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Research Article

CELL FORMATION IN CELLULAR MANUFACTURING SYSTEMS USING ARTIFICIAL IMMUNE SYSTEM

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ABSTRACT

This paper presents an Artificial Immune System (AIS) algorithm for the cell formation problem. This algorithm is used for manufacturing cells and part families in the cellular manufacturing systems. This algorithm is suitable for forming a good block diagonal matrix for a cell formation problem with Machine Part Incidence Matrix (MPIM) as input. The objective of this algorithm is the maximization of Grouping Efficacy (GE), which is one of the most widely, used measures of quality for cellular configurations. A comparison of the proposed algorithm is made with other proven methods of cell formation problems by found in the literature and that the proposed algorithm is performing much better than the others.

INTRODUCTION

In today's competitive world, every organization tries to be on top of its competitors by providing better quality product at lower product prices. Globalization also demands for an entirely different method of production, which can accommodate continuous and rapid changes in the product design and market demand. This intensified rivalry places persistent pressure on manufacturing systems to be enhanced both in efficiency and effectiveness. This is manifested in the rising tendency of greater varieties of products with shrunk product life cycles. The traditional manufacturing systems are not able to satisfy these requirements. Hence, batch shop production has gained more importance. In batch shop production, a batch of one product is made after which the facility is changed to produce the batch of the next product and so on.

In batch shop production environment, the cost of manufacturing is inversely proportional to the batch size and the batch size determines productivity. In real time environment, the batch size of the components is often small leading to frequent changeovers, larger machine idleness and so lesser productivity. To alleviate this problem, Group Technology (GT) can be implemented to accommodate small batches without losing much of production run time. GT is a manufacturing philosophy based on the principle that similar things should be done similarly.

The Cellular Manufacturing System (CMS) is one of the most important applications of GT to production. CMS is used to divide the manufacturing facility into small cells in which the similar parts and its associated machines are grouped together to form a manufacturing cell. The primary concern in CMS is to identify the machine cells and part families such

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that the movement of parts from one cell to another cell is kept in minimum numbers. The identification of part family and its associated machine cells are called Cell Formation (CF).

The CF problem is recognized as an NP (Non-polynomial) complete problem (Andres and Lozano, 2006). Thus, in order to reduce difficulties in the CF, there have been several methods to solve this CF problem. These methods produce good solutions for well structured small size matrices where part families and machine cells exist naturally. But, so far, they produce ill-structured large size matrices in the block diagonalization and end up with many Exceptional Elements (EE). (Goncalves and Resende, 2004; Manimaran, *et al*., 2010) have provided comprehensive reviews of the methodologies for CF problems.

The new approach based on Artificial Immune System (AIS) on the clonal selection principle to solve CF problems with an objective function of maximizing of Grouping Efficacy (GE). AIS is one of the recently developed evolutionary techniques, inspired by the theory of immunology or Immune System (IS). Immunology is the scientific discipline that studies the response of IS, when a non-self antigenic pattern is recognized by antibodies (Castro and Zuben, 2005).

The biological IS is a robust, complex, adaptive system that defends the body from foreign pathogens. It is able to categorize all cells (or molecules) within the body as self-cells or non -self cells. There are two major branches of the IS, namely, (i) Innate immune system and (ii) Adaptive immune system. The innate immune system is an unchanging mechanism that detects and destroys certain invading organisms, whilst the adaptive IS responds to previously unknown foreign cells and builds a response to them that can remain in the body over a long period of time. This remarkable information processing biological system has caught the attention of solving optimization problems in recent years (Omkar, *et al*., 2008). A novel computational intelligence technique, inspired by immunology, has emerged, known as AIS. Several concepts from immunology have been extracted and applied for the solution of real-world science and engineering problems such as pattern recognition (Carter, 2000) scheduling (Chandrasekaran, *et al*., 2006) multi objective optimization (Tan, *et al*., 2008), and batch scheduling problem (Balaji and Porselvi, 2014). It should be noted that as AIS is still a young and emerging field, there is not yet a fixed algorithm template and hence, actual implementations may differ from time to time and types of problems.

PROBLEM FORMULATION

The most commonly used objectives in cell formation are to minimize intercellular movements and maximize machines utilization (Zolfaghari and Liang 1997). Analyse the performance of the proposed algorithm and to assess the quality of solutions based on a number of criteria. The criteria adopted for the comparison are the number of the exceptional elements, and the number of the voids inside cells. These criteria will be incorporated into very well known performance measure widely used in the literature to quantitatively evaluate and compare the solution matrices known as Grouping Efficacy (GE) which is proposed by (Kumar and Chandrasekharan, 1990). A mathematical definition of this measure is given as

Maximum GE $(\tau) = \frac{e - e_e}{e + e_0}$

e -Number of 1s in the matrix.

e_o - Total number of 1s in the off diagonal blocks

e_o - Total number of 0s (blanks) in the diagonal blocks

According to (Kumar and Chandrasekharan, 1990), the GE has more discriminating power than the grouping efficiency. For this reason, the GE is a better performance measure to distinguish ill-structured matrices from well-structured matrices especially when the matrix size increases.

SOLUTION METHODOLOGY

The clonal selection principle describes the basic features of an immune response to an antigenic stimulus. It establishes the idea that only those cells that recognize the antigen proliferate, thus, being selected against those that do not. The main features of the clonal selection theory are

1. The new cells are copies of their parents (clone) subjected to a mutation mechanism with high rates.

2. Elimination of newly differentiated lymphocytes carrying self-reactive receptors.

3. Proliferation and differentiation of mature cells on contact with antigens.

When an antibody strongly matches an antigen, the corresponding B-cell is stimulated to produce clones of its kind which then produce more antibodies. This mutation is quite rapid, often as much as "one mutation per cell division'' and this allows a very quick response to the antigens. It should be noted that, in the AIS literature, often, no distinction is

considered between B-cells and the antibodies they produce. Both are subsumed under the word "antibody" and statements such as mutation of antibodies (rather than mutation of B-cells) are common. There are many more features of the IS, including adaptation, immunological memory and protection against auto-immune attacks.

DISCUSSION

In this work, the principles of AIS are clonal selection, mutation and receptor editing, which are used to solve CF problems. The proposed AIS used in this work is taken from Chandrasekaran *et a.l* (2006) and modified slightly. Clonal selection maintains the quality of the solution by triggering growth of lower affinity antibodies. Mutation is used to diverse the search process and receptor editing helps in escaping from the local optimal solutions (Das and Gonzalez, 2002).

Cell Formation

To explain the logic of the AIS for CF, a 5 × 7 Machine Part incidence Matrix (MPIM) is selected for illustration. The data set contains 5 machines and 7 parts and the number of cells is considered as two. Table 1 shows a block diagonal matrix. The rows indicate machines and columns represent parts or components. When the input Machine Part Incidence Matrix (MPIM) is presented to the algorithm as shown in Table 2, the result is obtained in the form of a block diagonal structure where each block represents a cell. The elements outside the block diagonal structure are termed as Exceptional Elements (EE) that represents inter-cell moves. Thus, the primary objective of CF is to identify part families and machine cells that are, the parts with similar characteristics are processed within the same family, and machines are grouped into cells to maximize the GE.

Table 1. Block diagonal matrix

		Parts						
		1	7	2	3	4	5	6
Machines	1	1	1				1	1
	4	1		1	1	1		
	2			1	1	1	1	
	3				1	1	1	1
	5			1		1	1	1

Table 2. Machines parts incident matrix.

		Parts						
		1	2	3	4	5	6	7
Machines	1	1				1	1	1
	2		1	1	1	1		
	3			1	1	1	1	
	4	1	1	1	1			
	5		1		1	1	1	

Step 1: Initialization

Initialization plays a key role in the development of AIS. Each problem is a M×N MPIM as a input of the initialization. A string with a length of M+N needs to be encoded. The first M bits of the string represent the sequence of machines that appear in the rows of the MPIM, while the last N bits of the string represent the sequence of parts appearing in the columns of the MPIM. An initial population (initial solutions) of the desired size is generated randomly. The population size depends on the problem size. The number of initial solutions to be included in the population is called population size. In this problem, 20 samples are generated randomly.

Step 2: Individual candidate solution

The AIS computes the objective function GE for each antibody of the solution space, so that, the string with the maximize objective function value is determined.

Step 3: Evaluation

Calculate the affinity value of each antibody using the following equation. $Affinity = \frac{1}{GE}$

Step 4: Cloning

Cloning is a mitotic process that produces exact copies of the parent cells. Based on the affinity value of the individual string, the numbers of clones are calculated for the population by the equation

Number of clones =

$$\frac{Individual\ affinity}{Total\ affinity} x Population\ size$$

Step 5: Genetic operations

Genetic operations on clones are known as crossover and mutation.

Step 6: Evaluation

Evaluate the newly generated antibodies. The antibody–antigen affinities of antibodies generated in Step 5 are evaluated.

Step 7: Generate memory set

Memory set Q, which is analogous to memory cells in biological IS, is a group of antibodies with higher affinities.

Step 8: Receptor editing

Receptor editing is held after cloning and mutation processes. In this step, a percentage of the antibodies

(worst percentage B of the whole population) in the memory set Q are eliminated and randomly created antibodies are replaced with them.

Step 9: Examination

Examine the termination criterion. If the termination criterion is satisfied, the computation procedure stops, otherwise, Steps 2 to 8 are repeated until the mentioned maximum number of iterations has been reached

For the performance of the above algorithm, it is tested with different benchmark datasets that are collected from the literature. The first 36 datasets were collected from the (Goncalves and Resende, 2004) and the last four data sets were collected from (Unler and Gungor, 2009). All the forty datasets were tested with AIS with an objective of GE. These data sets reflect a balance of several critical factors for CF research that consists of small (5 × 7) as well as large (40 × 100), structured and ill structured matrices for obtaining the GE as shown in Table 3. In terms of GE, the proposed AIS are compared with Evolutionary

Table 3. Comparative results for GE

Pro. No.	Source		Other approaches			Proposed Method
		Size	EGA	HERBAL	KHMCF	AIS
1	King andNakornchai (1982)	5 x 7	73.68	-	73.68	73.68
2	Waghodekar and Sahu (1984)	5 x 7	62.50	70.00	62.50	62.50
3	Seifoddini (1989)	5 x 18	79.59	77.40		79.59
4	Kusiak (1992)	6 x 8	76.92		76.92	76.92
5	Kusiak and Chow (1987)	7 x 11	53.13	58.60	53.13	53.13
6	Boctor (1991)	7 x 11	70.37		70.37	70.37
7	Seifoddini and Wolfe (1986)	8 x 12	68.3			68.30
8	Chandrasekharan and Rajagopalan (1986a)	8 x 20	85.25	85.20		85.25
9	Chandrasekharan and Rajagopalan (1986b)	8 x 20	58.72	58.30		57.39
10	Mosier and Taube (1985a)	10 x 10	70.59	70.60	76.47	70.59
11	Chan and Milner (1982)	10 x 15	92.00	92.00		92.00
12	Askin and Subra-manian (1987)	14 x 24	69.86		65.75	65.38
13	Stanfel (1985)	14 x 24	69.33		69.33	65.48
14	McCormick et al (1972)	16 x 24	52.58		50.48	52.58
15	Srinivasan et al (1990)	16 x 30	67.83		67.83	67.83
16	King (1980)	16 x 43	54.86	54.40		44.23
17	Carrie (1973)	18 x 24	54.46		52.83	52.83
18	Mosier and Taube (1985b)	20 x 20	42.96	41.90	40.29	42.96
19	Kumar et al (1986)	20 x 23	49.65	49.30		45.68
20	Carrie (1973)	20 x 35	76.22	75.70		76.22
21	Boe and Cheng (1991)	20 x 35	58.07			55.94
22	Chandrasekharan and Rajagopalan (1989)	24 x 40	100.00	100.00	100.00	100.00
23	Chandrasekaran and Rajagopalan (1989)	24 x 40	85.11	85.11		85.11
24	Chandrasekharan and Rajagopalan (1989)	24 x 40	73.51	73.51		73.51
25	Chandrasekharan and Rajagopalan (1989)	24 x 40	51.97	50.90		51.97
26	Chandrasekharan and Rajagopalan (1989)	24 x 40	47.06	46.50	47.17	47.06
27	Chandrasekharan and Rajagopalan (1989)	24 x 40	44.87	44.30		44.87
28	McCormick et al. (1972)	27 x 27	54.27			51.37
29	Carrie (1973)	28 x 46	44.62			44.62
30	Kumar and Vannelli (1987)	30 x 41	58.48	59.30		58.48
31	Stanfel (1985)	30 x 50	59.66		59.43	59.66
32	Stanfel (1985)	30 x 50	50.51		58.86	50.51
33	King andNakornchai (1982)	36 x 90	42.64			42.64
34	McCormick et al. (1972)	37 x 53	56.42		56.42	59.29
35	Chandrasekharan and Rajagopalan (1987)	40 x100	84.03	84.03		84.03
36	Goncalves and Resende (2004)	15 x 12	86.67		86.67	86.67
37	Car and Mikac (2006)	8 x 10			66.67	66.67
38	Chu and Hayya (1991)	9 x 9			73.53	74.29
39	Jayakrishnan and Narendran (1998)	20 x 8			83.37	82.26
40	Masnata and Settineri (1997)	24 x 10			63.93	67.53

Table 4. Summary of results for GE

Comparisons	Total Number of problems	Preeminent		Identical		Inferior	
		Number of problems	%	Number of problems	%	Number of problems	%
EGA	36	08	22	27	75	01	03
Herbal	19	06	34	06	33	06	33
KHMCF	22	06	27	10	46	06	27

Genetic Algorithm (EGA) by (Goncalves and Resende, 2004), HERBAL by (Vitanov, *et al*., 2007) and K-Harmonic Means Cell Formation (KHMCF) by (Unler and Gungor, 2009). These results are summarized in Table 4.

From Table 4, AIS results are equal to the reference solutions for 75%, 34% and 46% of problems of EGA, HERBAL and KHMCF respectively. 22%, 34%, and 27% of solutions gives high GE when compared to the reference solutions. Meanwhile, the results of very few problems are inferior while comparing with existing approaches.

CONCLUSION

The proposed AIS approach has been used for solving CF problems with an objective of maximizing the GE. The algorithm uses simple but effective techniques for solving CF problems by calculating cloning process, genetic operations, and a receptor editing procedure. The proposed AIS algorithm is competent and proves to be a good problem-solving technique for CF problems.

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