

2.2. Analytical Hierarchy Process (AHP)

The AHP was proposed by Saaty (1980) to resolve complex multi-criteria decision-making problems. In AHP, the decision problem under study is divided into a hierarchical system of criteria, sub-criteria etc. Indirect evaluation in the form of pair-wise comparisons is made for the elements of each level in the hierarchy, with respect to all the components of the immediate higher level elements using a nominal scale. The eigenvalues of the matrix are then derived, which signify the comparative weight of the various elements of a certain matrix. The consistency ratios of the comparative matrix are determined based upon the suitability of the information. AHP comprises five main steps (Saaty, 1980) for determination of the weight of the criteria, as follows.

Step 1. Define the evaluative criteria and establish a hierarchical framework

Step 2. Establish pair-wise comparison matrices. In this step, the elements of a particular level are compared pair-wise, with respect to a specific element in the immediate upper level.

Let the judgment matrix, denoted as A, be represented by $A = [a_{ij}]$, $i, j = 1; 2; \ldots ; n$.

where a_{ij} represents the comparison between any two criteria Ci and Cj. This comparison with respect to the goal or specific immediate higher-level criteria is made using a 9-point scale, as suggested by Saaty (1980).

The entries a_{ij} are governed by the following rules:

$$a_{ij}.a_{ji} \tag{1}$$

Obviously, $a_{ii} = 1$ for all i. If $a_{ij} > 1$, then the i^{th} criterion is more important than the j^{th} criterion, while if $a_{ij} < 1$, then the j^{th} criterion is more important than the i^{th} criterion. If two criteria have the same importance, then the entry a_{ij} is 1.

Step 3: Calculate the eigenvalue and eigenvector. In this step, first all the a_{ij} are normalised as

$$\hat{a}_{ij} = \frac{a_{ij}}{\sum_{i=1}^{n} a_{ij}} \tag{2}$$

Finally, the weight of the i^{th} criterion is calculated by using Equation 3.

$$w_i = \frac{\sum_{i=1}^{n} \hat{a}_{ij}}{n} \tag{3}$$

Step 4: Perform a consistency test

$$CI = \frac{\lambda_{\max} - n}{n-1} \tag{4}$$

where $\lambda_{\max}$ is the maximum eigenvalue, and n is the number of factors in the judgment matrix.

Step 5: Calculate the overall level hierarchy weight. All level weights should be normalized by dividing them by their sum. The obtained weight vector is multiplied by the weight coefficients of the criteria at the higher levels, until the top of the hierarchy is reached.

3. PROPOSED METHODOLOGY

Modular design strategies facilitate the management and development of complex products by decomposing them into modules. Over the years, many strategies have focused on possible approaches to product modularization. Taking into consideration the shortcomings of the existing methods of modularization or module identification in existing products, as well as in product families, in this paper an AHP, DSM and GA-based methodology is proposed to achieve optimal modular architecture. The overall methodology is divided into seven steps.

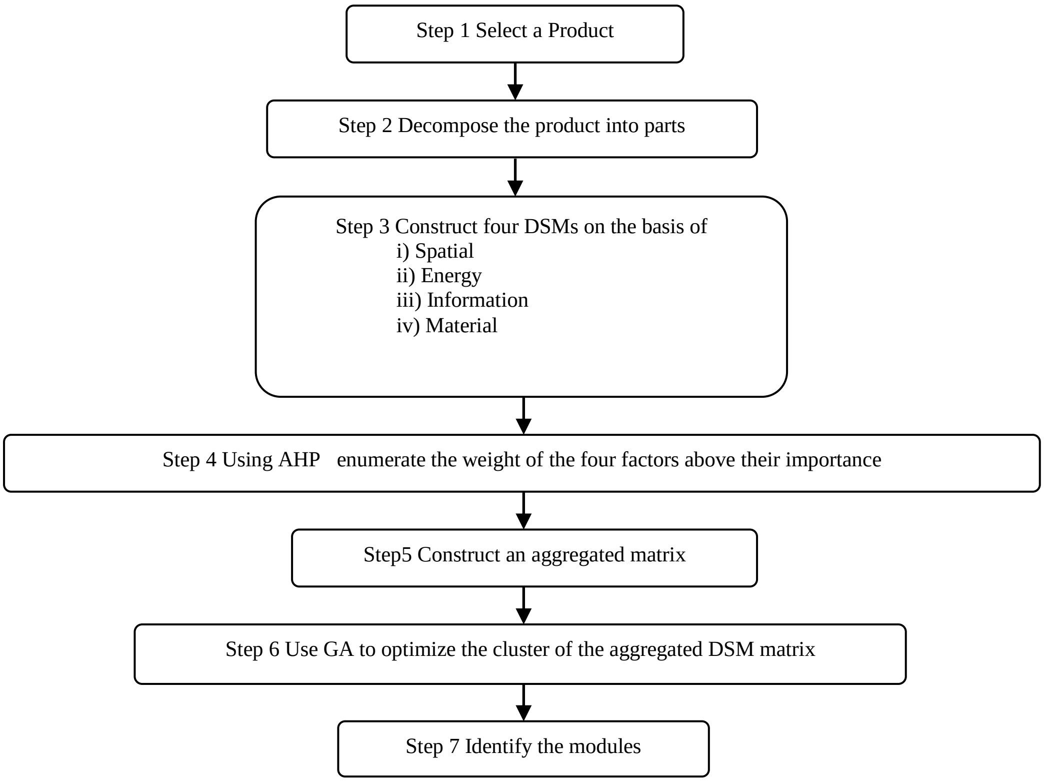


Figure 1 Methodology flow chart

Step 1: A product or product family is selected on the basis of factors such as commonalities, demand pattern, or number of existing product variants.

Step 2: The approach proposed by Yassine and Sharman (2004) has been used for the decomposition of products into elements, using existing documentation such as design manuals, process sheets, IDEF models etc., followed by validation by interviews with experts.

Step 3: The interactions between the various product elements are determined with respect to four factors, namely: (1) Spatiality – the associations between physical space and alignment; (2) Energy– the associations between energy exchange; (3) Information – the associations between information exchange; and (4) Material – the associations between material exchange.

With respect to four factors in step 3, four separate DSMs are prepared to identify the interactions between various decomposed elements. Depending upon the degree of interaction, classification of the degree of interaction can be made, as depicted in Table 2. The value of the cell in the diagonal may be considered as very high, i.e 4. The interaction matrix Dj can be expressed as:

$$Dj = \begin{array}{c|ccccc|} & A_1 & A_2 & A_3 & & A_n \\ \hline A_1 & \tilde{x}_{11} & \tilde{x}_{12} & \tilde{x}_{13} & \cdots & \tilde{x}_{1n} \\ A_2 & \tilde{x}_{21} & \tilde{x}_{22} & \tilde{x}_{23} & \cdots & \tilde{x}_{2n} \\ A_3 & \tilde{x}_{31} & \tilde{x}_{32} & \tilde{x}_{33} & \cdots & \tilde{x}_{3n} \\ \vdots & \vdots & & & & \\ A_n & \tilde{x}_{n1} & \tilde{x}_{n2} & \tilde{x}_{n3} & \cdots & \tilde{x}_{nn} \end{array} \tag{5}$$

where x_{i} is the degree of interaction between two elements, A_i and A_j, $i = 1,2, \ldots, n$, n is the number of elements, D_j is the interaction matrix/DSM$_j$ with respect to factor j, $j = 1,2,\ldots m$ and $m = 4$. D_1, $D_{2,}$, $D3$, D_4 represent the interaction matrix with respect to the spatial, energy, information and material factors, respectively.

Step 4: An aggregated DSM from the above four DSMs is constructed. As the importance of the four factors will vary from product to product, in order to enumerate their weights according to their importance with respect to goal, an AHP based method is proposed in this article. The hierarchy of the problem is shown in Figure 2.

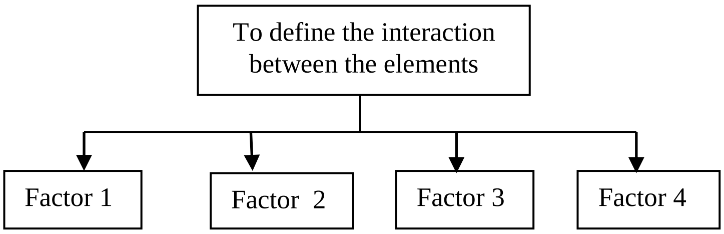


Figure 2 Hierarchy of the problem

Using Saaty's scale (1980), decision makers will prepare a pair-wise comparison matrix. The eigenvalues w_j of the 'm' number of factors using step1 to step 5 of section 2.2 are calculated.

Step 5: The aggregated matrix D_A is calculated:

$$f(D_A) = f(D_1, D_2, \ldots, D_m) \tag{6}$$

$$D_A = \sum\nolimits_{j=1}^{m} D_j w_j \tag{7}$$

Step 6: For the clustering in DSM, the GA attempts to move all the highest values off the diagonal elements of the DSM as close to the diagonal as possible.

Chromosome coding

The DSM is a square matrix used to map the interactions or coupling between the various product components. The order of appearance of the components in rows and columns is identical and can be represented by a string or chromosome, in which each gene in the chromosome represents a component.

P_1	$P_{2.}$	…	…	P_{n-1}	P_n

Figure 3 Chromosome coding

Initialization

If there are *n* number of components in the product, than factorial *n* combinations of the order of components is possible. In the initialization step, 100 random solutions, or combinations of the order of appearance generated randomly, are selected as the initial population.

Fitness function

For the purpose of clustering, it is necessary to bring all the higher value genes close to the diagonal. In the proposed fitness function, a penalty value is defined to calculate the fitness of each chromosome. In this paper, this value is fixed at 10. The objective is to minimize the total penalty imposed on a specific solution or chromosome.

If p is the penalty value and x_{ij} is the value in the i^{th} row and j^{th} column, the fitness value Z can be defined as:

$$Min\ Z = \sum_{j=1}^{n} \sum_{i=1}^{n} x_{ij} \times |j - i| \times p \tag{8}$$

s.t.

$$x_{ij} > \tau \tag{9}$$

$$i \neq j \tag{10}$$

$$m = n \tag{11}$$

where τ is a user defined cluster parameter.

For each off-diagonal cell that has a value greater than the cluster parameter τ, a fitness value is calculated. The value of the off-diagonal element is multiplied by the absolute value of the difference between the column number of the element and the diagonal or row number. This product is then multiplied by the penalty value, so that the farther away an element is from the diagonal, the greater its penalty value.

For example, if an off-diagonal element with a value of 3.5 is in row 3 column 8, and the cluster penalty is 10, the fitness for that element would be 3.5×[abs (8-3)]×10 or 175.

Mutation

In order to bring the large values close to the diagonal, the proposed GA changes the order of the components in the chromosome by using the mutation process. In this paper, heuristic mutation designed with an intensive search strategy, as proposed by Cheng and Gen (1994), is used. A set of chromosomes transformed from a given parent chromosome by exchanging no more than β genes is regarded as the neighbourhood of the parent chromosome.

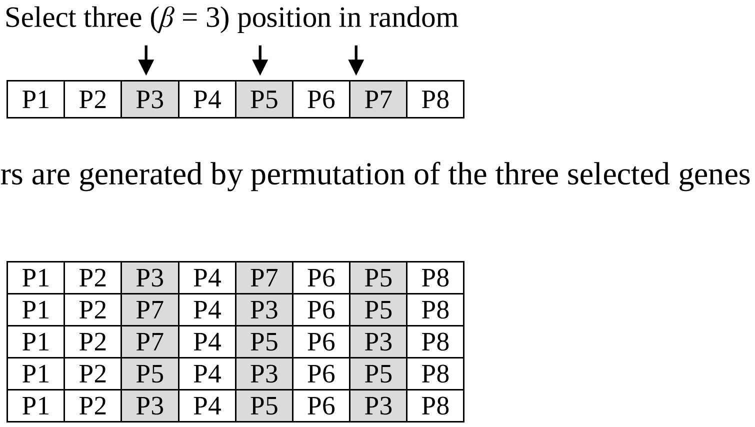
Mutation Procedure:

Step i. Pick β genes at random.

Step ii. Generate neighbours by all possible permutations of the selected genes.

Step iii. Evaluate all the neighbours and the select the best offspring.

This procedure is illustrated in Figure 4.



Select three (β = 3) position in random

P1	P2	P3	P4	P5	P6	P7	P8

All possible neighbours are generated by permutation of the three selected genes

P1	P2	P3	P4	P7	P6	P5	P8
P1	P2	P7	P4	P3	P6	P5	P8
P1	P2	P7	P4	P5	P6	P3	P8
P1	P2	P5	P4	P3	P6	P5	P8
P1	P2	P3	P4	P5	P6	P3	P8

Figure 4 Illustration of the heuristic mutation operator

Selection

Current selection procedures include the roulette wheel method of fitness-proportional selection. With this type of selection, if the five best chromosomes in the previous generation are superior to those in the new generation, five inferior individuals are removed randomly from the new population, and the best five of the previous population are added to the new population.

Other parameters: Maximum generations: 150; Population Size: 100; Cluster Parameter: 0.5; Cluster Penalty: 10.

The GA tends to move the highest valued off-diagonal elements closer to the diagonal, which moves the highly coupled processes closer to one another in the sequence. The chromosomes are of permutation types used for ordering problems. The string length is the same as the number of components involved; if ‘n’ components are considered, then all possible orders (n!) can be potential solutions. From these feasible solutions, the GA searches for the optimal solution, in which the objective function is minimized.

Step 7: Identify the modules

The modules are identified by grouping high value cells and the respective parts around the diagonal in the same module. The modules may be loosely coupled with other modules.

4. ILLUSTRATIVE EXAMPLE

In this section, a case example is used to illustrate and numerically validate the proposed AHP and the genetic algorithm based on clustering methodology for formation of the best modules. The step-wise application of the proposed methodology on the case example is discussed below. First, an example of five types of hand-held drills, heavy duty, high performance, high value, standard, and multipurpose (Choubey, 2007), is taken into consideration. In the second step, the physical decomposition of the product on the basis of functional characteristics is made, as shown in Table 3.

Table 3 Physical decomposition of the product

Nomenclature	Component Name	Nomenclature	Component Name
A	Encasing	L	Thin button to input speed
B	Rough palm	M	Wide button to input speed
C	Padded palm	N	16 slip clutch to transmit power
D	Diamond palm	O	22 slip clutch to transmit power
E	Bevel 2 point to lock/unlock battery	P	6 slip clutch to transmit power
F	Straight 2 point to lock/unlock r battery	Q	Solid shaft to transmit power
G	Square, 9.6 V, 2 pt. electricity transmission	R	Fine ring gear to switch speed
H	Open, 9.6 V, 2 pt. electricity transmission	S	Ring gear to switch speed
I	Chuck to secure/ unsecure bit	T	Black oval button to unlock switch
J	Chuck teeth to register/ unregister bit	U	Black button to unlock switch
K	Bit to act on object	V	Variable speed to switch power
		W	2 speed to switch power

In the third step, the interaction between components with respect to spatiality, energy, information and material, as shown in Table 1, is mapped in four DSMs, named D1, D2, D3, D4. The DSM with respect to the need for adjacency or orientation between two elements is shown in Figure 5.

	A	**B**	**C**	**D**	**…**	**…**	**V**	**W**
A	4	3	3	2	**…**	**…**	1	0
B	3	4	2	2	**…**	**…**	0	0
C	3	2	4	2	**…**	**…**	0	0
D	3	2	2	4	**…**	**…**	0	0
…	…	…	…	…	…	…	…	…
…	…	…	…	…	…	…	…	…
V	1	0	0	0	**…**	**…**	4	2
W	0	0	0	0	**…**	**…**	2	4

Figure 5 DSM constructed with respect to the spatial factor

In the next step, an analytical hierarchy process is used to map the importance of the spatial, energy, information and material factors with respect to drills. The opinion of decision makers is mapped in the pair-wise comparison matrix shown in Table 4a. The normalized pair-wise comparison matrix, along with the calculated weights of the test case, are shown in Table 4b. The weights of the spatial, energy, information and material factors are identified as W_1 = 0.694, W_2 = 0.158, W_3 = 0.096, W_4 = 0.052.

Table 4a Pair-wise comparison matrix

	Spatial	Energy	Information	Material
Spatial	1	7	9	9
Energy	1/7	1	3	3
Information	1/9	1/3	1	3
Material	1/9	1/3	1/3	1

Table 4b Normalized comparison matrix

	Spatial	Energy	Information	Material	Eigen value
Spatia;	0.733	0.808	0.675	0.563	0.694
Energy	0.105	0.115	0.225	0.188	0.158
Information	0.081	0.038	0.075	0.188	0.096
Material	0.081	0.038	0.025	0.063	0.052
	1	1	1	1	1

In the next step, the aggregated DSM is constructed by multiplying matrices D_1, D_2, D_3 and D_4 by their respective weights, W_1, W_2, W_3 and W_4 and adding the weighted matrices as defined by equations 6 and 7. Subsequently, the position of the components in the aggregated DSM is varied several times by the GA to form the clusters of parts. The chromosome represents the position of the component both in the row and column. An example of chromosome coding is shown in the string below.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W

For initialization, 100 random chromosomes are generated. The fitness value of the chromosome is calculated using equation 8, considering the cluster parameter τ as 0.15. Using the heuristic mutation method described in the previous section and the roulette wheel selection mechanism, the GA will rearrange the positions of the genes in the chromosome to obtain a least penalty situation. The following parameters are used for GA:

Maximum generations : 150   Population Size : 100
Cluster Parameter : 0.15   Cluster Penalty : 10

After 150 iterations, the least fitness value chromosome is obtained. The sequence of appearance of the various components in the chromosomes in the test case is shown below.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
D	B	C	H	E	F	G	A	L	M	N	O	P	Q	T	U	I	R	S	K	J	V	W

It was found that near this iteration, the variation in the fitness value is very small or negligible compared to previous iterations. The reduction in the fitness value in line with iteration is shown in figure 6.

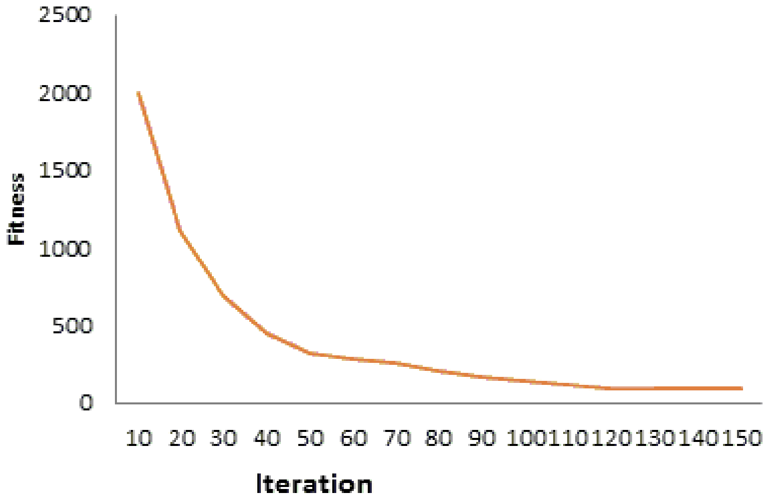


Figure 6 Fitness function with iteration

Step 7: Modules are identified by selecting high density clusters around the diagonal, as shown in Figure 7.

	D	**B**	**C**	**H**	**E**	**F**	**G**	**A**	**L**	**M**	**N**	**O**	**P**	**Q**	**T**	**U**	**I**	**R**	**S**	**K**	**J**	**V**	**W**
D	4	2.4	2.4	2.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B	2.4	4	1.6	1.6	0.8	0	0	0.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	2.4	1.75	4	1.6	0.8	0	0	0.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
H	2.4	1.6	1.6	4	0.8	0	0	0.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E	0	0.8	0.8	0.8	4	0.3	0.3	1.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
F	0	0	0	0	2.7	4	0.3	2.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
G	0	0	0	0	2.7	0.3	4	2.7	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A	0	0.8	0.8	0.8	1.9	0.3	0.3	4	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
L	0	0	0	0	0	0	0.1	0.2	4	1.9	2.4	0	0	0	0	0	0	0	0	0	0	0	0
M	0	0	0	0	0	0	0	0	1.9	4	2.4	0	0	0	0	0	0	0	0	0	0	0	0
N	0	0	0	0	0	0	0	0	2.7	2.7	4	0	0	0	0	0	0	0	0	0	0	0	0
O	0	0	0	0	0	0	0	0	0	0	0	4	2.7	0	0	0	0	0	0	0	0	0	0
P	0	0	0	0	0	0	0	0	0	0	0	2.5	4	0	0	0	0	0	0	0	0	0	0
Q	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2.4	2.4	2.4	2.4	2.4	0.2	0	0	0
T	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	4	2.4	2.4	2.4	2.4	0	0	0	0
U	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	2.4	4	2.4	2.4	2.4	0	0	0	0
I	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	2.4	2.7	4	2.4	2.4	0	0	0	0
R	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	2.4	2.4	2.4	4	2.4	0.2	0	0	0
S	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	2.55	2.4	2.4	2.4	4	0	0	0	0
K	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	4	2.4	2.4	2.4
J	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	4	2.7	2.7
V	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	2.4	4	2.4
W	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.4	2.4	2.4	4

Figure 7 Grouping of parts in the DSM rearranged by GA

5. RESULTS AND DISCUSSION

Figure 7 shows the module formation after applying the genetic algorithm to the Test case. In order to analyse the effect of weight on the formation of modules, experiments were conducted using different weight combinations. The following weights were used:

Category/ Weight	Test1	Test 2	Test 3	Test 4
Spatial (W1)	0.800	0.550	0.450	0.050
Energy (W2)	0.100	0.250	0.350	0.050
Information (W3)	0.050	0.100	0.100	0.100
Material (W4)	0.050	0.100	0.100	0.800
Total	1.000	1.000	1.000	1.000

Taking into account the above weights, four weighted aggregate matrices were constructed. After running the GA program for these, it was noticed that module formation changed with variation in weight. The following modules were obtained by using the proposed methodology for the above set of weights:

In the case of Test 1: Module-I [D, B, C, H, E, F, G, A], Module-II [L, M, N], Module-III [Q, T, U, I, R, S, K] and Module-IV [K, J, V, W]. It was observed that some components overlapped, which indicates that such components are suitable for all modules.

In the case of Test 2: Module-I [D, B, C, H, E, F, G], Module-II [L, M, N], Module-III [Q, T, U, I, R, S, K] and Module-IV [J, V, W]. In this case, component A does not fit into any module, so it is outside all of them. Unlike in Test 1, in Test 2 K is not an overlapping component.

In the case of Test 3: Module-I [D, B, C, H, E, F, G] and Module-II [Q, T, U, I, R, S, K]. In this case only two modules were formed, as many of the interaction values in the aggregated matrix decreased below the threshold value. This decrease in interaction value was due to the decrease in the weight values of the spatial criteria.

In the case of Test 4: Module-I [D, B, C, H, E, F] and Module-II [Q, T, U, I, R].

In this case, the number of modules also decreased, as well as the number of components inside them, due to the decrease in the weight of the spatial and energy criteria.

From the above observations, it can be interpreted that the criteria weights have a significant effect on the output of the proposed GA and AHP-based method. The method provides a consistent, systematic and automatic way to cluster DSMs, and the clustering results can be either used directly, or as an initial clustering arrangement for subsequent expert tuning.

6. CONCLUSION

For complex design projects, due to mass customization and shorter design times, the execution of design cycles has become a very difficult task. Product architecture selection directly affects the ease or difficulty of design. Adoption of integrated architecture leads to efficient product functionality, but exponentially increases the difficulty of design and manufacturing tasks. However, by adopting modular architecture a firm can rapidly and cost effectively introduce products that meet the varied customer demand.

Most of the available methods do not consider multiple DSMs for mapping the relationship between components. In DSM, off-diagonal elements show strong coupling between two elements. In this paper, a Genetic Algorithm (GA) and Analytical Hierarchy Process (AHP)-based methodology is propose for the development of modules (chunks). In the proposed method, multiple DSMs represent the interaction between components with respect to different factors, such as spatiality and energy.

A case study of portable drills has been made. The interaction between two corresponding elements has been measured on a scale of 1 to 4, as proposed by Pimmler and Eppinger (1994). Using AHP, the weights of the factors are determined, and an aggregate DSM is obtained by adding together all the weighted DSMs. The penalty concept is used to calculate the fitness value. Each cell with a value greater than the threshold value τ is multiplied by its distance from the diagonal. The problem is defined in terms of the minimization of the fitness value or the overall penalty. By using a heuristic mutation method, the GA rearranges the order of appearance of the components in the aggregated DSM to bring higher value cells near the diagonal. By rearranging the order of components, the GA tries to minimize the overall penalty. After 100 to 150 generations, negligible variation in the fitness value was observed.. Finally, clustering was achieved by keeping adjacent high-density items along the diagonal in the same cluster. This method is best suited for cases in which the number of elements is large, and it significantly reduces the time required for modularization.

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