

A NEW GENETIC ALGORITHM FOR THE CELL FORMATION PROBLEM
IN GROUP TECHNOLOGY

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To my dear grandmother and my first teacher İnci Oğuzülgen ..
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ABSTRACT

Cellular Manufacturing System (CMS) is considered as a competent strategy for batch type production. The motive behind using CMS is to reduce lead time and increase machine utilization. Zero-one machine part incidence matrix based on the machine part routing information is frequently used to form machine cells. In this study, a genetic algorithm is proposed to efficiently solve the Cell Formation (CF) problem considering the machine part incidence matrix. The algorithm is tested by using two different fitness functions on 35 problems from the literature and its performance is benchmarked with the outcomes of the three recent studies. Results are promising in both fitness score perspectives. The algorithm is then applied to datasets obtained from two supplier companies.

GRUP TEKNOLOJİSİNDE HÜCRE OLUŞTURMA PROBLEMİ İÇİN YENİ BİR
GENETİK ALGORİTMA

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ÖZET

Hücre İmalat Sistemi (HİS), toplu üretim için etkili bir sistem olarak görülmektedir. HİS kullanımının arkasında yatan neden, teslimat süresini en aza indirgeyip makine kullanımını eniyileme isteğidir. Genel olarak, parça-makine rotasından yola çıkılarak oluşturulmuş olan ikili tabanda atama matrisi kullanılmaktadır. Bu çalışmada, ikili atama matrisi göz önünde bulundurularak Hücre Oluşturma (HO) Problemi çözülmeye çalışılmıştır. Algoritma, iki farklı amaç fonksiyonu cinsinden, literatürde kullanılan karşılaştırma verileriyle denenmiş, performansı literatürdeki en yeni üç çalışma ile karşılaştırılmıştır. Her iki amaç fonksiyonundan da ümit veren sonuçlar elde edilmiştir. Ardından algoritma iki farklı tedarikçi firmadan edinilen veriler üzerinde denenmiştir.

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Chapter 1

1 INTRODUCTION

Group Technology (GT) is a management philosophy which is based on the principle that similar things, such as product design, process planning, fabrication, assembly and production control, should be done similarly (Askin and Standridge,1993). The main principle of GT is to decompose the organization area into sections, or cells, that behave like smaller organizational units which produce specific outputs. The cell, by its proper definition, is the essential unit of life. Since the early 1960s, similar to living organisms, manufacturing systems have also been said to possess cells that encourage continual performance improvements by closely locating people and equipment required for processing families of products. A cell, in this perspective, is a group of closely located workstations where multiple, sequential operations are performed on one or more families of similar raw materials, parts, components, products or information carriers (Hyer and Wemmerlöv, 2002). A manufacturing cell is a sole organizational unit within the manufacturing system, whose major goal is to physically process, transform, transmit, and add value to materials whose end state are products or components. If the cell concept is implemented to the shop floor-manufacturing area, the facility is said to operate in a Cellular Manufacturing (CM) environment. CM is favorable on reducing manufacturing costs as well as diminishing lead time of products in batch production. The most challenging problem in the implementation of CM systems is the cell formation (CF) problem. CF problem addresses the issues surrounding the creation of part families based on component processing requirements and the identification of machine groups based on their ability to process specific part families (Brown and Sumichrast, 2001).

The objective in CF problem is to minimize intercellular movements of the products while maximizing machine utilization (James et al, 2007). Formulated as an optimization problem, the CF problem has been shown to be a non-deterministic polynomial (NP) complete problem (Dimopoulos and Zalzal, 2000), that is, as the problem size increases the amount of computation also increases with an exponential

pattern. This occurrence results with an increase in the computational time. To solve the CF problem, we propose in this thesis a Genetic Algorithm (GA) approach. GAs are inspired by typical genetic development. Similar to that of biological process, GAs works with genes over the set of chromosomes performing crossover and mutation. Our aim is to construct an efficient and flexible algorithm for CF problem that can incorporate different fitness measures. The proposed algorithm is tested on 35 well-known instances from the literature and its performance is compared to those of hybrid grouping genetic algorithm (HGGA) in James et al. (2007) and enhanced grouping genetic algorithm (EnGGA) in Tunnukij and Hicks (2007). The organization of the thesis is as follows: In Chapter 2, we provide an overview of the CF problem and review the related literature. In Chapter 3, we describe the details of our algorithm. Chapter 4 is devoted to the computational study followed by two case studies in Chapter 5. Finally, Chapter 6 gives the concluding remarks and directions for future research.

Chapter 2

2 PROBLEM DESCRIPTION AND RELATED LITERATURE

CM is an application of the GT concepts to factory reconfiguration and shop floor layout design (Irani, 1999). There exist mainly three different traditional types of manufacturing facility layouts: product layout, cellular layout and functional layout. Some domains of application of cellular layout are machinery and machine tools, agricultural and construction equipment, hospital and medical equipment, defense products, automobiles and engines, piece parts and components, electronic products, chemical equipment and packaging industries (Irani, 1999). There are three different methods for cell design: visual inspection, production flow analysis (PFA) and part classification and coding (C&C). More detailed information about cellular manufacturing can be found in Irani's study on cellular manufacturing. There are three main phases in the design of a manufacturing cell (Dimopoulos and Zalzal, 2000):

- grouping of machines into cells, better known as the CF problem,
- layout of cells in the plant, and
- layout of machines within the cells.

Some of the recent studies are promising for CM area. Zolfaghari et al. (2005) compared the performance of a new hybrid manufacturing system (combination of job shop and CM) with a conventional CM System. Mahdavi and Mahadevan (2008) proposed an algorithm (CLASS) for cellular manufacturing system and layout design by using sequence data. Chtourou et al. (2007) offered a critical review of simulation studies in CM. The following sections describe the CF problem and review the relevant literature on CF problem including GA applications.

2.1 Description of the Cell Formation Problem

CF is the main step of the CM design process. The manufacturing system is divided into cells that work for producing a family of parts or components. The objective is mainly to minimize the inter-cell moves and obtain independently operating cells. The cell formation problem mainly constitutes grouping of machines into machine cells and parts into part families. This problem has a combinatorial pattern where there are m machines and n parts.

Selim et al. (1998) proposed a detailed review on CF techniques. These techniques can be classified into five main groups: descriptive procedures that are identified by Ballakur and Steudel (1987), cluster analysis, graph partitioning, artificial intelligence and mathematical programming. Figure 2.1.1 outlines the CF techniques (Selim et al., 1998)

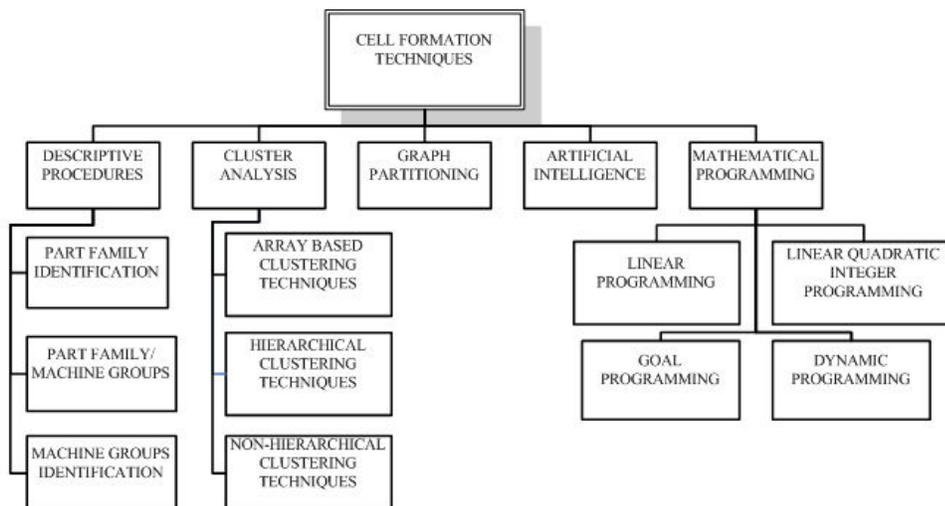


Figure 2.1.1 Outlines the CF techniques

Some early algorithms for cell formation are Production Flow Analysis (Burbidge, 1977), Rank Order Clustering (ROC) algorithm (King and Nakornchai, 1982) which is an array-based clustering technique, similarity-based clustering algorithm (McAuley, 1972), Zero-One Data-Ideal seed Algorithm for Clustering (ZODIAC), which is a non-hierarchical clustering algorithm (Chandrasekharan and Rajagopalan, 1989) and assignment model for cell formation (Srinivasan et al., 1990) which is a heuristic solution to p -median problem where the number of groups is not fixed (Onwubolu and Mutingi, 2001).

Originally, 0-1 linear programming p-median problem (Kusiak, 1987) seeks to form a fixed number of cells where the total similarity of machines in each cell is maximized. The formulation is as follows:

$$\text{Maximize} \quad \sum_{q=1}^m \sum_{j=1}^m \text{Similarity}_{qj} x_{qj} \quad (2.1)$$

Subject to

$$\sum_{j=1}^m x_{qj} = 1 \quad q = 1, 2, \dots, m \quad (2.2)$$

$$\sum_{p=1}^m x_{pj} = C \quad (2.3)$$

$$x_{qj} \leq x_{jj} \quad q = 1, 2, \dots, m, \quad j = 1, 2, \dots, m \quad (2.4)$$

$$x_{qj} = 0 \text{ or } 1 \quad q = 1, 2, \dots, m, \quad j = 1, 2, \dots, m \quad (2.5)$$

In the model, C is a parameter that represents the number of machine cells desired, so the user must know it a priori. The objective function (2.1) maximizes the total similarity of machines. Constraint (2.2) ensures that each machine belongs to one machine cell only and constraint (2.3) specifies the desired number of machine cells. Constraint (2.4) guarantees that machine q is assigned to machine cell j only when the machine cell is formed and constraint (2.5) represents either machine q belongs to machine cell j by using a binary decision variable, x_{qj} . (Heragu, 1998). Later, we will introduce a new similarity measure that addresses directly to machine similarities inside machine cells.

To reflect which part visits which machine, a binary machine-component incidence matrix is used. Although the binary representation does not reflect neither the varying lot sizes nor machine capacities and processing times, it is favorable because of the illustration simplicity. Machine-part incidence matrix is used in Rank Order Clustering (King and Nakornchai, 1982), ZODIAC (Chandrasekharan and Ragajopalan, 1989), MODROC that employs the ROC algorithm in conjunction with a block and slice method for obtaining a set of intersecting machine cells and non-intersecting part families followed by a hierarchical clustering method (Chandrasekharan and Ragajopalan, 1986), Bond Energy Algorithm which operates upon a raw input object-object or object-attribute data array by permuting its rows and columns in order to find informative variable groups and their interrelations (McCormick et al., 1972), Direct Clustering Algorithm in which families of

parts together during line-balancing optimization are grouped together (Chan and Milner, 1982) and Close Neighbor Algorithm where the user intervention is avoided (Boe and Cheng, 1991). By interchanging rows and columns of the incidence matrix, a block diagonal form is achieved (1s are brought to the diagonals). In an ideal solution, all the 1s will remain in the diagonal blocks of the incidence matrix and all the 0s in the off-diagonal blocks. Figure 2.1.2 shows an ideal solution to cell formation problem.

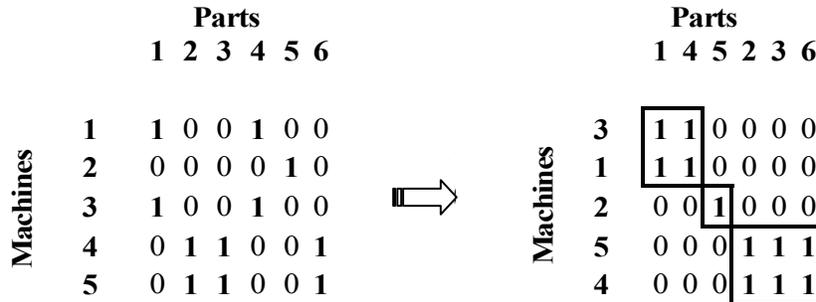


Figure 2.1.2 Ideal Case Solution to CF Problem

This implies that all the parts are produced entirely within their corresponding machine cells and the resulting manufacturing sub-systems achieve perfect independence that occurs rarely in practice (Won et al., 2004). If the perfect cell formation is not achieved, that means there are some exceptional machine-part incidences which remain outside the groups or some void incidences reduce machine utilization in the cell as shown in the figure 2.1.3.

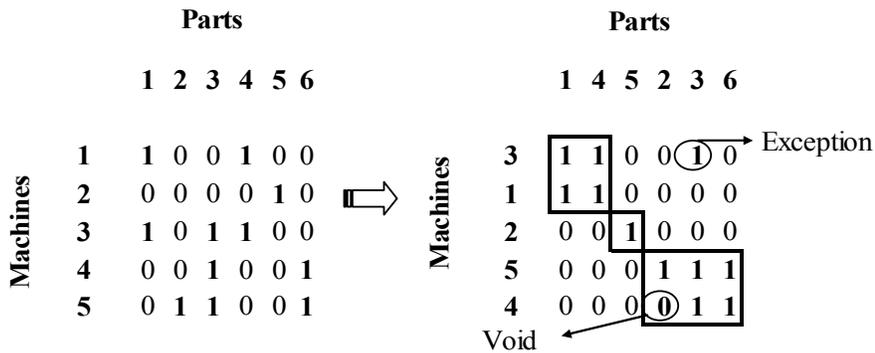


Figure 2.1.3 Exceptional and void elements

Some statistics in the literature are used to quantify the level of perfection of the resulting incidence matrix. These statistics are called performance measures. One of them is the grouping efficacy (Kumar and Chandrasekharan, 1990). This measure is meant to

find the goodness of block diagonal forms of binary matrices by using total number of nonzero incidences, e , number of voids, e_v , and number of exceptions, e_0 . The operational zone consists of the nonzero incidences and the voids. Finding the proportion of the sum of voids and exceptions in the operational zone will give us the inefficacy measure (2.6) of the incidence matrix as follows:

$$\frac{e_v + e_0}{e_v + e} \quad (2.6)$$

By subtracting the inefficacy measure from 1 we obtain the efficacy measure (2.7) of the incidence matrix as follows:

$$1 - \frac{e_v + e_0}{e_v + e} = \frac{e - e_0}{e + e_v} \quad (2.7)$$

Because the measure has a simple structure, it is widely used in recent studies in GT management philosophy where evolutionary algorithms exerted.

Grouping efficacy measure considers only 0-1 incidence matrix without making use of any similarity pattern between the machines other than part processing scheme. Alhourani and Seiffoddini (2007) proposed a new clustering technique for machine part grouping with a recently developed volume-based similarity coefficient that is based on the intercellular movement of parts. Wu et al.(2004) proposed a tabu search approach to CF problem. They introduced dynamic tabu tenure with a long term memory mechanism and two methods for quickly generating the initial solutions. Spilipoulos and Sofianopoulou (2008) proposed an efficient ant colony optimization system for the manufacturing CF problem that produces promising results for medium and large size instances. Yang and Yang (2008) proposed a modified adaptive resonance theory (ART1) neural network model where they evolve the ART1 model that was first used by Dagli and Huggahalli (1995). Dimopoulos and Mort (2004) proposed an evolutionary methodology for the construction of new similarity coefficients that can be used by standard hierarchical clustering techniques in CF. Yasuda and Yin (2005) introduced a comparative investigation on the similarity coefficients applied to CF problem and they founded out that Jaccard similarity coefficient is the most stable similarity coefficient.

2.2 Genetic Algorithm Approach to Cell Formation Problem

Invented in 1960 by John Holland, genetic algorithm (GA) is one of the most powerful algorithms developed in this century. GAs are favorable for solving complex problems with their ability to search large fitness landscapes. By means of its combinatorial nature, CF problem is an NP-complete problem where the traditional methods are incapable of finding optimal solutions to large instances within a reasonable amount of time (Dimopoulos and Zalzala 2000, Goncalves and Resende 2004). GAs, with their multi-directional searching ability in the fitness landscape, are less susceptible to becoming trapped in local optima (Yasuda et al, 2005) and more favorable than unidirectional stochastic searching methods such as Simulated Annealing (Kirkpatrick et al., 1983) and Tabu Search (Glover, 1989) where the search starts from a single state and converges to a local optima.

Unlike the mathematical programming approaches, GA does not need any complex mathematical representation. The main advantage of GA is that it only requires an objective function (or “fitness function”) that can be evaluated numerically (Tunnukij and Hicks, 2008). This function takes the required information from a string of numbers (binary, decimal, etc.) called as chromosome, where the necessary input to measure the performance of the current condition is given. To search a wide landscape, more than one chromosome is needed. These chromosomes are randomly initialized and form the initial population. Typically, the algorithm has three main operators:

- Selection Operator,
- Mutation Operator,
- Crossover Operator.

Selection operator provides fitter individuals to transfer their enclosed information to the next generations proportionally to their fitness scores or rankings. Some selection procedures are roulette wheel selection, ranking models, elitist methods and tournament selection. Selection mechanisms provide the transfer of the building blocks which are string templates (schemata) that match a short portion of the individuals and act as a unit to influence the fitness of individuals (Paz, 2000).

Mutation and crossover operators are mainly used to form new solutions from the existing ones. Some types of mutation are uniform mutation, multi-uniform mutation, non-uniform mutation, multi-non-uniform mutation and boundary mutation (Suresh and Kay, 1998). Mutation operators are used to find an alternative solution by only making a slight modification. As for the crossover operator, it is favorable to transfer a set of information from parents to offspring chromosomes. Like the mutation operator, crossover operator seeks to find an alternative solution to the current set of strings. Simple crossover, arithmetic crossover, cell-swap crossover and two-point crossover are different types of crossover operators.

The most common problem in using the GA is the computational speed. A way of reducing the computation time is to increase the computer power. Without upgrading the single computer, the power can be increased by using parallel GAs. The basic idea behind most parallel programs is to divide a task into chunks and to solve the chunks simultaneously using multiple processors (Paz, 2000). Paz classified parallel GAs into four categories: global master-slave parallelization, fine-grained algorithms, multiple-population and hierarchical parallel GAs.

Chaudhry and Luo (2005) proposed a survey on the application of GAs in production and operations management (POM). They reported that the use of GAs may be expanded to a broader range of areas instead of focusing onto specific studies. Nsakanda et al. (2007) prepared a technical note on ensuring the population diversity in GAs; they applied the experiment to the CF problem where they used the entropy-based and distance-based measures. Car and Mikac (2006) proposed a modified GA for solving CF problem based on emergent synthesis idea.

Faulkenhauer (1992) developed the Grouping Genetic Algorithm (GGA) where the drawbacks of the classical GAs are overcome significantly. GGA is a powerful algorithm that uses a special chromosome structure with its proper crossover, mutation and inversion operators. Brown and Sumichrast (2005) evaluated the performance advantages of GGA in three different types of problems and found that GGA performs well for solving grouping optimization problems.

James et al. (2007) proposed a Hybrid Grouping Genetic Algorithm (HGGA) where the standard GGA is coupled with a local search proposed by Gonçalves and Resende (2004). The algorithm makes use of the GGA with the chromosome encoding and the special crossover operator where they contribute a repair heuristic for the missing parts or machines. The chromosome encoding includes part families and machine groups as well as the machine-part cells. The crossover operation is different than normal crossover operators. The cross points are chosen from the cell numbers segment and part-machine segments are interchanged accordingly. Because there might be some missing parts or machines, a repair heuristic that takes the incidence matrix into consideration was used. Selection operator is the classical roulette wheel selection. They demonstrated that by incorporating the local search algorithm into a traditional grouping GA, they both improved the solution quality and reduced the variability of the solutions with fewer iterations than the traditional GGA. Results were tested with 35 well known instances from the literature and the performance of HGGA was shown to be at least as well as, and often better than, some of the best algorithms for the CF problem.

Tunnukij and Hicks (2008) developed an Enhanced Grouping Genetic Algorithm (EnGGA) where they introduced a new strategy that combines the elitist strategy with the rank-based roulette wheel strategy and configured the standard GGA replacement heuristic with a greedy heuristic. They compared their findings with 24 instances from the literature and obtained effective results that equal or outperform all the other methods considered including HGGA.

Mahdavi et al (2009) proposed a GA approach for solving the CF problem and obtained considerably good outcomes. The chromosome representation consists of two sections: the first section represents the parts and the second stands for machines. They introduced a non linear mathematical model based on the machine part incidence matrix and a new mutation operator. They benchmarked the results they found with other algorithms in the literature but did not take HGGA into consideration.

Since HGGA, EnGGA, and the algorithm proposed by Mahdavi et al. provide the best results, we use them in our computational study to benchmark the performance of our algorithm.

Chapter 3

3 PROPOSED ALGORITHM

The proposed algorithm is a GA used for assigning machines into machine cells via similarity based fitness measure and variable search mechanisms. Even though the diagonal structure gives a great deal of solutions, similarity based cell formation methods are more realistic for real life applications.

The proposed algorithm employs a variant of Jaccard similarity coefficient where the number of machines in a cell affects the total similarity measure of the instance. The randomness is carefully conserved during selection, crossover and mutation procedures. The selection operator is the classical roulette wheel mechanism where the chromosomes are valorized according to their fitness scheme and picked within a probability range of being selected. The crossover operator fragments the chromosome into three pieces and switches the intermediary sections. The uniformity of crossover points and the crossover rate are kept consistent in each generation. The mutation operator has two separate branches: random and guided mutation. Random mutation provides algorithm to search a wide landscape and guided mutation satisfies the need for converging to better results. The two mutation types are sequentially applied and the fitness landscape, in a broader view, looks like a sandglass that shrinks and enlarges consequently.

Although satisfactory percentages of the best individuals are reserved along the generations, the tendency of convergence cannot be overcome. In the case of aggregation into a single or two diverse chromosome structures, the best chromosome structure and the chromosomes with a constant survival probability are kept in hand whereas the remaining chromosomes are regenerated anew.

The chromosomes are assumed to be feasible if neither of machine cells disappear. To keep the feasibility intact, chromosome structures are continuously checked during the generation. The algorithm is run for a predetermined number of generations. We apply two search approaches: single population search and multiple populations search. The resulting best chromosome is given as an input to the part family formation procedure.

In this section, we briefly explain the performance measure and algorithm components to provide the reader detailed information on the steps and the characteristics of the proposed algorithm. The flowchart of the algorithm can be found in APPENDIX A.

3.1 Chromosome Structure

The algorithm has a simple chromosome structure where the genes correspond to cell numbers and the chromosome length corresponds to the total number of machines in the shop floor.

The general representation of the chromosome structure in this study is first used by Venugopal and Narendran (1992) and represents the simple machine assignment into cells. Figure 3.1.1 shows the chromosome structure of an example machine cell configuration. In this figure, machines {1, 3} are in cell 1, machine {2, 4, 7, 8} are in cell 2 and machines {5, 6} are in cell 3.

m_1	m_2	m_3	m_4	m_5	m_6	m_7	m_8
1	2	1	2	3	3	2	2

Figure 3.1.1 A chromosome structure example

Since the initial number of cells is defined at first, we assume that the least amount of machines in each cell must be equal to one.

3.2 Proposed Fitness Function

The fitness function for each chromosome is calculated by means of similarities between machines. Because Jaccard similarity coefficient (Jaccard, 1901) is found to be the most stable measure (Yin and Yasuda, 2005) for the CF problem, we preferred to use Jaccard measure instead of the other possible coefficients (Yin and Yasuda, 2006). The measure in equation (3.1) can be summarized as the proportion of the number of machines that operates on both of two parts to the number of machines occupied by either of the parts.

$$\frac{\text{\#Machines operating on Part A AND Part B}}{\text{\#Machines operating on Part A OR Part B}} = \frac{A \cap B}{A \cup B} \quad (3.1)$$

The incidence matrix in figure 3.2.1 is used for the example study in this chapter. Figure 3.2.2 shows an exemplar of the similarity coefficient matrix formed by using Jaccard measure. This matrix is generated in accordance with equation (3.1) and gives the similarities.

		Parts																				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
Machines	1	0	1	1	0	0	0	0	1	1	0	1	0	1	1	0	1	1	0	1	0	
	2	0	0	1	1	0	1	1	0	0	0	0	0	0	1	0	0	0	0	1	0	1
	3	0	1	0	0	0	0	0	1	1	0	1	0	1	1	0	1	1	0	1	0	
	4	0	0	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	1	0	1
	5	1	0	0	0	1	1	0	0	0	1	0	1	0	0	1	0	1	0	0	0	0
	6	1	0	0	0	1	0	0	0	1	1	0	1	0	0	1	0	0	0	0	0	1
	7	0	0	1	1	0	1	1	0	0	0	1	1	0	0	0	0	0	0	1	0	1
	8	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1

Figure 3.2.1 Incidence Matrix (Chandrasekharan and Rajagopalan, 1986a)

		Machines							
		1	2	3	4	5	6	7	8
Machines	1	-	0.13	0.90	0.06	0.06	0.06	0.13	0.07
	2		-	0.07	0.75	0.08	0.08	0.67	0.86
	3			-	0.00	0.07	0.07	0.06	0.00
	4				-	0.17	0.17	0.67	0.86
	5					-	0.56	0.15	0.08
	6						-	0.15	0.08
	7							-	0.75
	8								-

Figure 3.2.2 Similarity coefficient matrix

Fitness score reflects the quality of the resulting chromosome. In this study, we generated a fitness function, Fit (Equation 3.2), as the total average similarity score where the similarities between the machines and the number of machines in each cell are kept into account. Fit is equal to the sum of all average fitness scores per cell. S_{jkt} is the measure between two machines, k and t in cell j , d_j is the number of machines in cell j , C is the total number of machine cells, M is the total number of machines and i is the index for the evaluated chromosome.

$$Fit_i = \text{Fitness score for the chromosome}_i = \sum_{j=1}^C \frac{S_{jkt}}{d_j} \quad \forall k, t \quad (3.2)$$

Figure 3.2.1 also shows the machine assignments into three cells generated by James et al. (2005) for the given incidence matrix. By using this particular assignment as the chromosome structure, and similarity coefficient matrix, Fit is found to be 1.8647. The reason why we use the equation (3.2) is that finding the sum of all average fitness scores per cell gives much more reliable information on the total similarity score than finding the sum of similarities.

3.3 Selection Operator

The selection operator is roulette wheel selection. The values are normalized between 0 and 1 depending upon the fitness ensuring that the higher quality solutions are given a larger piece of the wheel (James et al., 2007). Because duplication is not allowed, chromosomes are avoided to mate with themselves. This constraint ensures that no fake convergence happens during crossover.

3.4 Crossover Operator

As a result of roulette wheel selection, the algorithm forms group of pairs of parent chromosomes, where the size of the group is half of the size of population. Then, two-point crossover is performed on the pair of chromosomes. By generating two rounded-up random points between 1 and $m-1$, we divide both of the parents into three sub-sections and interchange the intermediary parts to form a new pair of offspring chromosomes. Consider the two parent chromosomes in figure 3.4.1.

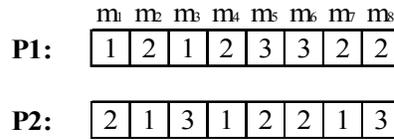


Figure 3.4.1 Randomly selected pair of chromosomes

The chromosomes are cut into three parts and intermediary sub-structures are swapped as shown in figure 3.4.2.

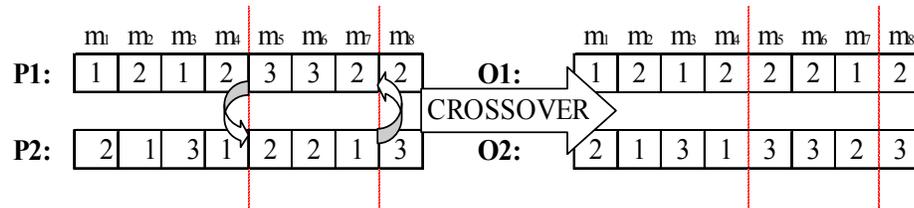


Figure 3.4.2 Two-point crossover

3.5 Infeasibility Check

Since the number of cells is pre-determined and empty cells are prohibited, the resulting offspring chromosome may be infeasible as is the case for O1 in figure 3.4.2. To overcome this problem, Gupta et al.(1995) used an adjustment operator where they iteratively search for locating a new machine into the empty cell so that no cell remains empty (Cheng Lee, 1998). We use the same procedure by making sure that a machine belonging to a singleton-cell with a single machine- is not selected for relocation. The infeasibility in offspring 1 in the example in figure 3.4.2 is eliminated by assigning either machine 5, 6 or 7 to cell 3 as seen in figure 3.5.1.

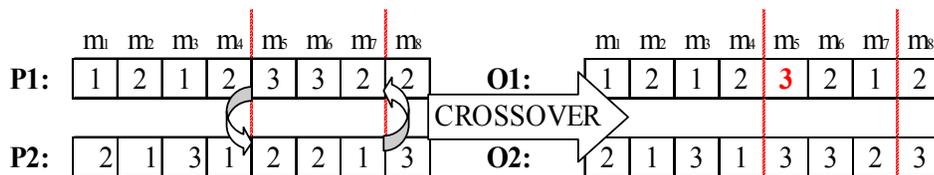


Figure 3.5.1 Feasible offsprings

3.6 Mutation Operator

To expand the search space, we use a dual mutation procedure. To prevent fast convergence, we apply different mutation rates within the generations. Once the mutation begins, the procedure is applied to all individuals of the population. By the time we increase the diversity among chromosomes, we use a mutation procedure to maximize the fitness score by relocating the least similar machine of the minimum scored cell to another cell where the similarity contribution is maximized. We name this method as guided mutation. Figure 3.6.1 describes the steps of the guided mutation.

- Step 1. Calculate the fitness scores for each cell
- Step 2. Find the cell with the minimum fitness score and check whether the cell is a singleton or not. If the cell is a singleton, check the second cell with the minimum fitness score. Continue until you find a non-singleton cell
- Step 3. Select the machine which is least similar to other machines in the cell
- Step 4. Relocate this machine iteratively to the other cells
- Step 5. For each iteration, calculate the contribution of changing the location of the machine to the fitness score
- Step 6. Put the machine to the cell where the highest contribution is achieved.

Figure 3.6.1 Steps of the guided mutation

Random mutation is performed to impede the convergence through local optimum. Each chromosome is randomly mutated by skipping the singletons.

3.7 Elitist Strategy

The elitist strategy is useful for keeping the best chromosome structures and progressively improving the set of chromosomes in every generation. To prevent fast convergence and increase diversity among chromosomes, elite individuals were selected according to their structures instead of their fitness scores. We also adopt an elitist strategy by replacing the least fit offsprings by the fittest parents. Figure 3.7.1 shows the steps of the elitist strategy.

- Step 1. Find l structurally different fittest individuals from the initial parent population where l is equal to 2 for the intervals A and C, and 6 for the intervals B and D.
- Step 2. Find l structurally different least fit individuals from the offspring population where l is equal to 2 for the intervals A and C, and 6 for the intervals B and D.
- Step 3. If the worst score of the set of fittest individuals is greater than the best score of the set of least fit individuals, replace the least fit individuals in the offspring population with the fittest individuals from the initial parent population.

Figure 3.7.1 Steps of the elitist strategy

3.8 Migration Strategy

If β percent of one type of chromosome or γ percent of two different types of chromosomes over the offspring population converges to the likewise structures, algorithm chooses to preserve a percentage of the fittest chromosomes with different structures over all the population, migrate ϕ chromosomes with a probability rate ν of being selected and store the remaining $1 - \phi$ chromosomes. The algorithm generates ν randomly thus ϕ value varies correspondingly. Figure 3.8.1 shows the states of the individuals before and after the migration.

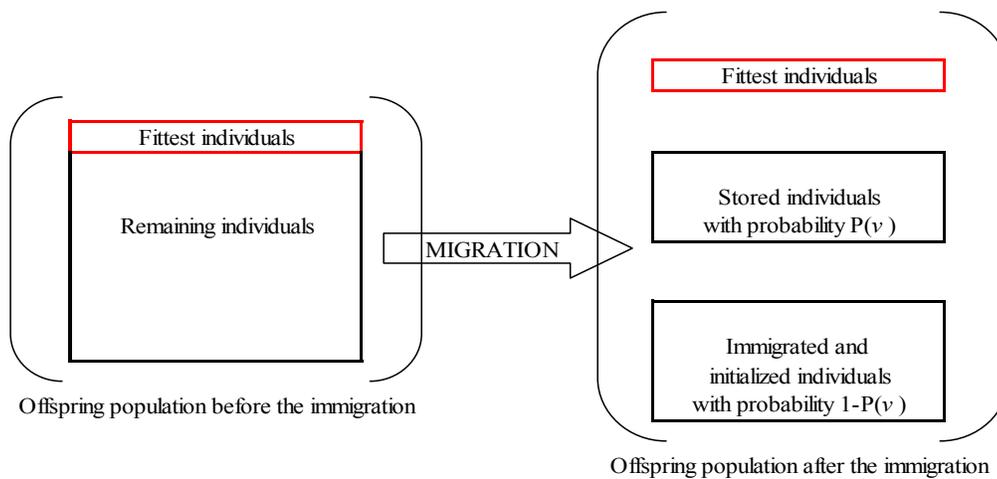


Figure 3.8.1 States of the individuals before and after the immigration.

3.9 Sequential Search Procedure

Running the algorithm for the given set of generation numbers just one time is mentioned as single search GA. Another way of searching is the parallel GAs. One of the parallel GAs is called multiple-population algorithm or the island strategy (Hartmann, 2000). The main idea behind this strategy is to select the fittest individuals (Equation 3.3) from ζ neighbor islands and bring them to the main island to produce offsprings. The environmental conditions are assumed to be constant in each island.

$$\# \text{ Fittest individuals} = \frac{\text{Population size}}{\zeta} \quad (3.3)$$

Figure 3.9.1 presents the procedure to locate individuals from neighbor islands to the main island. In this example, number of islands is taken as 5.

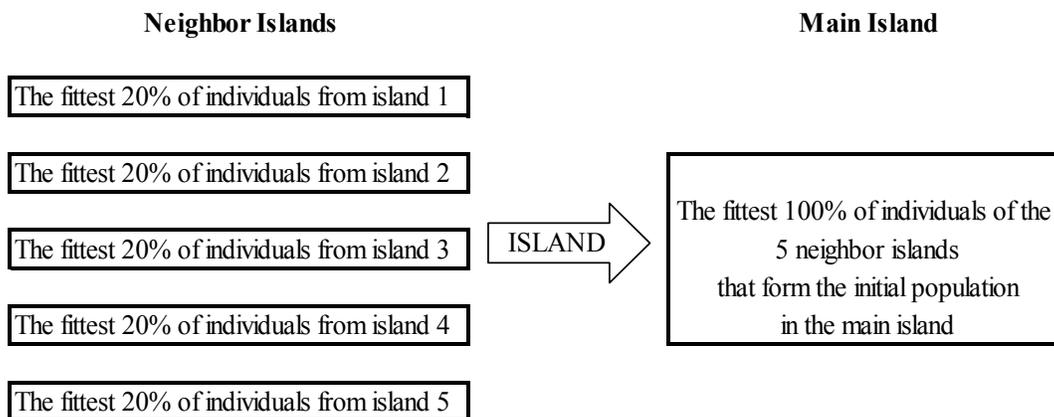


Figure 3.9.1 Formation of the main island population

Notice that the island strategy increases the search space by augmenting the number of iterations by $\zeta + 1$ times and provides opportunity to start with a better initial population. Also, it should be noted that island strategy is a kind of migration strategy where the best individuals are gathered together.

3.10 Part Family Formation Procedure

Once the machine groups are formed using the GA, the part families are constructed by using partial efficacy measure (Gonçalves and Resende, 2004). The idea behind this score

is mainly to put the part into the best possible cell to maximize the total efficacy of the incidence matrix. Figure 3.10.1 shows the steps of the part family formation procedure.

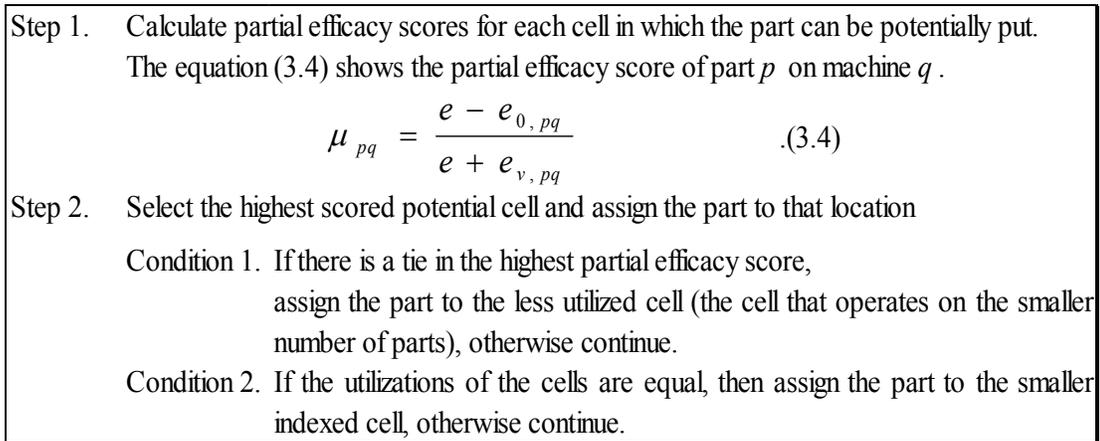


Figure 3.10.1 Steps of the part family formation procedure

After forming part families, we check whether there are missing families. If any, we randomly assign a part to the absent family (without perturbing singletons). The correction procedure is similar to the infeasibility check where we look for the missing machine cells in the chromosome structure.

Best chromosome structure is given as an input to the part family formation procedure by using partial efficacy measure. Note that the part families are formed only for the best fit chromosome.

Chapter 4

4 EXPERIMENTAL STUDY

The algorithm is tested with 35 well-known instances from the literature. The proposed GA was coded in MATLAB 7.0 (without using GA Toolbox) and run in high performance workstations (Intel (R) Core (TM)2 Quad CPU, Q6600 at 2.40GHz and 3.24GB of RAM). The information required to solve the algorithm included the part machine incidence matrix, the number of cells, the number of generations, and the size of the population.

4.1 Preliminary Experiments & Observations

The population size is set to 50. The probability of immigration is 0.3. The crossover rate is 0.5. The stopping criterion is determined as the number of generations. Different number of generations (120, 300, 900, 1800) and different run types (single population genetic algorithm and multiple population genetic algorithms) are applied and the best possible results are compared with the latest 2 methods performed on cell formation problem. The results over 5 different runs are explicitly given in APPENDIX B. The deviation of the results and the deviation from the best score in the literature for each search procedure are measured may also be checked from APPENDIX B.

Table 4.1 shows the chromosome length (#machines) and the corresponding best stopping criteria and search procedures in terms of two fitness measures (e.g. Instances with more than 30 machines and less than or equal to 40 machines converge to the highest similarity score by using 900 generations as stopping criterion and direct search (no island) procedure). The table is arranged by means of best scores with least deviation over 5 runs.

Efficacy Measure			Similarity Measure		
# Machines	Generation Size	Search Procedure	# Machines	Generation Size	Search Procedure
≤ 10	120	No island	≤ 10	120	No island
≤ 20	300	No island	≤ 14	120	No island
			≤ 16	300	Island-5
			≤ 20	900	Island-5
≤ 30	1800	Island-2	≤ 30	900	No island
≤ 40	1800	No island	≤ 40	1800	No island

Table 4.1 Generation size according to chromosome length

Figure 4.1.1 and 4.1.2 show the positive impact of the migration strategy over 5 runs. The same instance (instance 35) with the same number of machine cells and the same initial population are given as an input to the algorithm. As can be seen from Figure 4.1.1, 80% of the results converge through a local optima and only 20% give high scores. When the algorithm uses the migration strategy, 80% of the results converge to a favorable score.

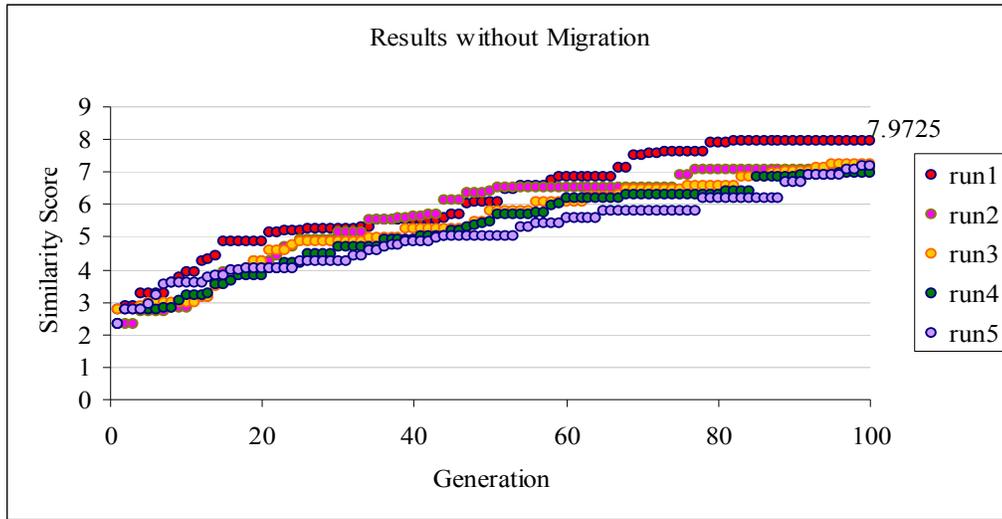


Figure 4.1.1 Results without migration

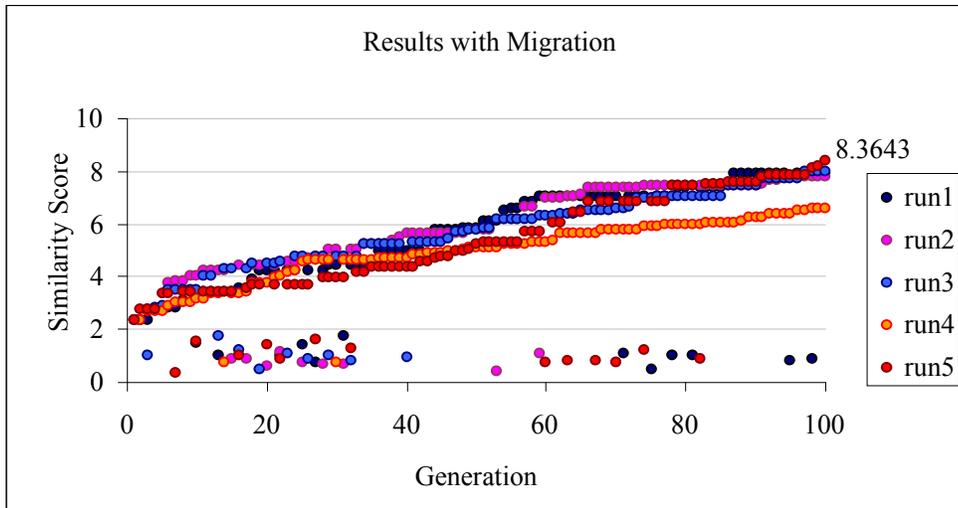


Figure 4.1.2 Results with migration

Figure 4.1.3 and 4.1.4, show the typical expected behavior of a 2-island strategy compared to a non-island strategy. If the same random initial population is used as a benchmark input for a single run of 20 generations and 2-island strategies, the island strategy gives better results. The instant drop in the island set 1 is caused by the migration operation and corresponds to a single value over 20 generations. The algorithm always keeps the best fitness score in hand and search for better results.

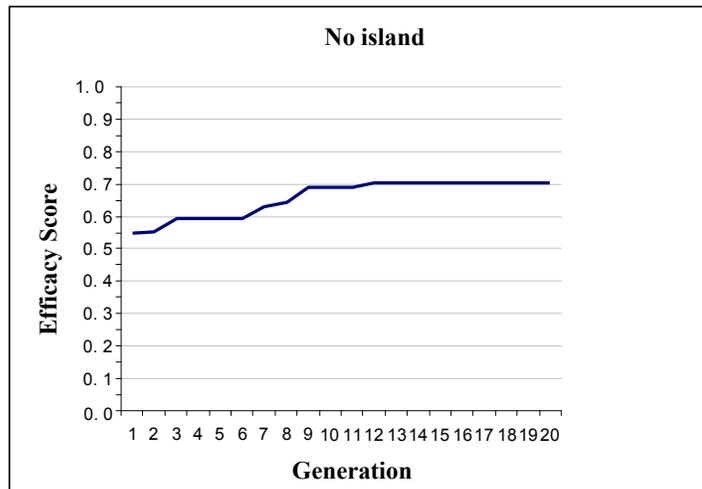


Figure 4.1.3 No-Island Strategy

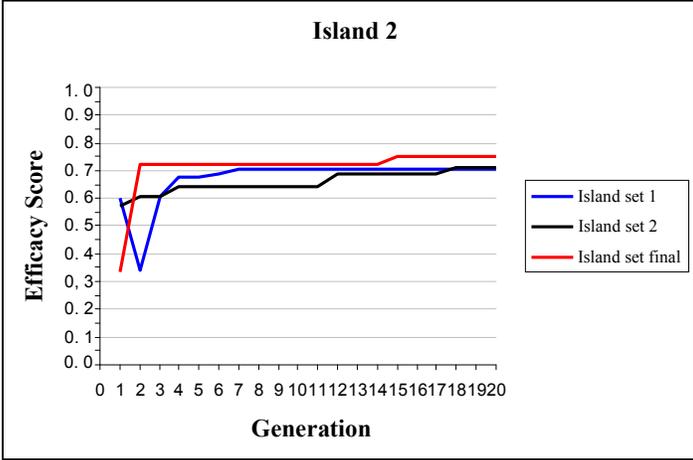


Figure 4.1.4 Island Strategy

It is important to note that our proposed algorithm is a sequential GA where the island strategy is used and run in a single processor. However, it can be converted by a slight modification into a parallel GA and run in multiple processors.

Figures 4.1.5 (a), 4.1.5 (b) and 4.1.5 (c) reflect the behavior of small instances while using the island strategy. It is obvious that island strategy is not useful on instances with small number of machines. The algorithm, within a single search, directly converges to the best solution found so far. Although the best solution can be found in early stages of the generations, to ensure that the results obtained are not trapped to the local optima, we preferred to run the instance until the stopping criteria is met. It can be seen that the island strategy may be useful when smaller number of iterations is chosen as a stopping criterion or more complex string of machines where a wider search space is required.

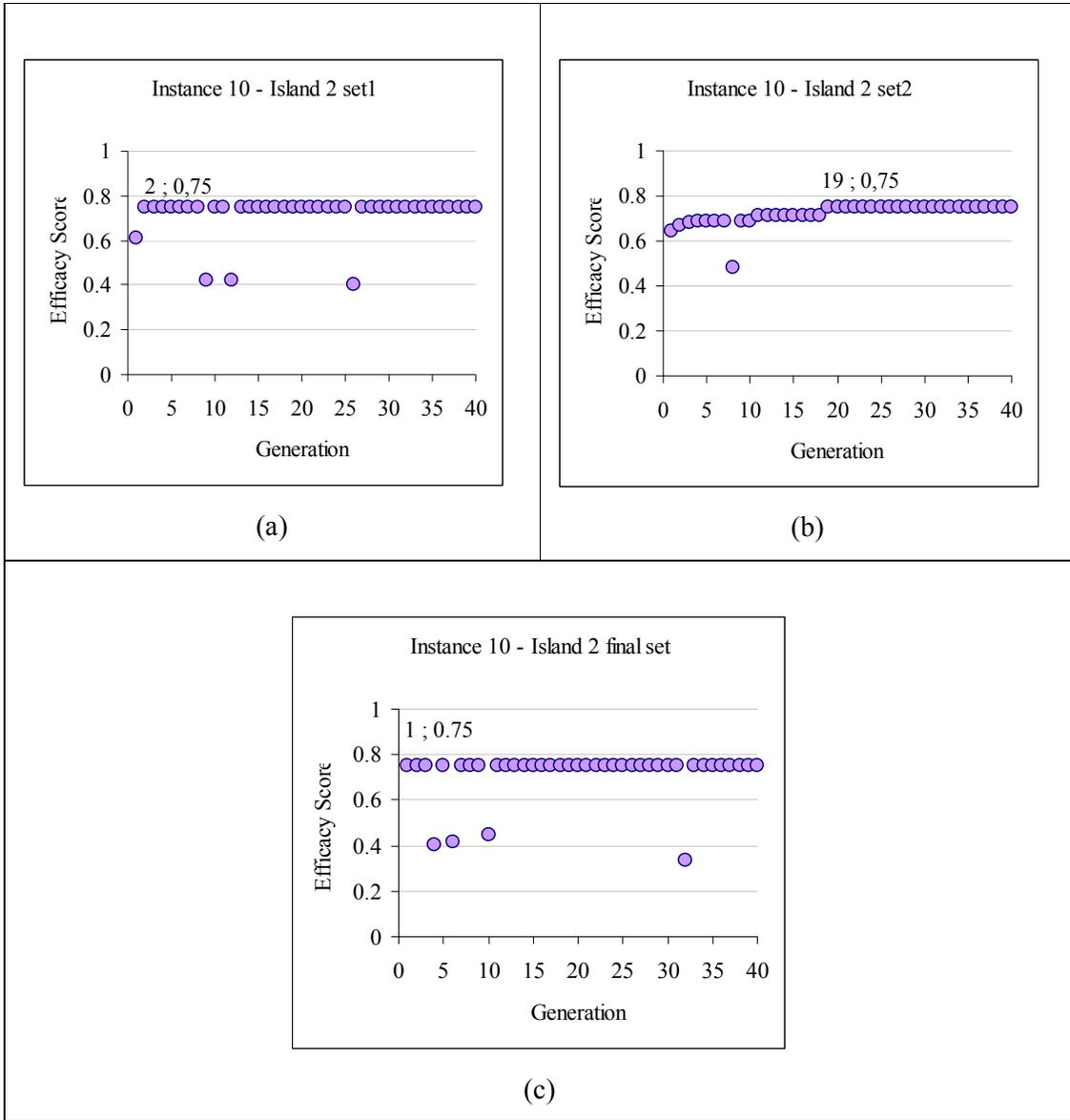


Figure 4.1.5 Convergence of the small sized instances (a) set1, (b) set2, (c) final set

Figure 4.1.6 shows the convergence of the algorithm with single search through the best score. The points that are apart from the convergence region symbolize the migration steps. Figure 4.1.7 shows the behavior of a large problem with 40 machines (instance 35) in case of 5-island procedure with 1800 generations. Each sub-procedure is run for 300 generations and structurally the best 10% of the chromosomes are collected and undergone 300 generations. A considerable increase in the results from the island run is detected.

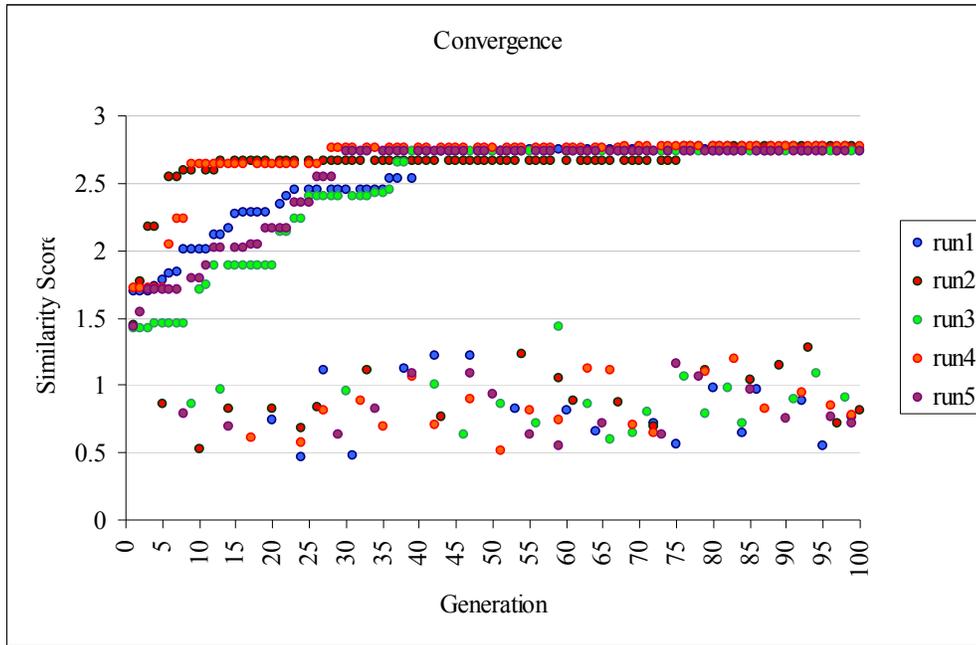


Figure 4.1.6 Convergence of the algorithm with single search through the best score

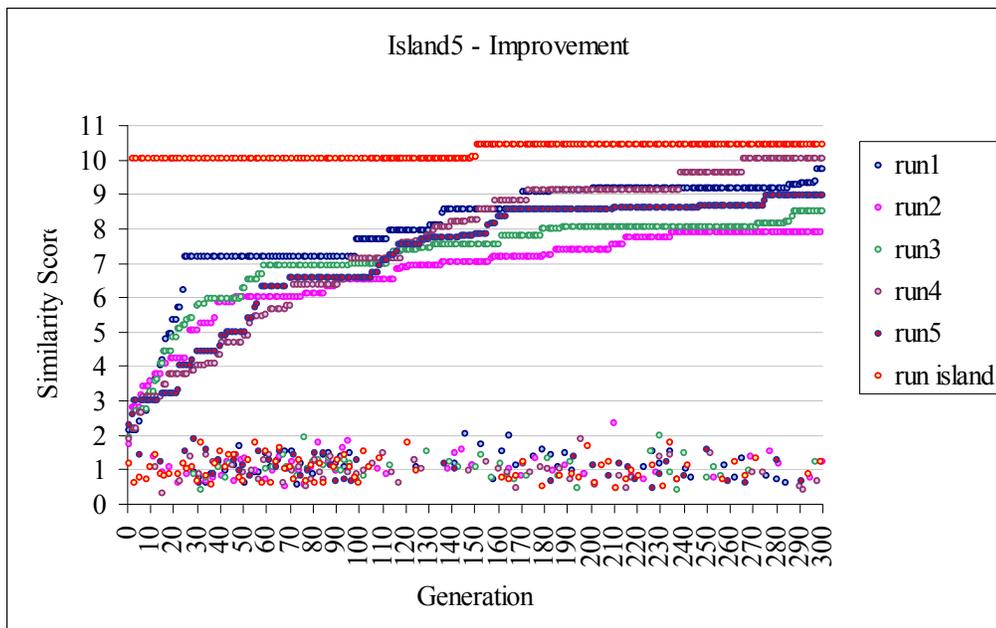


Figure 4.1.7 Behavior of instance 35 - 5-island-1800 generations

The mutation procedure is a dual mutation procedure where the mutation types differ according to generation number. Table 4.2 shows the behavior of the results in case of using two mutation types consecutively (e.g. random – guided means that we first use random mutation then we use guided mutation). Results demonstrate that higher results

using efficacy measure are obtained for large sized instances with a dual mutation procedure where the fitness landscape first shrinks and then enlarges by using first guided then random mutation. By taking similarity measure as the fitness function, we see that higher results are obtained by using either first random then guided mutation or fully random mutation.

Efficacy Measure						
Instance	Source	Size	Random - Guided	Guided - Random	Random - Random	Guided - Guided
18	Mosier and Taube	20 x 20	42.36%	43.36%	43.07%	43.07%
25	Chandrasekharan and Rajagopalan	24 x 40	52.63%	52.63%	52.41%	52.63%
26	Chandrasekharan and Rajagopalan	24 x 40	48.63%	48.61%	48.32%	48.32%
27	Chandrasekharan and Rajagopalan	24 x 40	46.26%	46.21%	45.89%	46.58%
28	McCormick et al.	27 x 27	54.52%	54.52%	54.45%	54.27%
29	Carrie	28 x 46	45.87%	46.48%	45.24%	46.46%
30	Kumar and Vannelli	30 x 41	63.31%	62.33%	61.54%	62.59%
31	Stanfel	30 x 50	59.66%	59.77%	58.48%	59.66%
32	Stanfel	30 x 50	50.55%	50.56%	50.55%	50.54%
33	King and Nakornchai	36 x 90	45.88%	46.61%	45.14%	45.75%
34	McCormick et al.	37 x 53	58.37%	58.86%	58.25%	58.37%
35	Chandrasekharan and Rajagopalan	40 x 100	78.74%	83.81%	83.81%	81.82%

Similarity Measure						
Instance	Source	Size	Random - Guided	Guided - Random	Random - Random	Guided - Guided
18	Mosier and Taube	20 x 20	2.3962	2.3962	2.3962	2.3962
25	Chandrasekharan and Rajagopalan	24 x 40	1.9761	1.9761	1.9761	1.9761
26	Chandrasekharan and Rajagopalan	24 x 40	1.6091	1.6079	1.6091	1.6109
27	Chandrasekharan and Rajagopalan	24 x 40	1.4662	1.4648	1.4662	1.4662
28	McCormick et al.	27 x 27	4.6528	4.6528	4.6528	4.6282
29	Carrie	28 x 46	2.4042	2.3909	2.4042	2.3562
30	Kumar and Vannelli	30 x 41	4.2765	4.1443	4.2765	4.2765
31	Stanfel	30 x 50	3.5298	3.5823	3.5823	3.5220
32	Stanfel	30 x 50	2.7592	2.7429	2.7592	2.7445
33	King and Nakornchai	36 x 90	2.0383	2.0276	2.0383	1.9803
34	McCormick et al.	37 x 53	8.8944	8.9150	8.9150	8.9122
35	Chandrasekharan and Rajagopalan	40 x 100	9.8432	9.5757	9.8432	9.4811

Table 4.2 Comparison on the sequence of dual mutation procedure (300 generations)

However, as can be seen in Table 4.3, for higher number of generations, there is no change on the highest results while using random-guided, guided-random or fully random mutations. In our calculations, we used first guided then random mutation.

			Similarity Measure			
			Random - Guided	Guided - Random	Random - Random	Guided - Guided
18	Mosier and Taube	20 x 20	2.3962	2.3962	2.3962	2.3962
25	Chandrasekharan and Rajagopalan	24 x 40	1.9761	1.9761	1.9761	1.9761
26	Chandrasekharan and Rajagopalan	24 x 40	1.6130	1.6130	1.6130	1.6130
27	Chandrasekharan and Rajagopalan	24 x 40	1.4662	1.4662	1.4546	1.4662
28	McCormick et al.	27 x 27	4.6528	4.6528	4.6528	4.6305
29	Carrie	28 x 46	2.3909	2.4042	2.4042	2.3909
30	Kumar and Vannelli	30 x 41	4.2765	4.2765	4.2765	4.2765
31	Stanfel	30 x 50	3.6171	3.6171	3.6171	3.5939
32	Stanfel	30 x 50	2.7592	2.7592	2.7575	2.7592
33	King and Nakornchai	36 x 90	2.0788	2.0788	2.0788	2.0763
34	McCormick et al.	37 x 53	8.9584	8.9584	8.9584	8.9584
35	Chandrasekharan and Rajagopalan	40 x 100	10.4205	10.4205	10.4205	10.1287

Table 4.3 Comparison on the sequence of dual mutation procedure for the similarity measure (1800 generations)

Figure 4.1.8 shows the intervals for the mutation rates and mutation types. Assume that the total generation number is 100. In case of mutation, the chromosomes in the generations between [1, 30] (Interval A) and the generations between [51, 80] (Interval C) are updated by using guided mutation whereas the rest of the chromosomes in the rest of the generations are randomly mutated.

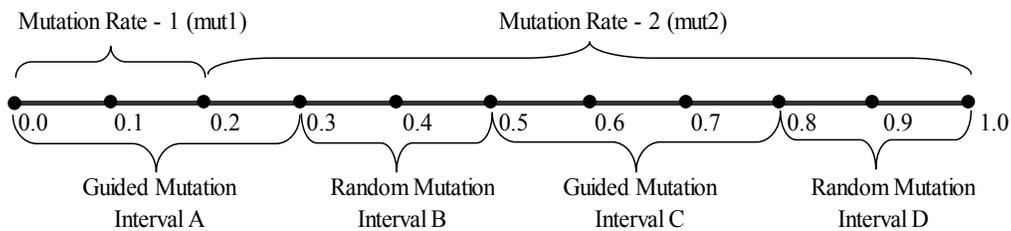


Figure 4.1.8 Intervals for the mutation rates and mutation types

Figure 4.1.9 shows the behavior of the algorithm in extreme crossover and mutation rates for different problems. As the chromosome lengths increase, crossover and mutation operators affect the fitness scores. Lack of both crossover and mutation operators results with poor scores whereas the application of both operators in every generation gives the highest scores.

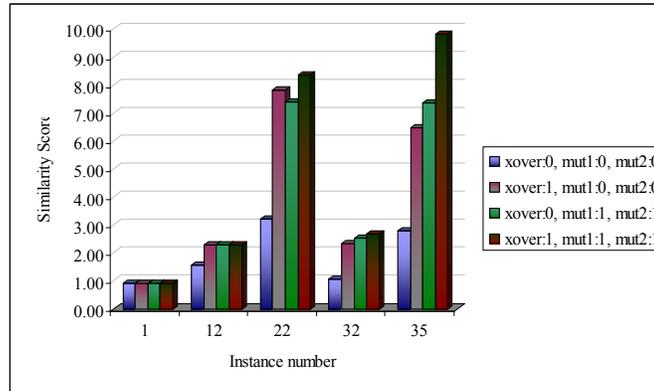


Figure 4.1.9 Impact of crossover and mutation rates to the average of the maximum of 5 runs

Crossover operator has a positive influence depending on the chromosome length. Mutation operator has better impact on higher chromosome lengths; however, it has slightly lower results in instance 22. The motive behind is the ideal case nature of the problem. If mutation operation is solely or predominantly applied, the results diverge through lower scores (Figure 4.1.9 and 4.1.10) A number of different crossover and mutation rates are experimented on the same set of instances and the average of the maximum results over 5 runs are compared in Figure 4.1.10. Because the rate of occurrences directly strikes the randomness, set [1, 1, 1] is directly eliminated. The best two set of rates are [0.9, 0.4, 0.2] and [0.5, 0.2, 0.1]. Set [0.9, 0.4, 0.2] gives better results on larger instances with lower number of generations. However, final results do not change and we used set [0.5, 0.2, 0.1] in our calculations.

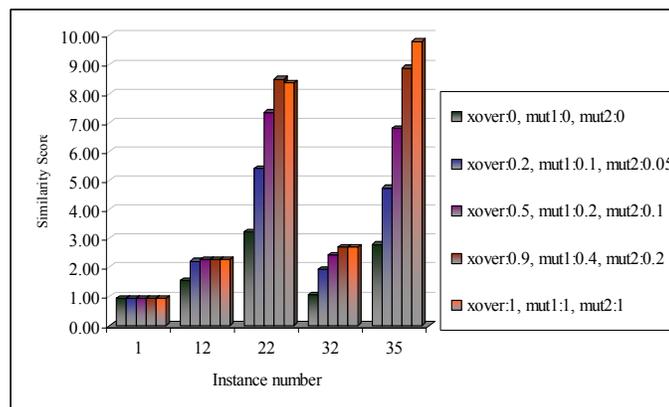


Figure 4.1.10 Average of the maximum of 5 runs vs. different crossover and mutation rates

4.2 Computational Results

All of the instances are taken from the original source to be sure that no error in the data occurs. The HGGA efficacy scores are also recalculated and the same observation that is made by Tunnukij and Hicks (2008) on the miscalculation of the instance-25 was also corrected.

Since both HGGA and EnGGA methods allow singletons, we can directly compare them in terms of efficacy and the similarity scores. However, because machine cells are not explicitly defined for EnGGA method, we can only measure the performance of the corresponding machine cell assignments with efficacy measure. We preferred not to show the results from the former methods because these two algorithms outperform the other results in the literature.

Table 4.3 shows the maximum scores found by using efficacy measure and the similarity measure in the genetic algorithm. The gaps between the best solution in the literature and our findings show that the new algorithm performs adequately well with the efficacy measure on the majority of the instances as well as the similarity measure always gives favorable results.

The best results for all the instances (Table 4.3) are chosen by taking into consideration the least deviation over 5 runs per instance in APPENDIX B. The corresponding incidence matrices are available in APPENDIX C and APPENDIX D.

The results from the literature defeats the outcomes of the proposed algorithm while using similarity measure as the fitness function. The reason behind this is that the final efficacy score found by using the proposed algorithm is calculated without making any local search throughout the part families.

One single generation, typically takes on average 1 second. The time it takes to converge directly depends on the generation number where the highest score over the set of generations is hit upon. Likewise, chromosome length, number of cells and probable use of operators straightforwardly influence the number of generations for convergence.

Instance	Source	Size	Efficacy Measure				Similarity Measure				
			Best Score	Source*	Proposed GA (%)	Gap (%)	Best Score (HGGA)	Proposed GA	Gap (%)	Corresponding Efficacy Score(%)	Gap (%)
1	King and Nakornchai	5 × 7	82.35	H, E	82.35	0.00	0.9306	0.9306	0.00	82.35	0.00
2	Waghodekar and Sahu	5 × 7	69.57	H, E, M	69.57	0.00	0.7667	0.7667	0.00	69.57	0.00
3	Seifoddini	5 × 18	79.59	H, E, M	79.59	0.00	0.9637	0.9637	0.00	79.59	0.00
4	Kusiak and Cho	6 × 8	76.92	H, E, M	76.92	0.00	1.3587	1.3587	0.00	76.92	0.00
5	Kusiak and Chow	7 × 11	60.87	H, E, M	60.87	0.00	0.2917	0.2917	0.00	58.33	-2.54
6	Boctor	7 × 11	70.83	H, E, M	70.83	0.00	0.7500	0.7500	0.00	70.83	0.00
7	Seifoddini and Wolfè	8 × 12	69.44	H, E	69.44	0.00	1.4111	1.4111	0.00	69.44	0.00
8	Chandrasekharan and Rajagopalan	8 × 20	85.25	H, E, M	85.25	0.00	1.8647	1.8647	0.00	85.25	0.00
9	Chandrasekharan and Rajagopalan	8 × 20	58.72	H, E, M	58.72	0.00	1.3779	1.4274	3.59	57.66	-1.06
10	Mosier and Taube	10 × 10	75.00	H, M	75.00	0.00	1.4375	1.4583	1.45	69.23	-5.77
11	Chan and Milner	10 × 15	92.00	H, M	92.00	0.00	2.9167	2.9167	0.00	92.00	0.00
12	Askin and Subramanian	14 × 24	72.06	H	72.06	0.00	2.1960	2.2933	4.43	69.70	-2.36
13	Stanfel	14 × 24	71.83	H, M	71.83	0.00	2.0368	2.1683	6.45	70.59	-1.24
14	McCormick et al.	16 × 24	53.26	H, E, M	53.26	0.00	1.4550	1.5116	3.89	51.09	-2.17
15	Srinivasan et al.	16 × 30	68.99	H, E	68.99	0.00	2.7690	2.7690	0.00	68.99	0.00
16	King	16 × 43	57.53	H, E	57.53	0.00	1.7193	1.8223	5.99	53.69	-2.43
17	Carrie	18 × 24	57.73	H, E	57.29	-0.44	1.8306	2.2306	21.85	56.25	-1.48
18	Mosier and Taube	20 × 20	43.18	H, M	43.18	0.00	2.1243	2.3962	12.80	40.16	-3.02
19	Kumar et al.	20 × 23	50.81	H	50.81	0.00	1.1360	2.9517	159.84	47.29	-3.52
20	Carrie	20 × 35	77.91	H, E, M	77.91	0.00	4.9661	4.9664	0.01	73.94	-3.97
21	Boe and Cheng	20 × 35	57.98	H, E	57.98	0.00	3.3295	3.3625	0.99	56.68	-1.30
22	Chandrasekharan and Rajagopalan	24 × 40	100.00	H, E, M	100.00	0.00	8.5000	8.5000	0.00	100.00	0.00
23	Chandrasekharan and Rajagopalan	24 × 40	85.11	H, E, M	85.11	0.00	6.2459	6.2459	0.00	85.11	0.00
24	Chandrasekharan and Rajagopalan	24 × 40	73.51	H, E, M	73.51	0.00	4.3729	4.3729	0.00	73.51	0.00
25	Chandrasekharan and Rajagopalan	24 × 40	53.29	H, E, M	52.63	-0.66	1.9473	1.9761	1.48	49.33	-3.96

* H: HGGA, E: EnGGA, M: Mahdavi et al

Table 4.4 Comparison of the proposed genetic algorithm with results from the literature

Instance	Source	Size	Efficacy Measure				Similarity Measure				
			Best Score	Source	Proposed GA (%)	Gap (%)	Best Score (HGGA)	Proposed GA	Gap (%)	Corresponding Efficacy Score(%)	Gap (%)
26	Chandrasekharan and Rajagopalan	24 × 40	48.95	H, E, M	48.95	0.00	1.5348	1.6130	5.10	46.90	-2.05
27	Chandrasekharan and Rajagopalan	24 × 40	47.26	H	46.81	-0.45	1.3008	1.4662	12.71	41.89	-5.37
28	McCormick et al.	27 × 27	54.82	E	54.52	-0.30	4.3823	4.6528	6.17	48.71	-6.11
29	Carrie	28 × 46	46.91	H	47.08	0.17	2.2180	2.4042	8.40	44.40	-1.13
30	Kumar and Vannelli	30 × 41	63.31	H, E	63.31	0.00	3.9587	4.2765	8.03	59.57	-3.74
31	Stanfel	30 × 50	60.12	H, M	59.77	-0.35	3.4633	3.6171	4.44	58.96	-0.81
32	Stanfel	30 × 50	50.83	H, M	50.83	0.00	0.7606	2.7592	262.76	48.94	-1.89
33	King and Nakornchai	36 × 90	46.35	H	46.78	0.43	0.5627	2.0788	269.43	42.82	-2.99
34	McCormick et al.	37 × 53	60.64	H, E	60.36	-0.28	8.6598	8.9584	3.45	49.95	-9.26
35	Chandrasekharan and Rajagopalan	40 × 100	84.03	H, M	83.81	-0.22	10.4205	10.4205	0.00	83.81	-0.22

*H: HGGA, E: EnGGA, M: Mahdavi et al.

Table 4.4 Comparison of the proposed genetic algorithm with results from the literature (Continued)

Chapter 5

5 CASE STUDY

The algorithm is applied to two supplier companies which currently operate on job shop environment.

5.1 General Information about the Cases

The first company, MERCAN MAKİNA A.Ş., is a small-medium sized supplier company with 1 factory in İzmir Kemalpaşa Industrial District. They supply various parts and components for 3 manufacturers in Turkey. There are a total of 13 active machines and 213 dynamically produced parts. Originally they have divided shop-floor layout into 7 sections. Because this study has never done before, the incidence matrix of the shop floor is made up anew.

The second company, KONVEYOR A.Ş., is a big company with 6 factories in Istanbul, Eskişehir and Manisa and 1300 employees in total. As of 2007, the company has reached an annual turnover volume of 80M €. They supply various parts and components for all appliance manufacturers in Turkey and for many other companies spread in Europe, Asia, Africa and South and North America. This study is performed in the factory (5000 sqm area with 2 floors) that is located in Istanbul Tuzla Industrial District. The approximate production capacity (in 2007) of the factory is 80000 parts /day. 387 workers work in 2-shifts and 7-days per week.

There are a total of 155 active machines and 767 dynamically produced parts. Originally they have divided shop-floor layout into 20 sections in accordance with 26 different operations. However, the company faced with lead time problems and they decided to analyze the factory configuration by using Cellular Manufacturing.

Because the visiting sequence of machines and parts are not separately defined, we formed the incidence matrix, from fresh, by using operation-part information. We maintained the same input parameters and assumptions that we used in the computational study.

We analyzed datasets for both fitness measures with different number of clusters for 1800 generations. The results found by using fitness measure over 5 runs and the corresponding efficacy score and the corresponding machine-part assignments are exposed in table 5.1

	Similarity Measure				Efficacy Measure	
	#Cells	Proposed GA	Deviation (%) over 5 Runs	Final Efficacy Scores (%)	#Cells	Efficacy Scores (%)
Mercan Makina A.Ş.	2	0.8933	0.00	42.33	2	48.08
	3	0.9438	0.00	54.21	3	55.62
	4	0.9864	0.00	54.29	4	56.42
	5	0.9864	0.00	54.50	5	56.60
	6	0.9652	0.00	54.86	6	56.77
	7	0.9158	0.00	56.18	7	56.60
	8	0.8521	0.00	55.81	8	56.54
	9	0.7799	0.00	55.54	9	56.62
	10	0.6728	0.00	55.70	10	55.63
	11	0.5432	0.00	55.57	11	55.49
	Konveyor A.Ş.	2	1.0417	0.00	32.14	2
3		1.2043	0.00	40.36	3	44.30
4		1.3091	2.07	41.70	4	46.20
5		1.3695	0.54	42.11	5	47.26
6		1.4177	0.47	46.21	6	47.99
7		1.4585	0.29	46.84	7	48.42
8		1.5001	0.37	46.98	8	48.66
9		1.5023	0.00	47.07	9	48.69
10		1.4979	0.23	47.11	10	48.84
11		1.4850	0.06	47.21	11	48.91
12		1.4712	0.00	47.44	12	48.93
13		1.4424	0.11	47.36	13	48.94
14		1.4111	0.00	47.50	14	48.99
15		1.3754	0.58	47.46	15	49.00
16		1.3291	0.00	47.83	16	49.00
17		1.2735	0.00	47.92	17	48.98
18		1.2025	0.09	48.43	18	48.93
19		1.1281	0.00	48.04	19	48.84
20		1.0533	0.00	48.05	20	48.70
21		0.9647	0.00	48.03	21	48.31

Table 5.1 Case results

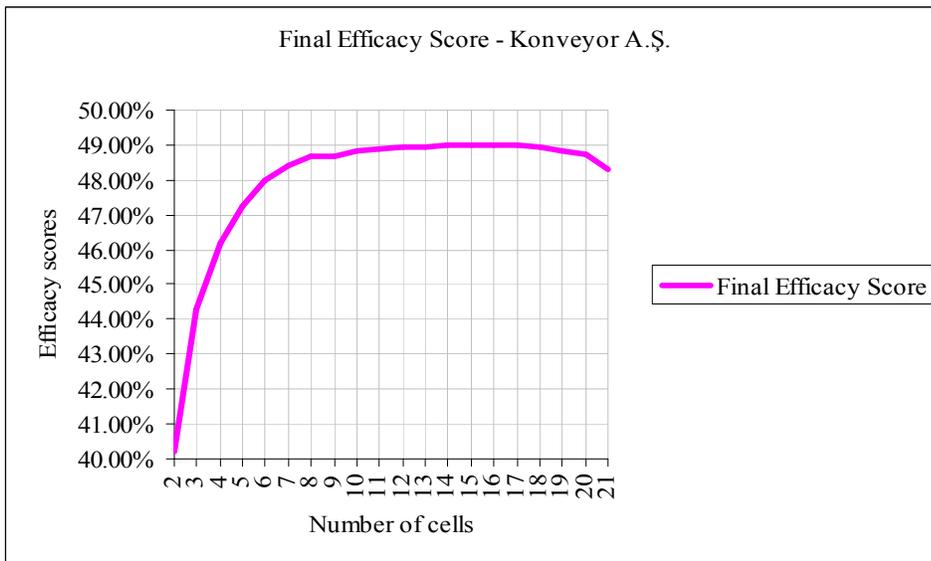
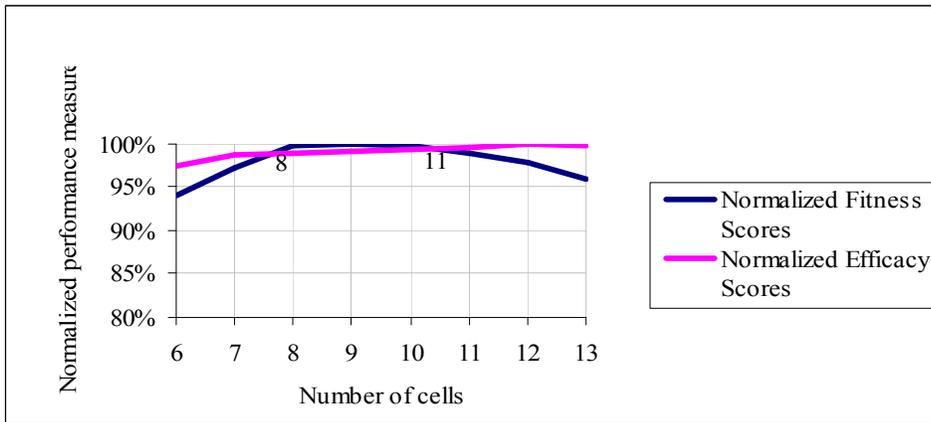
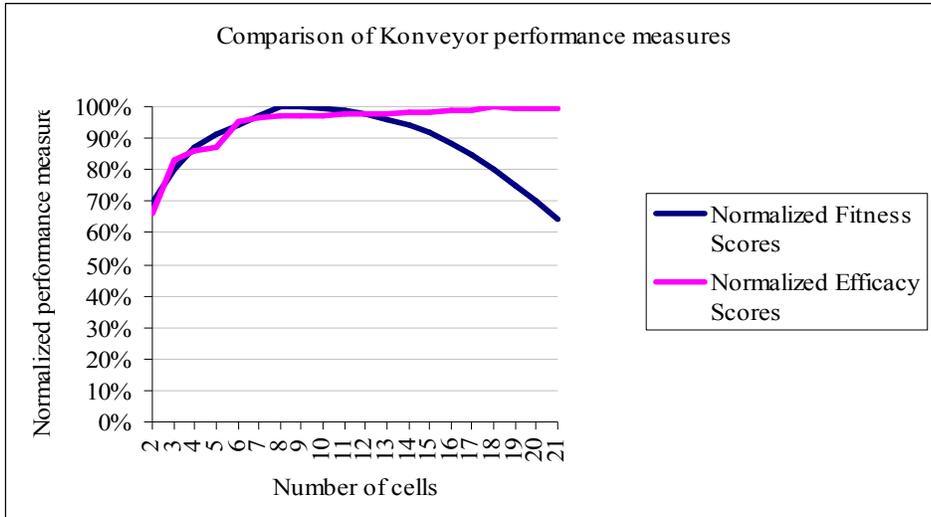


Figure 5.1.1 Konveyor A.Ş. performance measures vs. number of cells

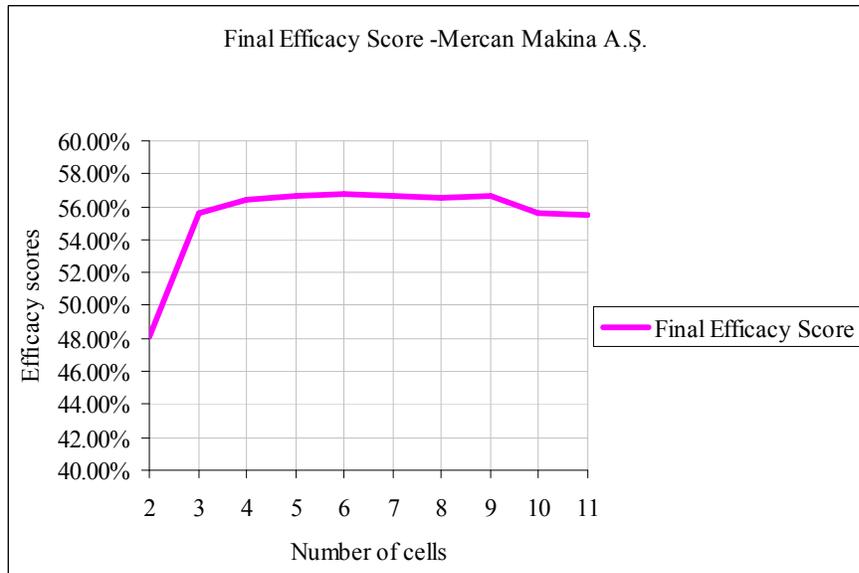
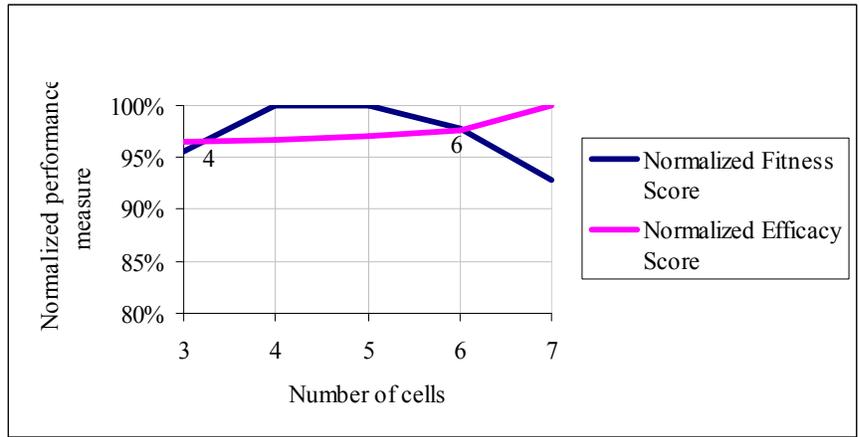
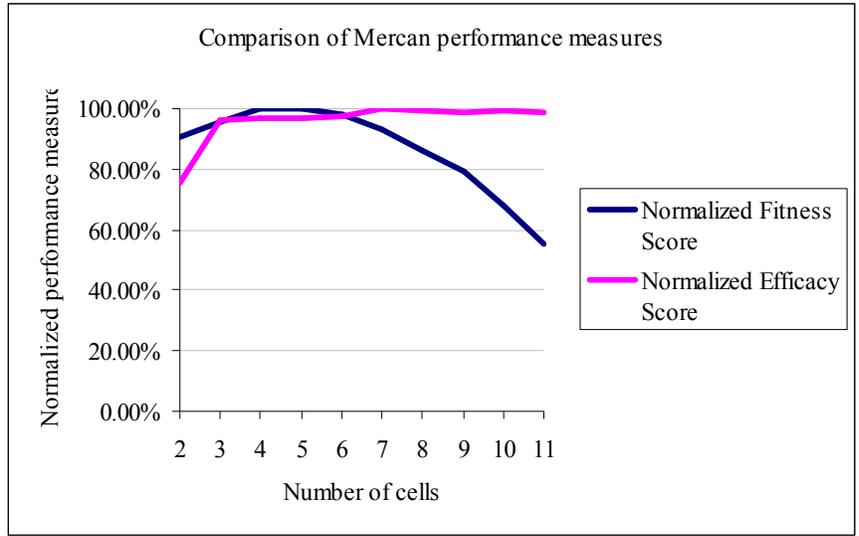


Figure 5.1.2 Mercan Makina A.Ş. performance measures vs. number of cells

Results show that our algorithm works well on real life cases. There is consistency of change in pattern of the fitness score versus number of cells. To compare the results of the similarity score more adequately, we normalized machine cell assignment scores and final efficacy scores by means of maximum score. Results show that, if the firm wants to form the clusters according to similarity between machine processes, we should suggest Mercan Makina A.Ş. to use between 4 – 6 cells and Konveyor A.Ş. between 8 – 11 cells. Exemplary machine part assignment schemes for both cases are given in APPENDIX E.

Figure 5.1.3 shows the convergence scheme, in terms of similarity score, of Mercan Makina A.Ş. Results show that the best score found as 0.9864 in the 50th generation and all of the 5 runs converged to the highest score in 129th generation.

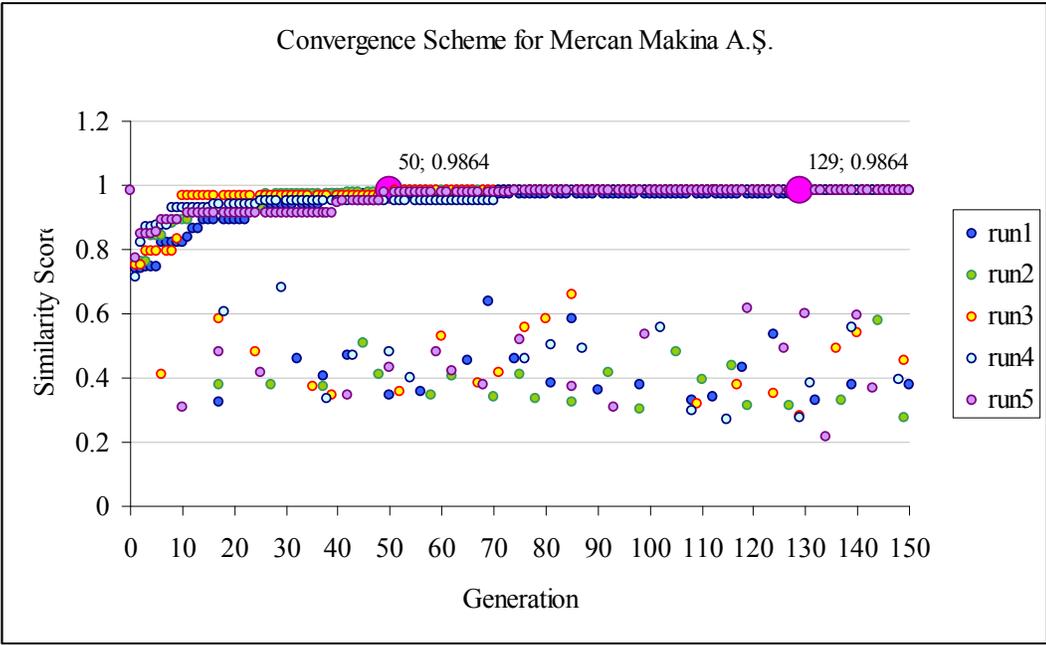


Figure 5.1.3 Convergence scheme for Mercan Makina A.Ş.

Figure 5.1.4 shows the convergence scheme, in terms of similarity score, of Konveyor A.Ş. Results show that the best score found as 1.5023 in the 729th generation and all of the 5 runs converged to the highest score in 1506th generation.

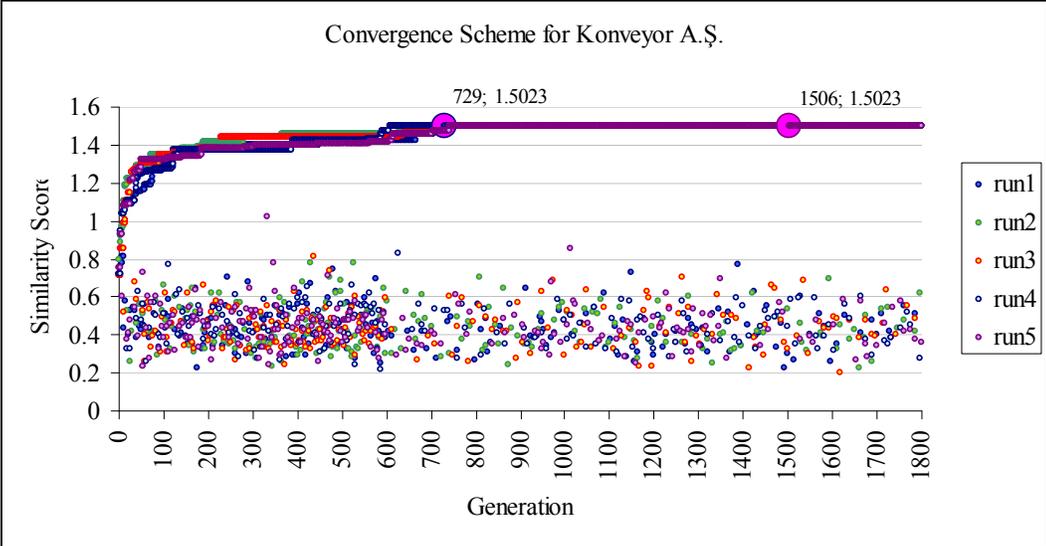


Figure 5.1.4 Convergence scheme for Konveyor A.Ş.

Both cases were run for 1800 generations with the standard parameters of the algorithm. Since the algorithm found the same results by using island strategies, the number of generations may be decreased by making a slight modification and running the cases in parallel machines instead of a single machine.

Chapter 6

6 CONCLUSION AND FUTURE WORK

This thesis proposes a GA approach for the machine cell formation problem utilizing a Jaccard-based similarity coefficient as the fitness function. However, the algorithm may be easily adapted for any other similarity measure. In GA, we use a simple chromosome structure that only contains machine cell information. Even though complex chromosome structures are favorable for holding more information to simultaneously form machine groups and part families, the simple structure is powerful on choosing the best machine cell configuration in a reasonable amount of computational time.

The roulette wheel selection procedure, a two-point crossover mechanism, random and guided mutation operators with an elitist strategy are applied for a pre-determined number of generations. The random mutation operator allows the algorithm to search a broad landscape whereas the guided mutation attempts to converge to better results in the neighborhood. The two mutation types are applied consecutively and the fitness landscape, in a broader sight, looks like a sandglass that shrinks and enlarges accordingly.

The performance of the proposed GA method is tested on 35 well-known problems and is compared to that of other GA approaches in the literature, which are known as best-in-class algorithms. Our comparison is based on both our similarity measure and the grouping efficacy measure. The results are promising with respect to the similarity measure and competitive with respect to the efficacy measure.

The proposed approach is also applied to two real life data that were collected from two plants operating in a job-shop environment. Different machine cell configurations are reported for varying cell numbers and sizes. The results show that the algorithm may be efficiently used in a real-life setting.

Further research on this topic may focus on the following extensions. First, the island strategy and the parameter selection may be investigated through a more in-depth experimental analysis. Second, other similarity measures may be considered to test the robustness of the algorithm. However, the comparison will be limited by the availability of benchmark data in the literature. A similarity measure based on production volumes may be particularly more realistic in an industrial environment. Furthermore, parallel computing may be used in the experiments with multiple populations to reduce the computational effort. The algorithm can be easily adapted to a parallel setting.

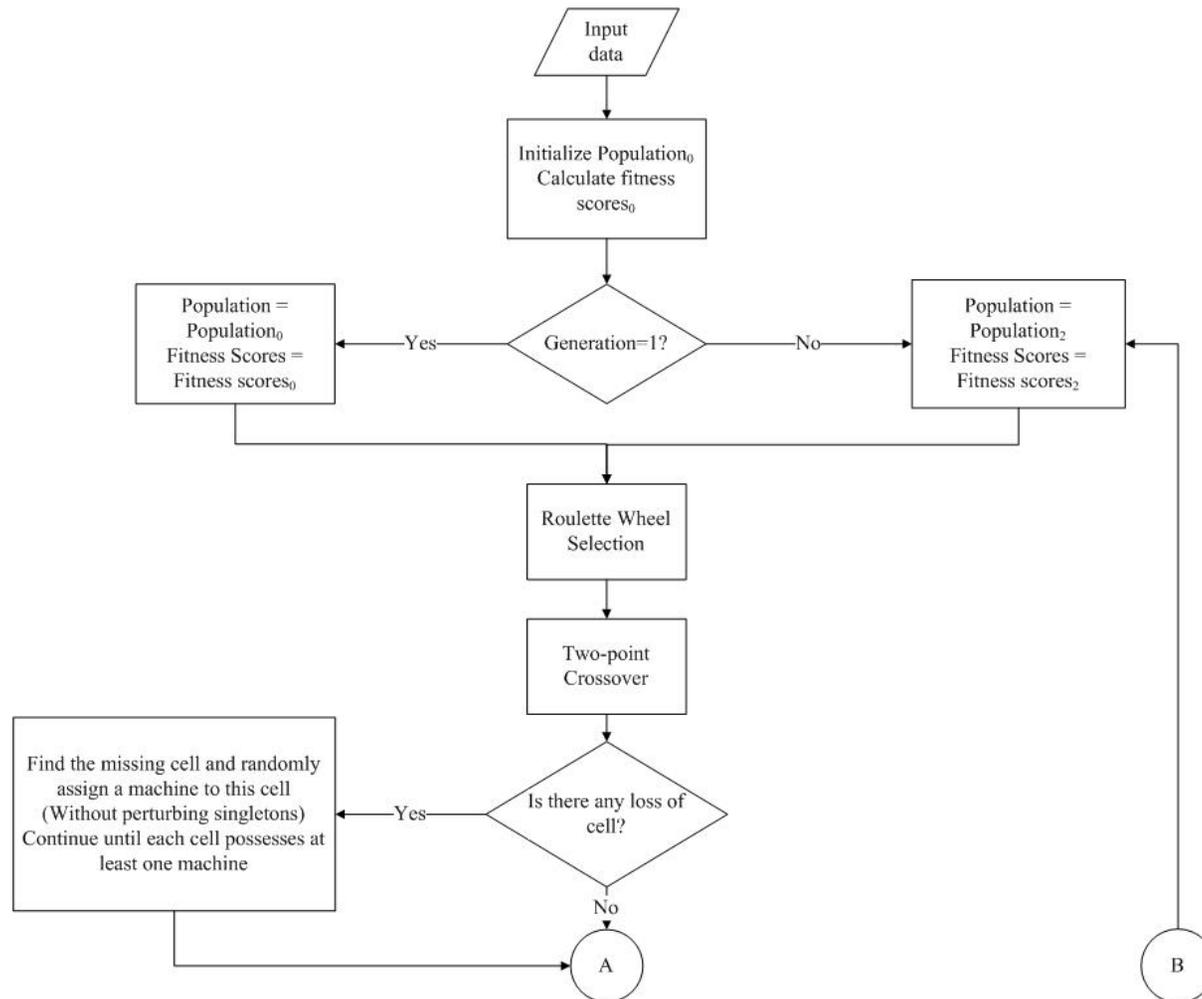
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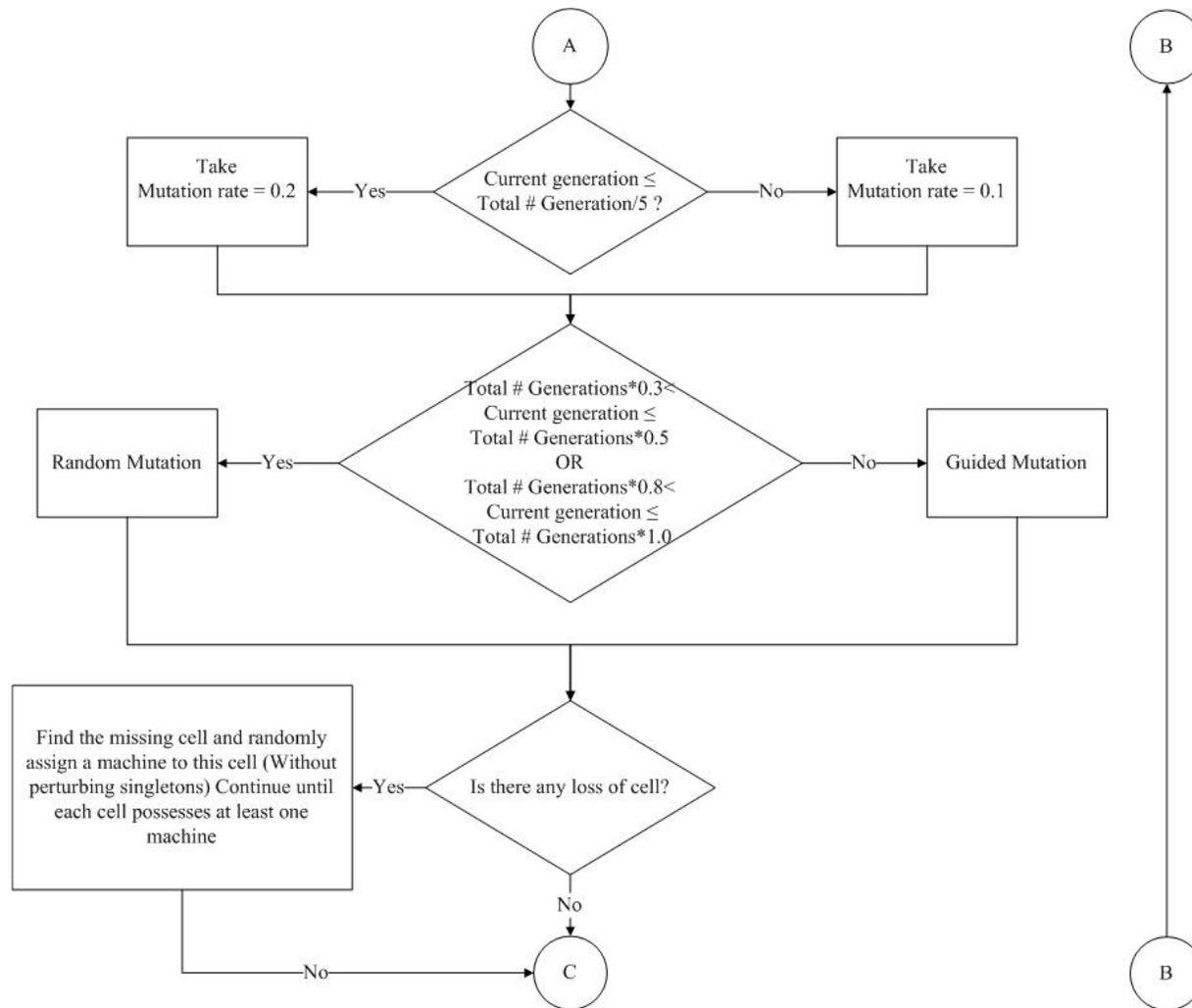
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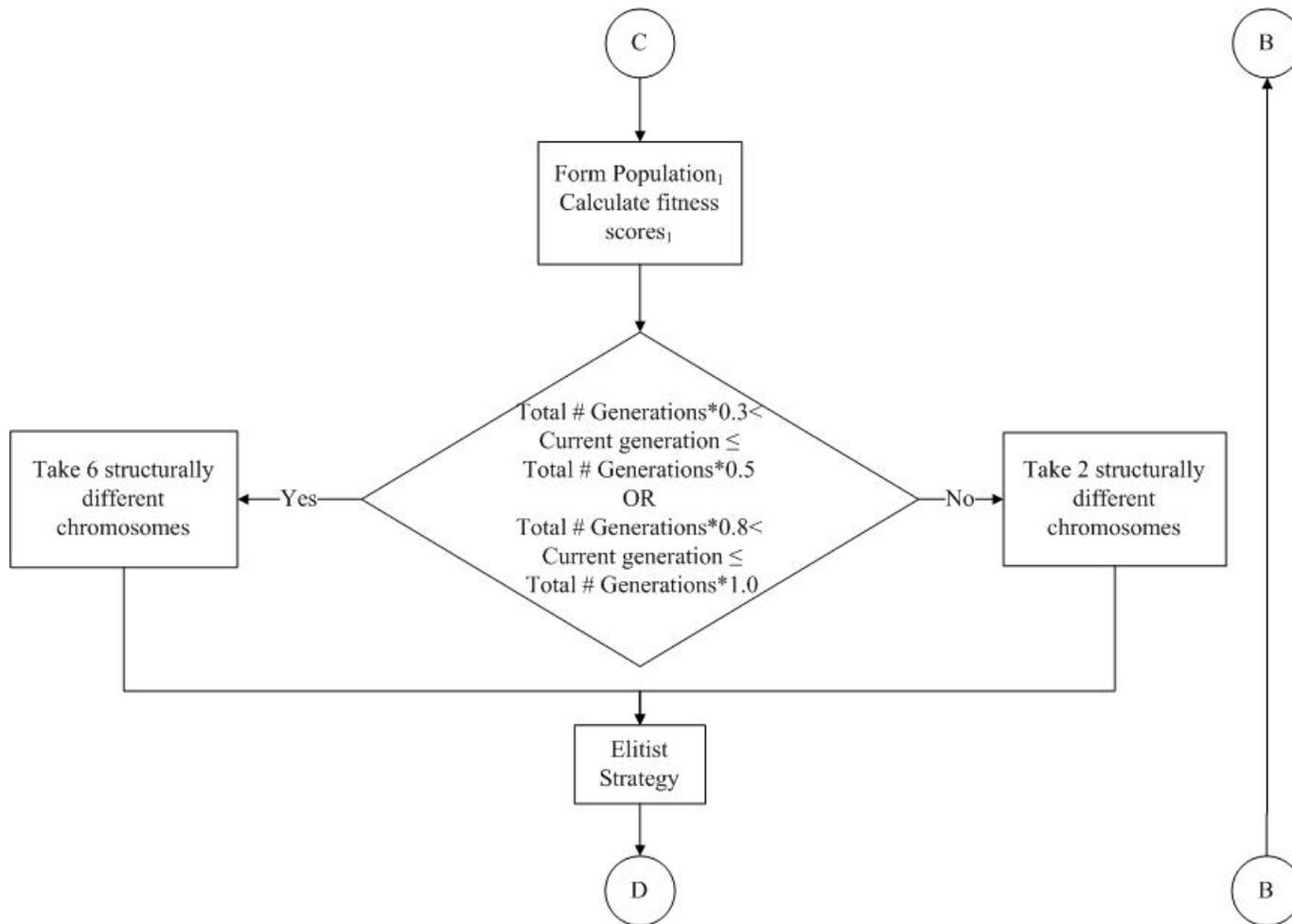
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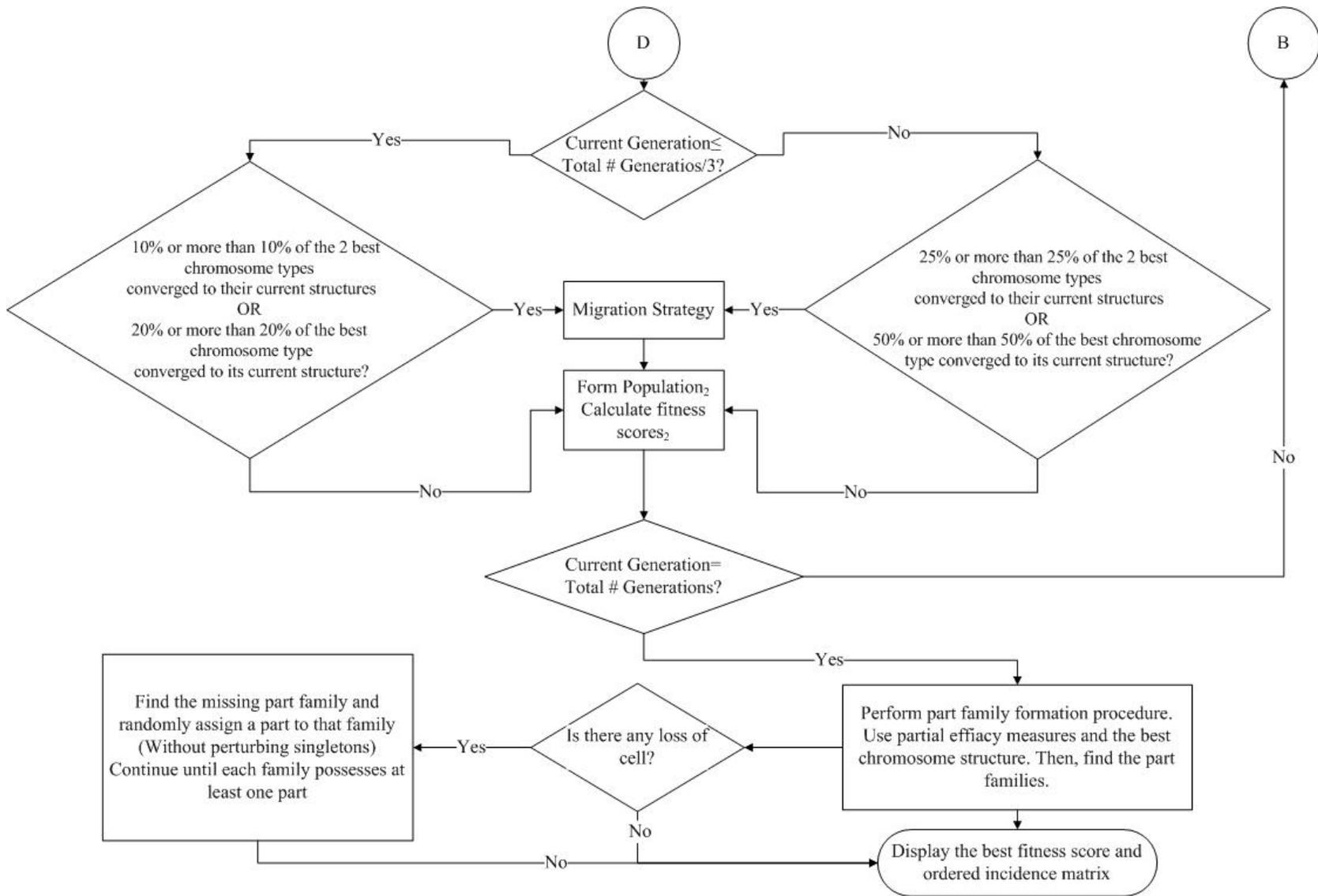
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8 APPENDIX A – Flowchart of the Proposed Algorithm









9 APPENDIX B – Detailed Computational Results of 5 Runs

Instance Size Number of cells	HGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
1 5 × 7 2	0.9306	120	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%
		300	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%
		900	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%
		1800	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%	0.9306	0.00%	0.00%
2 5 × 7 2	0.7667	120	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%
		300	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%
		900	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%
		1800	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%	0.7667	0.00%	0.00%
3 5 × 18 2	0.9637	120	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%
		300	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%
		900	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%
		1800	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%	0.9637	0.00%	0.00%
4 6 × 8 2	1.3587	120	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%
		300	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%
		900	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%
		1800	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%	1.3587	0.00%	0.00%
5 7 × 11 5	0.2917	120	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%
		300	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%
		900	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%
		1800	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%	0.2917	0.00%	0.00%
6 7 × 11 4	0.7500	120	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%
		300	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%
		900	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%
		1800	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%	0.7500	0.00%	0.00%
7 8 × 12 4	1.4111	120	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%
		300	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%
		900	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%
		1800	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%	1.4111	0.00%	0.00%

Instance Size Number of cells	HGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
8 8 × 20 3	1.8647	120	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%
		300	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%
		900	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%
		1800	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%	1.8647	0.00%	0.00%
9 8 × 20 2	1.3779	120	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%
		300	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%
		900	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%
		1800	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%	1.4274	0.00%	3.59%
10 10 × 10 5	1.4375	120	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%
		300	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%
		900	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%
		1800	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%	1.4583	0.00%	1.45%
11 10 × 15 3	2.9167	120	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%
		300	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%
		900	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%
		1800	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%	2.9167	0.00%	0.00%
12 14 × 24 7	2.1960	120	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%
		300	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%
		900	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%
		1800	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%	2.2933	0.00%	4.43%
13 14 × 24 7	2.0368	120	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%
		300	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%
		900	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%
		1800	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%	2.1683	0.00%	6.45%
14 16 × 24 8	1.4550	120	1.5116	0.35%	3.89%	1.5116	1.69%	3.89%	1.5116	2.70%	3.89%
		300	1.5116	0.00%	3.89%	1.5116	1.08%	3.89%	1.5116	0.80%	3.89%
		900	1.5116	1.32%	3.89%	1.5116	0.00%	3.89%	1.5116	0.00%	3.89%
		1800	1.5116	0.00%	3.89%	1.5116	0.00%	3.89%	1.5116	0.00%	3.89%

Instance Size Number of cells	HGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
15 16 × 30 6	2.7690	120	2.7651	5.17%	-0.14%	2.7690	0.21%	0.00%	2.7690	0.79%	0.00%
		300	2.7690	1.25%	0.00%	2.7690	0.00%	0.00%	2.7690	0.93%	0.00%
		900	2.7690	0.00%	0.00%	2.7690	0.00%	0.00%	2.7690	0.00%	0.00%
		1800	2.7690	0.00%	0.00%	2.7690	0.00%	0.00%	2.7690	0.00%	0.00%
16 16 × 43 8	1.7193	120	1.8223	0.00%	5.99%	1.8223	1.89%	5.99%	1.8223	5.58%	5.99%
		300	1.8223	0.00%	5.99%	1.8223	0.00%	5.99%	1.8223	0.00%	5.99%
		900	1.8223	0.00%	5.99%	1.8223	0.00%	5.99%	1.8223	0.00%	5.99%
		1800	1.8223	0.00%	5.99%	1.8223	0.00%	5.99%	1.8223	0.00%	5.99%
17 18 × 24 9	1.8306	120	2.2306	0.00%	21.85%	2.2306	5.38%	21.85%	2.2306	5.90%	21.85%
		300	2.2306	0.00%	21.85%	2.2306	0.00%	21.85%	2.2306	0.00%	21.85%
		900	2.2306	0.00%	21.85%	2.2306	0.00%	21.85%	2.2306	0.00%	21.85%
		1800	2.2306	0.00%	21.85%	2.2306	0.00%	21.85%	2.2306	0.00%	21.85%
18 20 × 20 6	2.1243	120	2.3131	4.15%	8.89%	2.3310	6.67%	9.73%	2.2688	9.92%	6.80%
		300	2.3962	3.09%	12.80%	2.3962	4.90%	12.80%	2.3185	2.55%	9.14%
		900	2.3962	2.09%	12.80%	2.3962	2.71%	12.80%	2.3962	1.71%	12.80%
		1800	2.3962	1.71%	12.80%	2.3962	1.71%	12.80%	2.3962	1.71%	12.80%
19 20 × 23 7	1.1360	120	2.8983	1.08%	155.13%	2.9517	5.09%	159.84%	2.9014	10.17%	155.41%
		300	2.9517	3.60%	159.84%	2.9517	1.19%	159.84%	2.9364	3.21%	158.48%
		900	2.9517	0.00%	159.84%	2.9517	0.00%	159.84%	2.9517	0.00%	159.84%
		1800	2.9517	0.00%	159.84%	2.9517	0.00%	159.84%	2.9517	0.00%	159.84%
20 20 × 35 5	4.9661	120	4.9664	3.82%	0.01%	4.9664	20.94%	0.01%	4.8828	42.93%	-1.68%
		300	4.9664	3.22%	0.01%	4.9664	3.16%	0.01%	4.9664	3.17%	0.01%
		900	4.9664	0.01%	0.01%	4.9664	0.01%	0.01%	4.9664	0.00%	0.01%
		1800	4.9664	0.00%	0.01%	4.9664	0.00%	0.01%	4.9664	0.00%	0.01%
21 20 × 35 5	3.3295	120	3.3545	14.64%	0.75%	3.3407	5.96%	0.34%	3.3545	9.56%	0.75%
		300	3.3625	3.63%	0.99%	3.3625	3.42%	0.99%	3.3625	4.12%	0.99%
		900	3.3625	0.44%	0.99%	3.3625	0.44%	0.99%	3.3625	0.00%	0.99%
		1800	3.3625	0.36%	0.99%	3.3625	0.44%	0.99%	3.3625	0.00%	0.99%

Instance Size Number of cells	HGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
22 24 × 40 7	8.5000	120	7.5000	41.59%	-11.76%	7.8333	54.92%	-7.84%	6.8333	32.56%	-19.61%
		300	8.5000	44.72%	0.00%	8.5000	0.00%	0.00%	8.5000	43.20%	0.00%
		900	8.5000	0.00%	0.00%	8.5000	0.00%	0.00%	8.5000	0.00%	0.00%
		1800	8.5000	0.00%	0.00%	8.5000	0.00%	0.00%	8.5000	0.00%	0.00%
23 24 × 40 7	6.2459	120	6.2459	29.32%	0.00%	6.0538	22.73%	-3.08%	5.5937	48.25%	-10.44%
		300	6.2459	26.83%	0.00%	6.2459	8.59%	0.00%	6.0538	36.03%	-3.08%
		900	6.2459	0.00%	0.00%	6.2459	10.06%	0.00%	6.2459	0.00%	0.00%
		1800	6.2459	0.00%	0.00%	6.2459	0.00%	0.00%	6.2459	0.00%	0.00%
24 24 × 40 7	4.3729	120	4.3729	39.39%	0.00%	4.3729	41.35%	0.00%	3.8576	37.77%	-11.78%
		300	4.3729	0.00%	0.00%	4.3729	24.64%	0.00%	4.3729	21.12%	0.00%
		900	4.3729	0.00%	0.00%	4.3729	0.00%	0.00%	4.3729	0.00%	0.00%
		1800	4.3729	0.00%	0.00%	4.3729	0.00%	0.00%	4.3729	0.00%	0.00%
25 24 × 40 11	1.9473	120	1.9682	14.17%	1.07%	1.9428	2.72%	-0.23%	1.9111	15.24%	-1.86%
		300	1.9761	6.17%	1.48%	1.9761	2.92%	1.48%	1.9375	3.78%	-0.50%
		900	1.9761	2.71%	1.48%	1.9761	1.09%	1.48%	1.9761	0.00%	1.48%
		1800	1.9761	1.46%	1.48%	1.9761	0.00%	1.48%	1.9761	0.00%	1.48%
26 24 × 40 12	1.5348	120	1.6017	5.98%	4.36%	1.5806	5.14%	2.98%	1.4706	4.09%	-4.18%
		300	1.6079	1.94%	4.76%	1.6130	2.47%	5.10%	1.6074	4.52%	4.73%
		900	1.6130	0.25%	5.10%	1.6130	0.28%	5.10%	1.6130	0.12%	5.10%
		1800	1.6130	0.00%	5.10%	1.6130	0.21%	5.10%	1.6130	0.12%	5.10%
27 24 × 40 12	1.3008	120	1.4629	5.97%	12.46%	1.3831	3.31%	6.33%	1.3642	4.46%	4.87%
		300	1.4648	3.16%	12.61%	1.4662	4.57%	12.71%	1.4581	2.36%	12.10%
		900	1.4662	1.20%	12.71%	1.4662	2.01%	12.71%	1.4662	1.74%	12.71%
		1800	1.4662	0.78%	12.71%	1.4662	0.00%	12.71%	1.4662	1.74%	12.71%
28 27 × 27 6	4.3823	120	4.4860	11.90%	2.37%	4.4384	12.16%	1.28%	4.1307	21.02%	-5.74%
		300	4.6528	7.29%	6.17%	4.4503	2.75%	1.55%	4.5330	11.56%	3.44%
		900	4.6528	12.78%	6.17%	4.6528	6.66%	6.17%	4.6528	3.12%	6.17%
		1800	4.6528	10.52%	6.17%	4.6528	7.11%	6.17%	4.6528	3.12%	6.17%

Instance Size Number of cells	HGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
29 28 × 46 10	2.2180	120	2.3113	4.92%	4.21%	2.2197	10.98%	0.08%	2.2177	15.98%	-0.01%
		300	2.3909	3.48%	7.80%	2.3673	5.19%	6.73%	2.3857	6.61%	7.56%
		900	2.4042	2.10%	8.40%	2.4042	2.16%	8.40%	2.3857	1.05%	7.56%
		1800	2.4042	1.97%	8.40%	2.4042	1.80%	8.40%	2.3857	1.05%	7.56%
30 30 × 41 14	3.9587	120	4.2394	25.68%	7.09%	4.1099	24.46%	3.82%	3.8787	33.07%	-2.02%
		300	4.1443	8.89%	4.69%	4.1765	5.06%	5.50%	4.2479	11.32%	7.31%
		900	4.2765	2.03%	8.03%	4.2765	0.00%	8.03%	4.2765	1.64%	8.03%
		1800	4.2765	6.09%	8.03%	4.2765	0.00%	8.03%	4.2765	1.64%	8.03%
31 30 × 50 13	3.4633	120	3.4583	14.39%	-0.14%	3.3843	15.66%	-2.28%	3.0728	15.61%	-11.28%
		300	3.5823	7.93%	3.44%	3.4662	7.29%	0.08%	3.5375	12.93%	2.14%
		900	3.5939	3.51%	3.77%	3.5491	7.19%	2.48%	3.6171	6.95%	4.44%
		1800	3.5298	0.80%	1.92%	3.6171	3.85%	4.44%	3.6171	6.95%	4.44%
32 30 × 50 14	0.7606	120	2.6864	21.64%	253.19%	2.6407	9.73%	247.18%	2.2874	25.20%	200.73%
		300	2.7429	10.98%	260.63%	2.7320	10.94%	259.19%	2.6254	5.11%	245.17%
		900	2.7592	0.54%	262.76%	2.7592	2.05%	262.76%	2.7592	0.08%	262.76%
		1800	2.7592	0.00%	262.76%	2.7592	0.43%	262.76%	2.7592	0.08%	262.76%
33 36 × 90 17	0.5627	120	2.0521	20.00%	264.70%	1.8282	8.51%	224.90%	1.6167	7.27%	187.31%
		300	2.0276	6.47%	260.34%	2.0744	13.26%	268.66%	1.9583	9.72%	248.01%
		900	2.0788	5.92%	269.43%	2.0788	4.29%	269.43%	2.0779	3.87%	269.28%
		1800	2.0788	0.14%	269.43%	2.0779	0.37%	269.28%	2.0779	3.87%	269.28%
34 37 × 53 3	8.6598	120	8.6617	32.86%	0.02%	8.8392	37.99%	2.07%	8.4875	40.65%	-1.99%
		300	8.9150	21.16%	2.95%	8.9118	27.11%	2.91%	8.3785	10.10%	-3.25%
		900	8.9584	2.43%	3.45%	8.9584	4.02%	3.45%	8.9584	2.87%	3.45%
		1800	8.9584	3.56%	3.45%	8.9584	3.60%	3.45%	8.9584	2.87%	3.45%
35 40 × 100 10	10.4205	120	9.0348	119.32%	-13.30%	7.3890	62.33%	-29.09%	6.1221	50.80%	-41.25%
		300	9.5757	70.30%	-8.11%	9.7907	47.16%	-6.04%	8.5676	58.02%	-17.78%
		900	10.4205	30.33%	0.00%	10.0264	15.34%	-3.78%	10.4205	42.68%	0.00%
		1800	10.4205	19.84%	0.00%	10.4205	40.16%	0.00%	10.4205	42.68%	0.00%

Minimum Deviations for Similarity Measure

		No-Island			2-Island			5-Island					No-Island			2-Island			5-Island					No-Island			2-Island			5-Island																														
5	120	0.00%	0.00%	0.00%	10	120	0.00%	0.00%	0.00%	20	120	1.08%	5.09%	9.56%	30	120	14.39%	9.73%	15.61%	10	120	0.00%	0.00%	0.00%	300	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	3.09%	1.19%	2.55%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	7.93%	5.06%	5.11%	900	0.54%	0.00%	0.08%	1800	0.00%	0.00%	0.08%
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	14.39%	9.73%	15.61%		300	0.00%	0.00%	0.00%		300	0.00%	0.00%		0.00%	300	3.09%		1.19%	2.55%	300		7.93%	5.06%	5.11%		300	0.00%	0.00%		0.00%	300	7.93%		5.06%	5.11%									
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	14.39%	9.73%	15.61%		900	0.54%	0.00%	0.08%		900	0.00%	0.00%		0.00%	900	0.00%		0.00%	0.00%	900		0.00%	0.00%	0.00%		900	0.54%	0.00%		0.08%	900	0.00%		0.00%	0.08%	900		0.00%	0.00%	0.08%				
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	14.39%	9.73%	15.61%		1800	0.00%	0.00%	0.08%		1800	0.00%	0.00%		0.00%	1800	0.00%		0.00%	0.00%	1800		0.00%	0.00%	0.00%		1800	0.00%	0.00%		0.00%	1800	0.00%		0.00%	0.08%	1800		0.00%	0.00%	0.08%				
6	120	0.00%	0.00%	0.00%	14	120	0.00%	0.00%	0.00%	24	120	5.97%	2.72%	4.09%	36	120	20.00%	8.51%	7.27%	14	120	0.00%	0.00%	0.00%	300	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	0.00%	0.00%	2.36%	900	5.92%	4.29%	3.87%	1800	0.14%	0.37%	3.87%												
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	0.00%	0.00%	2.36%		300	20.00%	8.51%	7.27%		300	6.47%	13.26%	9.72%		300	0.00%	0.00%		0.00%	300	0.00%		0.00%	0.00%	300		0.00%	0.00%	2.36%		300	6.47%	13.26%		9.72%	300	5.92%	4.29%	3.87%	300	5.92%	4.29%	3.87%						
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	20.00%	8.51%	7.27%		900	5.92%	4.29%	3.87%		900	0.00%	0.00%		0.00%	900	0.00%		0.00%	0.00%	900		0.00%	0.00%	0.00%		900	0.00%	0.00%		0.00%	900	0.00%	0.00%	0.00%	900	5.92%	4.29%	3.87%	900	5.92%	4.29%	3.87%		
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	20.00%	8.51%	7.27%		1800	0.14%	0.37%	3.87%		1800	0.00%	0.00%		0.00%	1800	0.00%		0.00%	0.00%	1800		0.00%	0.00%	0.00%		1800	0.00%	0.00%		0.00%	1800	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%		
7	120	0.00%	0.00%	0.00%	16	120	0.00%	0.21%	0.79%	27	120	11.90%	12.16%	21.02%	37	120	32.86%	37.99%	40.65%	16	120	0.00%	0.00%	0.00%	300	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	7.29%	2.75%	11.56%	900	2.43%	4.02%	2.87%	1800	3.56%	3.60%	2.87%												
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	11.90%	12.16%	21.02%		300	32.86%	37.99%	40.65%		300	21.16%	27.11%	10.10%		300	0.00%	0.00%		0.00%	300	0.00%		0.00%	0.00%	300		7.29%	2.75%	11.56%		300	2.43%	4.02%		2.87%	300	2.43%	4.02%	2.87%	300	2.43%	4.02%	2.87%						
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	11.90%	12.16%	21.02%		900	32.86%	37.99%	40.65%		900	2.43%	4.02%	2.87%		900	0.00%	0.00%		0.00%	900	0.00%		0.00%	0.00%	900		7.29%	2.75%	11.56%		900	2.43%	4.02%		2.87%	900	2.43%	4.02%	2.87%	900	2.43%	4.02%	2.87%						
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	11.90%	12.16%	21.02%		1800	32.86%	37.99%	40.65%		1800	3.56%	3.60%	2.87%		1800	0.00%	0.00%		0.00%	1800	0.00%		0.00%	0.00%	1800		7.29%	2.75%	11.56%		1800	2.43%	4.02%		2.87%	1800	2.43%	4.02%	2.87%										
8	120	0.00%	0.00%	0.00%	18	120	0.00%	5.38%	5.90%	28	120	4.92%	10.98%	15.98%	40	120	119.32%	62.33%	50.80%	18	120	0.00%	0.00%	0.00%	300	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	3.48%	5.19%	6.61%	900	30.33%	15.34%	42.68%	1800	19.84%	40.16%	42.68%												
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	4.92%	10.98%	15.98%		300	119.32%	62.33%	50.80%		300	70.30%	47.16%	58.02%		300	0.00%	0.00%		0.00%	300	0.00%		0.00%	0.00%	300		3.48%	5.19%	6.61%		300	30.33%	15.34%		42.68%	300	30.33%	15.34%	42.68%										
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	4.92%	10.98%	15.98%		900	119.32%	62.33%	50.80%		900	70.30%	47.16%	58.02%		900	0.00%	0.00%		0.00%	900	0.00%		0.00%	0.00%	900		3.48%	5.19%	6.61%		900	30.33%	15.34%		42.68%	900	30.33%	15.34%	42.68%										
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	4.92%	10.98%	15.98%		1800	119.32%	62.33%	50.80%		1800	19.84%	40.16%	42.68%		1800	0.00%	0.00%		0.00%	1800	0.00%		0.00%	0.00%	1800		3.48%	5.19%	6.61%		1800	30.33%	15.34%		42.68%	1800	30.33%	15.34%	42.68%										

Maximum Deviations for Similarity Measure

		No-Island			2-Island			5-Island					No-Island			2-Island			5-Island					No-Island			2-Island			5-Island																																					
5	120	0.00%	0.00%	0.00%	10	120	0.00%	0.00%	0.00%	20	120	14.64%	20.94%	42.93%	30	120	25.68%	24.46%	33.07%	m	300	0.00%	0.00%	0.00%	m	300	0.00%	0.00%	0.00%	m	300	10.98%	10.94%	12.93%	s	900	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	900	2.09%	2.71%	1.71%	900	3.51%	7.19%	6.95%	1800	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	1800	1.71%	1.71%	1.71%	1800	6.09%	3.85%	6.95%
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	3.63%	4.90%	4.12%		300	10.98%	10.94%	12.93%		900	3.51%	7.19%	6.95%	900	2.09%	2.71%	1.71%	900	3.51%	7.19%	6.95%	900	2.09%		2.71%	1.71%	900	3.51%	7.19%	6.95%																										
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	2.09%	2.71%	1.71%		900	3.51%	7.19%	6.95%		900	3.51%	7.19%	6.95%	900	2.09%	2.71%	1.71%	900	3.51%	7.19%	6.95%	900	2.09%		2.71%	1.71%	900	3.51%	7.19%	6.95%																										
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	1.71%	1.71%	1.71%		1800	6.09%	3.85%	6.95%		1800	6.09%	3.85%	6.95%	1800	1.71%	1.71%	1.71%	1800	6.09%	3.85%	6.95%	1800	6.09%		3.85%	6.95%	1800	6.09%	3.85%	6.95%																										
6	120	0.00%	0.00%	0.00%	14	120	0.00%	0.00%	0.00%	24	120	41.59%	54.92%	48.25%	36	120	20.00%	8.51%	7.27%	s	300	0.00%	0.00%	0.00%	m	300	0.00%	0.00%	0.00%	m	300	6.47%	13.26%	9.72%	900	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	900	2.71%	10.06%	1.74%	900	5.92%	4.29%	3.87%	1800	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	1800	1.46%	0.21%	1.74%	1800	0.14%	0.37%	3.87%	
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	44.72%	24.64%	43.20%		300	6.47%	13.26%	9.72%		300	6.47%	13.26%	9.72%	300	0.00%	0.00%	0.00%	300	6.47%	13.26%	9.72%	300	6.47%		13.26%	9.72%	300	6.47%	13.26%	9.72%																										
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	2.71%	10.06%	1.74%		900	5.92%	4.29%	3.87%		900	5.92%	4.29%	3.87%	900	0.00%	0.00%	0.00%	900	5.92%	4.29%	3.87%	900	5.92%		4.29%	3.87%	900	5.92%	4.29%	3.87%																										
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	1.46%	0.21%	1.74%		1800	0.14%	0.37%	3.87%		1800	0.14%	0.37%	3.87%	1800	0.00%	0.00%	0.00%	1800	0.14%	0.37%	3.87%	1800	0.14%		0.37%	3.87%	1800	0.14%	0.37%	3.87%																										
7	120	0.00%	0.00%	0.00%	16	120	5.17%	1.89%	5.58%	27	120	11.90%	12.16%	21.02%	37	120	32.86%	37.99%	40.65%	m	300	0.00%	0.00%	0.00%	m	300	1.25%	1.08%	0.93%	s	300	7.29%	2.75%	11.56%	900	0.00%	0.00%	0.00%	900	1.32%	0.00%	0.00%	900	12.78%	6.66%	3.12%	900	2.43%	4.02%	2.87%	1800	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	1800	10.52%	7.11%	3.12%	1800	3.56%	3.60%	2.87%	
	300	0.00%	0.00%	0.00%		300	1.25%	1.08%	0.93%		300	7.29%	2.75%	11.56%		300	21.16%	27.11%	10.10%		300	7.29%	2.75%	11.56%	300	1.25%	1.08%	0.93%	300	7.29%	2.75%	11.56%	300	7.29%		2.75%	11.56%																														
	900	0.00%	0.00%	0.00%		900	1.32%	0.00%	0.00%		900	12.78%	6.66%	3.12%		900	2.43%	4.02%	2.87%		900	2.43%	4.02%	2.87%	900	0.00%	0.00%	0.00%	900	2.43%	4.02%	2.87%	900	2.43%		4.02%	2.87%																														
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	10.52%	7.11%	3.12%		1800	3.56%	3.60%	2.87%		1800	3.56%	3.60%	2.87%	1800	0.00%	0.00%	0.00%	1800	3.56%	3.60%	2.87%	1800	3.56%		3.60%	2.87%																														
8	120	0.00%	0.00%	0.00%	18	120	0.00%	5.38%	5.90%	28	120	4.92%	10.98%	15.98%	40	120	119.32%	62.33%	50.80%	m	300	0.00%	0.00%	0.00%	s	300	0.00%	0.00%	0.00%	s	300	3.48%	5.19%	6.61%	900	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	900	2.10%	2.16%	1.05%	900	30.33%	15.34%	42.68%	1800	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	1800	1.97%	1.80%	1.05%	1800	19.84%	40.16%	42.68%	
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	3.48%	5.19%	6.61%		300	70.30%	47.16%	58.02%		300	3.48%	5.19%	6.61%	300	0.00%	0.00%	0.00%	300	3.48%	5.19%	6.61%	300	70.30%		47.16%	58.02%																														
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	2.10%	2.16%	1.05%		900	30.33%	15.34%	42.68%		900	2.10%	2.16%	1.05%	900	0.00%	0.00%	0.00%	900	2.10%	2.16%	1.05%	900	30.33%		15.34%	42.68%																														
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	1.97%	1.80%	1.05%		1800	19.84%	40.16%	42.68%		1800	19.84%	40.16%	42.68%	1800	0.00%	0.00%	0.00%	1800	19.84%	40.16%	42.68%	1800	19.84%		40.16%	42.68%																														

Instance Size Number of cells	HGGA	EnGGA	Genera- tion	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
1 5 × 7 2	82.35%	82.35%	120	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%
			300	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%
			900	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%
			1800	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%	82.35%	0.00%	0.00%
2 5 × 7 2	69.57%	69.57%	120	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%
			300	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%
			900	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%
			1800	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%	69.57%	0.00%	0.00%
3 5 × 18 2	79.59%	79.59%	120	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%
			300	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%
			900	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%
			1800	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%	79.59%	0.00%	0.00%
4 6 × 8 2	76.92%	76.92%	120	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%
			300	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%
			900	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%
			1800	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%	76.92%	0.00%	0.00%
5 7 × 11 5	60.87%	60.87%	120	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%
			300	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%
			900	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%
			1800	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%	60.87%	0.00%	0.00%
6 7 × 11 4	70.83%	70.83%	120	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%
			300	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%
			900	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%
			1800	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%	70.83%	0.00%	0.00%
7 8 × 12 4	69.44%	69.44%	120	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%
			300	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%
			900	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%
			1800	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%	69.44%	0.00%	0.00%

Instance Size Number of cells	HGGA	EnGGA	Genera- tion	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
8 8 × 20 3	85.25%	85.25%	120	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%
			300	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%
			900	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%
			1800	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%	85.25%	0.00%	0.00%
9 8 × 20 2	58.72%	58.72%	120	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%
			300	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%
			900	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%
			1800	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%	58.72%	0.00%	0.00%
10 10 × 10 5	75.00%	-	120	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%
			300	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%
			900	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%
			1800	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%	75.00%	0.00%	0.00%
11 10 × 15 3	92.00%	-	120	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%
			300	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%
			900	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%
			1800	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%	92.00%	0.00%	0.00%
12 14 × 24 7	72.06%	-	120	72.06%	0.85%	0.00%	72.06%	1.06%	0.00%	72.06%	1.49%	0.00%
			300	72.06%	0.00%	0.00%	72.06%	0.00%	0.00%	72.06%	0.00%	0.00%
			900	72.06%	0.00%	0.00%	72.06%	0.00%	0.00%	72.06%	0.00%	0.00%
			1800	72.06%	0.00%	0.00%	72.06%	0.00%	0.00%	72.06%	0.00%	0.00%
13 14 × 24 7	71.83%	-	120	71.83%	0.00%	0.00%	71.83%	0.00%	0.00%	71.83%	0.54%	0.00%
			300	71.83%	0.00%	0.00%	71.83%	0.00%	0.00%	71.83%	0.00%	0.00%
			900	71.83%	0.00%	0.00%	71.83%	0.00%	0.00%	71.83%	0.00%	0.00%
			1800	71.83%	0.00%	0.00%	71.83%	0.00%	0.00%	71.83%	0.00%	0.00%
14 16 × 24 8	52.75%	53.26%	120	53.26%	0.49%	0.00%	53.26%	0.69%	0.00%	52.17%	0.80%	-1.09%
			300	53.26%	0.49%	0.00%	53.26%	0.00%	0.00%	53.26%	0.60%	0.00%
			900	53.26%	0.00%	0.00%	53.26%	0.00%	0.00%	53.26%	0.00%	0.00%
			1800	53.26%	0.00%	0.00%	53.26%	0.00%	0.00%	53.26%	0.00%	0.00%

Instance Size Number of cells	HGGA	EnGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
15 16 × 30 6	68.99%	68.99%	120	68.99%	0.00%	0.00%	68.99%	1.51%	0.00%	68.99%	0.91%	0.00%
			300	68.99%	0.00%	0.00%	68.99%	0.00%	0.00%	68.99%	0.00%	0.00%
			900	68.99%	0.00%	0.00%	68.99%	0.00%	0.00%	68.99%	0.00%	0.00%
			1800	68.99%	0.00%	0.00%	68.99%	0.00%	0.00%	68.99%	0.00%	0.00%
16 16 × 43 8	57.53%	57.53%	120	57.53%	0.00%	0.00%	57.53%	0.68%	0.00%	57.43%	0.76%	-0.10%
			300	57.53%	0.00%	0.00%	57.53%	0.00%	0.00%	57.53%	0.05%	0.00%
			900	57.53%	0.00%	0.00%	57.53%	0.00%	0.00%	57.53%	0.00%	0.00%
			1800	57.53%	0.00%	0.00%	57.53%	0.00%	0.00%	57.53%	0.00%	0.00%
17 18 × 24 9	57.73%	57.73%	120	57.29%	0.70%	-0.44%	57.29%	0.82%	-0.44%	55.67%	0.36%	-2.06%
			300	57.29%	0.00%	-0.44%	57.29%	0.26%	-0.44%	57.29%	0.22%	-0.44%
			900	57.29%	0.00%	-0.44%	57.29%	0.00%	-0.44%	57.29%	0.00%	-0.44%
			1800	57.29%	0.00%	-0.44%	57.29%	0.00%	-0.44%	57.29%	0.00%	-0.44%
18 20 × 20 6	43.18%	-	120	42.75%	0.26%	-0.43%	42.34%	0.46%	-0.84%	41.98%	1.09%	-1.20%
			300	43.36%	0.78%	0.18%	42.96%	0.38%	-0.22%	43.07%	0.44%	-0.11%
			900	42.86%	0.37%	-0.32%	43.36%	0.33%	0.18%	43.18%	0.06%	0.00%
			1800	43.36%	0.55%	0.18%	43.36%	0.28%	0.18%	43.36%	0.36%	0.18%
19 20 × 23 7	50.81%	-	120	50.00%	1.07%	-0.81%	48.85%	1.38%	-1.96%	47.58%	0.50%	-3.23%
			300	50.81%	1.44%	0.00%	50.81%	0.93%	0.00%	50.81%	1.23%	0.00%
			900	50.81%	0.22%	0.00%	50.81%	1.18%	0.00%	50.40%	0.18%	-0.41%
			1800	50.81%	0.00%	0.00%	50.81%	0.00%	0.00%	50.81%	0.00%	0.00%
20 20 × 35 5	77.91%	77.91%	120	77.91%	1.07%	0.00%	77.91%	3.23%	0.00%	76.36%	5.66%	-1.55%
			300	77.91%	0.77%	0.00%	77.91%	0.36%	0.00%	77.91%	0.57%	0.00%
			900	77.91%	0.00%	0.00%	77.91%	0.00%	0.00%	77.91%	0.00%	0.00%
			1800	77.91%	0.00%	0.00%	77.91%	0.00%	0.00%	77.91%	0.00%	0.00%
21 20 × 35 5	57.98%	57.98%	120	57.98%	0.54%	0.00%	57.98%	1.32%	0.00%	55.96%	3.38%	-2.02%
			300	57.98%	0.70%	0.00%	57.98%	0.64%	0.00%	57.98%	0.83%	0.00%
			900	57.98%	0.00%	0.00%	57.98%	0.00%	0.00%	57.98%	0.37%	0.00%
			1800	57.98%	0.00%	0.00%	57.98%	0.00%	0.00%	57.98%	0.00%	0.00%

Instance Size Number of cells	HGGA	EnGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
22 24 × 40 7	100.00%	100.00%	120	100.00%	10.42%	0.00%	100.00%	8.25%	0.00%	94.12%	11.33%	-5.88%
			300	100.00%	2.63%	0.00%	100.00%	3.24%	0.00%	100.00%	3.57%	0.00%
			900	100.00%	0.00%	0.00%	100.00%	0.00%	0.00%	100.00%	0.00%	0.00%
			1800	100.00%	0.00%	0.00%	100.00%	0.00%	0.00%	100.00%	0.00%	0.00%
23 24 × 40 7	85.11%	85.11%	120	85.11%	7.15%	0.00%	80.82%	2.12%	-4.29%	67.72%	4.88%	-17.39%
			300	85.11%	0.00%	0.00%	85.11%	2.47%	0.00%	80.82%	1.49%	-4.29%
			900	85.11%	0.00%	0.00%	85.11%	0.00%	0.00%	85.11%	0.00%	0.00%
			1800	85.11%	0.00%	0.00%	85.11%	0.00%	0.00%	85.11%	0.00%	0.00%
24 24 × 40 7	73.51%	73.51%	120	69.87%	1.91%	-3.64%	73.51%	6.81%	0.00%	60.37%	3.13%	-13.14%
			300	73.51%	1.43%	0.00%	73.51%	0.00%	0.00%	73.51%	3.10%	0.00%
			900	73.51%	0.00%	0.00%	73.51%	0.00%	0.00%	73.51%	0.00%	0.00%
			1800	73.51%	0.00%	0.00%	73.51%	0.00%	0.00%	73.51%	0.00%	0.00%
25 24 × 40 11	53.29%	53.29%	120	52.63%	1.12%	-0.66%	51.97%	1.77%	-1.32%	49.67%	2.70%	-3.62%
			300	52.63%	0.32%	-0.66%	52.63%	0.53%	-0.66%	52.29%	1.34%	-1.00%
			900	52.63%	0.10%	-0.66%	52.63%	0.00%	-0.66%	52.63%	0.11%	-0.66%
			1800	52.63%	0.11%	-0.66%	52.63%	0.00%	-0.66%	52.63%	0.11%	-0.66%
26 24 × 40 12	48.95%	48.95%	120	48.61%	0.69%	-0.34%	47.52%	1.06%	-1.43%	45.16%	0.86%	-3.79%
			300	48.61%	0.24%	-0.34%	48.61%	0.37%	-0.34%	48.03%	0.60%	-0.92%
			900	48.61%	0.17%	-0.34%	48.95%	0.29%	0.00%	48.95%	0.36%	0.00%
			1800	48.61%	0.14%	-0.34%	48.95%	0.27%	0.00%	48.95%	0.29%	0.00%
27 24 × 40 12	47.26%	46.58%	120	45.58%	0.37%	-1.68%	45.89%	0.63%	-1.37%	44.83%	1.16%	-2.43%
			300	46.21%	0.25%	-1.05%	46.26%	0.44%	-1.00%	46.21%	0.51%	-1.05%
			900	46.81%	0.35%	-0.45%	46.58%	0.14%	-0.68%	46.58%	0.26%	-0.68%
			1800	46.58%	0.27%	-0.68%	46.81%	0.10%	-0.45%	46.58%	0.19%	-0.68%
28 27 × 27 6	54.02%	54.82%	120	54.39%	2.36%	-0.43%	52.82%	1.15%	-2.00%	51.19%	1.85%	-3.63%
			300	54.52%	0.83%	-0.30%	54.45%	0.47%	-0.37%	54.15%	1.32%	-0.67%
			900	54.52%	0.80%	-0.30%	54.52%	0.50%	-0.30%	54.52%	0.31%	-0.30%
			1800	54.52%	0.46%	-0.30%	54.52%	0.03%	-0.30%	54.52%	0.06%	-0.30%

Instance Size Number of cells	HGGA	EnGGA	Generation	No island	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island2	Deviation from the sample of 5 runs	Gap between the best solution and our result	Island5	Deviation from the sample of 5 runs	Gap between the best solution and our result
29 28 × 46 10	46.91%	-	120	44.79%	0.51%	-2.12%	43.96%	1.15%	-2.95%	43.54%	0.88%	-3.37%
			300	46.31%	0.84%	-0.60%	46.06%	0.13%	-0.85%	46.25%	0.46%	-0.66%
			900	46.10%	0.16%	-0.81%	47.08%	0.33%	0.17%	46.77%	0.18%	-0.14%
			1800	46.25%	0.20%	-0.66%	46.44%	0.24%	-0.47%	46.24%	0.24%	-0.67%
30 30 × 41 14	63.31%	63.31%	120	60.00%	2.20%	-3.31%	61.38%	1.80%	-1.93%	58.78%	3.44%	-4.53%
			300	62.33%	0.87%	-0.98%	62.14%	1.20%	-1.17%	60.14%	1.15%	-3.17%
			900	62.94%	0.41%	-0.37%	63.31%	0.53%	0.00%	63.31%	0.68%	0.00%
			1800	62.59%	0.39%	-0.72%	63.31%	0.38%	0.00%	63.31%	0.61%	0.00%
31 30 × 50 13	59.77%	-	120	58.96%	1.57%	-0.81%	55.19%	2.13%	-4.58%	53.07%	1.93%	-6.70%
			300	59.77%	1.22%	0.00%	59.65%	0.85%	-0.12%	56.91%	0.94%	-2.86%
			900	59.77%	0.05%	0.00%	59.77%	0.05%	0.00%	59.77%	0.63%	0.00%
			1800	59.77%	0.15%	0.00%	59.77%	0.00%	0.00%	59.77%	0.06%	0.00%
32 30 × 50 14	50.83%	-	120	50.00%	1.38%	-0.83%	49.19%	2.43%	-1.64%	44.50%	1.17%	-6.33%
			300	50.56%	0.67%	-0.27%	50.28%	0.87%	-0.55%	49.21%	0.42%	-1.62%
			900	50.83%	0.12%	0.00%	50.56%	0.13%	-0.27%	50.82%	0.36%	-0.01%
			1800	50.83%	0.15%	0.00%	50.83%	0.14%	0.00%	50.56%	0.12%	-0.27%
33 36 × 90 17	46.35%	-	120	45.71%	1.55%	-0.64%	44.59%	1.72%	-1.76%	44.14%	2.30%	-2.21%
			300	46.56%	1.16%	0.21%	45.33%	0.64%	-1.02%	45.60%	0.92%	-0.75%
			900	46.61%	0.12%	0.26%	46.37%	0.12%	0.02%	46.37%	0.39%	0.02%
			1800	46.31%	0.09%	-0.04%	46.78%	0.11%	0.43%	46.24%	0.14%	-0.11%
34 37 × 53 3	60.64%	60.64%	120	58.37%	0.20%	-2.27%	58.49%	0.04%	-2.15%	58.37%	0.72%	-2.27%
			300	58.37%	0.00%	-2.27%	60.14%	0.36%	-0.50%	60.14%	0.01%	-0.50%
			900	60.36%	0.72%	-0.28%	58.62%	0.00%	-2.02%	58.86%	0.00%	-1.78%
			1800	58.49%	0.00%	-2.15%	58.49%	0.72%	-2.15%	58.62%	0.00%	-2.02%
35 40 × 100 10	84.03%	-	120	74.30%	4.80%	-9.73%	68.31%	7.12%	-15.72%	50.83%	2.21%	-33.20%
			300	83.81%	5.09%	-0.22%	76.01%	2.96%	-8.02%	68.39%	4.11%	-15.64%
			900	83.81%	2.26%	-0.22%	83.81%	1.46%	-0.22%	83.81%	3.18%	-0.22%
			1800	83.81%	0.00%	-0.22%	83.81%	0.00%	-0.22%	83.81%	1.81%	-0.22%

Maximum Deviations - Efficacy Measure

		No-Island			2-Island			5-Island					No-Island			2-Island			5-Island					No-Island			2-Island			5-Island																																										
5	120	0.00%	0.00%	0.00%	10	120	0.00%	0.00%	0.00%	20	120	1.07%	3.23%	5.66%	30	120	2.20%	2.43%	3.44%	10	120	0.00%	0.00%	0.00%	300	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	1.44%	0.93%	1.23%	900	0.37%	1.18%	0.37%	1800	0.55%	0.28%	0.36%	300	1.22%	1.20%	1.15%	900	0.41%	0.53%	0.68%	1800	0.39%	0.38%	0.61%
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	1.44%	0.93%	1.23%		300	1.22%	1.20%	1.15%																																																					
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.37%	1.18%	0.37%		900	0.41%	0.53%	0.68%																																																					
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.55%	0.28%	0.36%		1800	0.39%	0.38%	0.61%																																																					
6	120	0.00%	0.00%	0.00%	14	120	0.85%	1.06%	1.49%	24	120	10.42%	8.25%	11.33%	36	120	1.55%	1.72%	2.30%	14	120	0.00%	0.00%	0.00%	300	0.00%	0.00%	0.00%	900	0.00%	0.00%	0.00%	1800	0.00%	0.00%	0.00%	300	2.63%	3.24%	3.57%	900	0.35%	0.29%	0.36%	1800	0.27%	0.27%	0.29%	300	1.16%	0.64%	0.92%	900	0.12%	0.12%	0.39%	1800	0.09%	0.11%	0.14%												
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	2.63%	3.24%	3.57%		300	1.16%	0.64%	0.92%																																																					
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.35%	0.29%	0.36%		900	0.12%	0.12%	0.39%																																																					
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.27%	0.27%	0.29%		1800	0.09%	0.11%	0.14%																																																					
7	120	0.00%	0.00%	0.00%	16	120	0.49%	1.51%	0.91%	27	120	2.36%	1.15%	1.85%	37	120	0.20%	0.04%	0.72%	16	120	0.49%	0.00%	0.60%	300	0.83%	0.47%	1.32%	900	0.80%	0.50%	0.31%	1800	0.46%	0.03%	0.06%	300	0.00%	0.36%	0.01%	900	0.72%	0.00%	0.00%	1800	0.00%	0.72%	0.00%																								
	300	0.00%	0.00%	0.00%		300	0.49%	0.00%	0.60%		300	0.83%	0.47%	1.32%		300	0.00%	0.36%	0.01%																																																					
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.80%	0.50%	0.31%		900	0.72%	0.00%	0.00%																																																					
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.46%	0.03%	0.06%		1800	0.00%	0.72%	0.00%																																																					
8	120	0.00%	0.00%	0.00%	18	120	0.70%	0.82%	0.36%	28	120	0.51%	1.15%	0.88%	40	120	4.80%	7.12%	2.21%	18	120	0.70%	0.26%	0.22%	300	0.84%	0.13%	0.46%	900	0.16%	0.33%	0.18%	1800	0.20%	0.24%	0.24%	300	5.09%	2.96%	4.11%	900	2.26%	1.46%	3.18%	1800	0.00%	0.00%	1.81%																								
	300	0.00%	0.00%	0.00%		300	0.00%	0.26%	0.22%		300	0.84%	0.13%	0.46%		300	5.09%	2.96%	4.11%																																																					
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.16%	0.33%	0.18%		900	2.26%	1.46%	3.18%																																																					
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.20%	0.24%	0.24%		1800	0.00%	0.00%	1.81%																																																					

Minimum Deviations - Efficacy Measure

		No-Island	2-Island	5-Island			No-Island	2-Island	5-Island			No-Island	2-Island	5-Island			No-Island	2-Island	5-Island
5 m	120	0.00%	0.00%	0.00%	10 m	120	0.00%	0.00%	0.00%	20 m	120	0.26%	0.46%	0.50%	30 m	120	1.38%	1.80%	1.17%
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	0.70%	0.36%	0.44%		300	0.67%	0.85%	0.42%
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.05%	0.05%	0.36%
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.15%	0.00%	0.06%
6 s	120	0.00%	0.00%	0.00%	14 m	120	0.00%	0.00%	0.54%	24 m	120	0.37%	0.63%	0.86%	36 s	120	1.55%	1.72%	2.30%
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.51%		300	1.16%	0.64%	0.92%
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.12%	0.12%	0.39%
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.09%	0.11%	0.14%
7 m	120	0.00%	0.00%	0.00%	16 m	120	0.00%	0.68%	0.76%	27 s	120	2.36%	1.15%	1.85%	37 s	120	0.20%	0.04%	0.72%
	300	0.00%	0.00%	0.00%		300	0.00%	0.00%	0.00%		300	0.83%	0.47%	1.32%		300	0.00%	0.36%	0.01%
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.80%	0.50%	0.31%		900	0.72%	0.00%	0.00%
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.46%	0.03%	0.06%		1800	0.00%	0.72%	0.00%
8 m	120	0.00%	0.00%	0.00%	18 s	120	0.70%	0.82%	0.36%	28 s	120	0.51%	1.15%	0.88%	40 s	120	4.80%	7.12%	2.21%
	300	0.00%	0.00%	0.00%		300	0.00%	0.26%	0.22%		300	0.84%	0.13%	0.46%		300	5.09%	2.96%	4.11%
	900	0.00%	0.00%	0.00%		900	0.00%	0.00%	0.00%		900	0.16%	0.33%	0.18%		900	2.26%	1.46%	3.18%
	1800	0.00%	0.00%	0.00%		1800	0.00%	0.00%	0.00%		1800	0.20%	0.24%	0.24%		1800	0.00%	0.00%	1.81%

10 APPENDIX C – Diagonal Matrices Obtained Using the Efficacy Measure as the Fitness Score

Instance 1

		1	1	1	2	2
		5	2	3	4	1
1	1	1	1	1		
1	3		1	1		
1	7	1		1		
2	2				1	1
2	4				1	1
2	5					1
2	6				1	1

Instance 2

		1	1	1	1	2
		3	5	2	4	1
1	2	1	1	1		
1	3	1		1	1	
1	4	1	1	1	1	
1	5	1	1	1		1
2	1				1	1
2	6	1	1			1
2	7					1

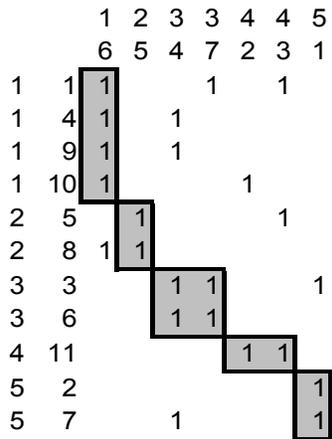
Instance 3

			1	1	1	2	2
			5	3	2	1	4
1	4	1	1	1			
1	7		1	1			
1	9	1					
1	10	1	1	1			
1	15	1	1	1			
1	18	1	1	1			
2	1				1	1	1
2	2					1	1
2	3				1	1	1
2	5					1	1
2	6				1	1	1
2	8				1	1	1
2	11				1	1	1
2	12				1	1	1
2	13				1	1	1
2	14					1	1
2	16					1	1
2	17					1	1

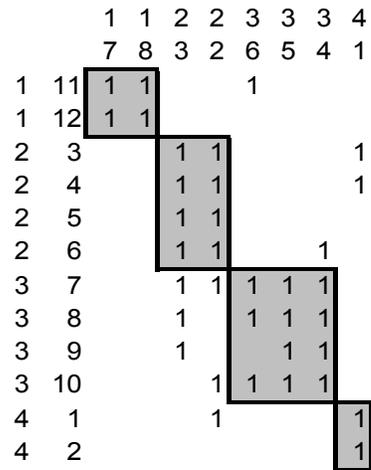
Instance 4

			1	1	1	2	2	2
			3	5	2	4	6	1
1	1	1	1	1				
1	3	1	1	1				
1	5		1	1				
1	6	1	1	1				
1	8	1	1	1				
2	2				1			1
2	4					1	1	1
2	7				1	1	1	1

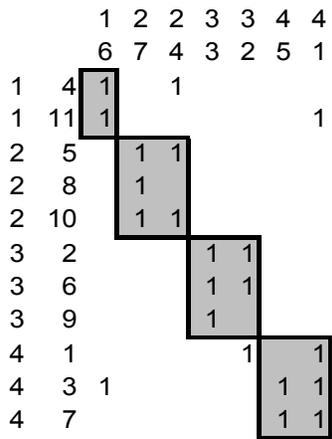
Instance 5



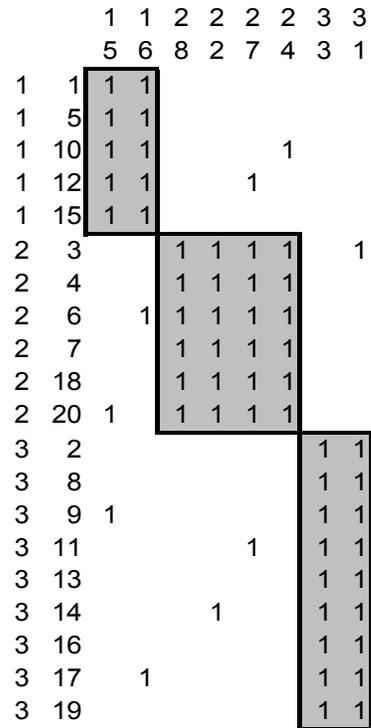
Instance 7



Instance 6



Instance 8



Instance 9

	1	1	1	2	2	2	2	2
	3	7	5	1	2	4	6	8
1 5	1	1					1	1
1 6	1	1	1		1			
1 11	1	1		1		1		
1 12	1	1	1				1	
1 13	1	1	1	1				1
1 16	1	1	1			1	1	1
1 17	1	1	1	1				1
1 19	1	1	1	1		1	1	
1 20	1	1	1	1	1			
2 1		1			1	1	1	1
2 2		1		1		1	1	
2 3		1	1	1	1		1	
2 4			1	1	1		1	
2 7	1	1		1	1		1	
2 8	1	1		1			1	1
2 9			1	1	1		1	
2 10		1		1		1	1	1
2 14			1		1	1	1	1
2 15		1		1		1	1	
2 18			1	1	1	1	1	

Instance 11

	1	1	1	1	2	2	2	3	3	3
	3	4	6	9	2	5	8	1	7	10
1 1	1	1	1	1						
1 4	1		1	1	1					
1 6	1	1		1						
1 9	1	1	1	1	1					
1 14	1	1	1	1	1					
2 3					1	1	1			
2 5					1	1	1			
2 8					1	1	1			
2 13					1	1	1			
2 15					1	1	1			
3 2								1	1	1
3 7								1	1	
3 10								1	1	1
3 11								1	1	1
3 12								1	1	1

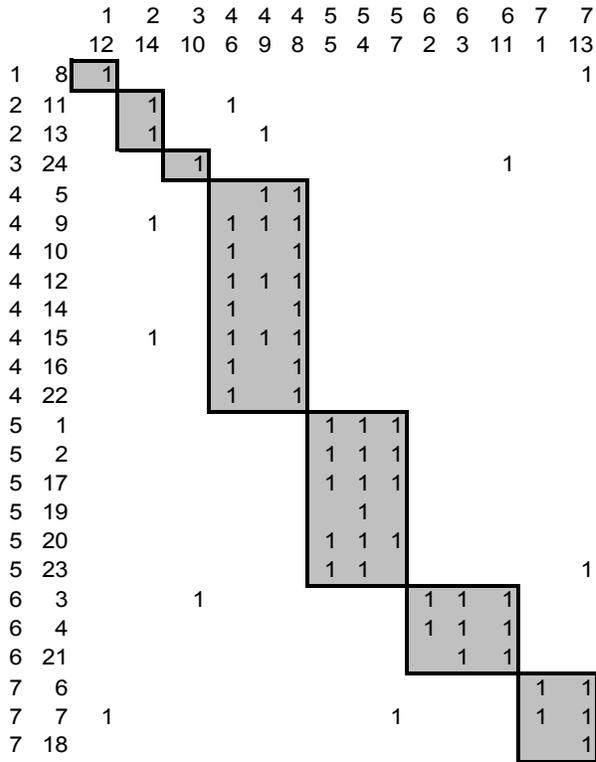
Instance 10

	1	2	3	3	4	4	5	5	5	5
	8	3	5	6	4	1	7	2	10	9
1 6	1		1							
1 9	1									
2 5		1								
3 7			1	1						
3 10			1	1		1				
4 1				1	1	1				
5 2								1	1	
5 3								1	1	1
5 4								1	1	1
5 8								1	1	1

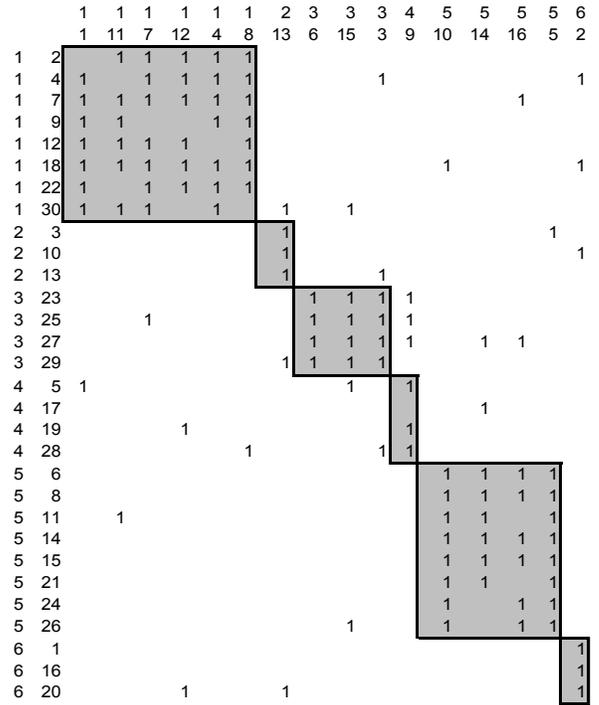
Instance 12

	1	2	2	2	3	4	4	4	5	6	6	6	7	7
	14	9	6	8	10	5	4	7	12	2	3	11	1	13
1 11	1				1									
1 13	1			1										
2 1					1	1								
2 6					1	1	1							
2 10		1			1	1	1	1						
2 12					1	1	1	1						
2 14						1	1	1						
2 15		1				1	1	1	1					
2 16						1	1	1						
3 22										1				
3 24										1				
4 2										1	1	1		
4 3										1	1	1		
4 17										1	1	1		
4 19											1			
4 20											1	1	1	
4 23											1	1		
5 9												1		1
6 4							1					1	1	1
6 5												1	1	1
6 21												1	1	
7 7													1	1
7 8										1	1		1	1
7 18													1	1

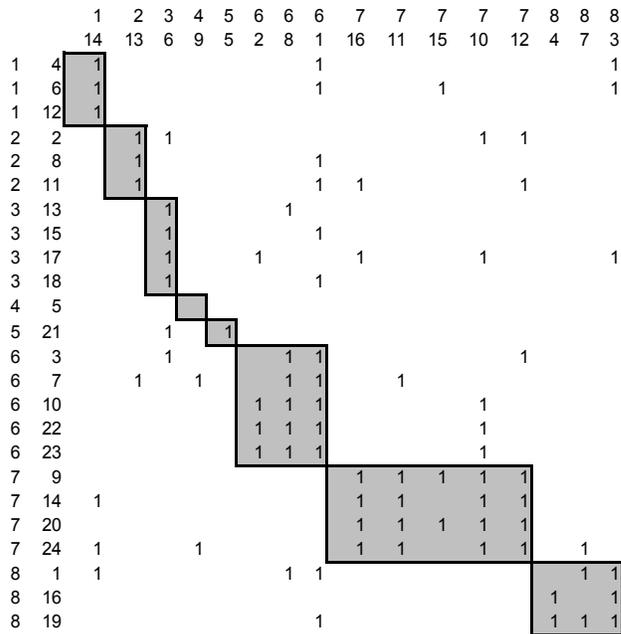
Instance 13



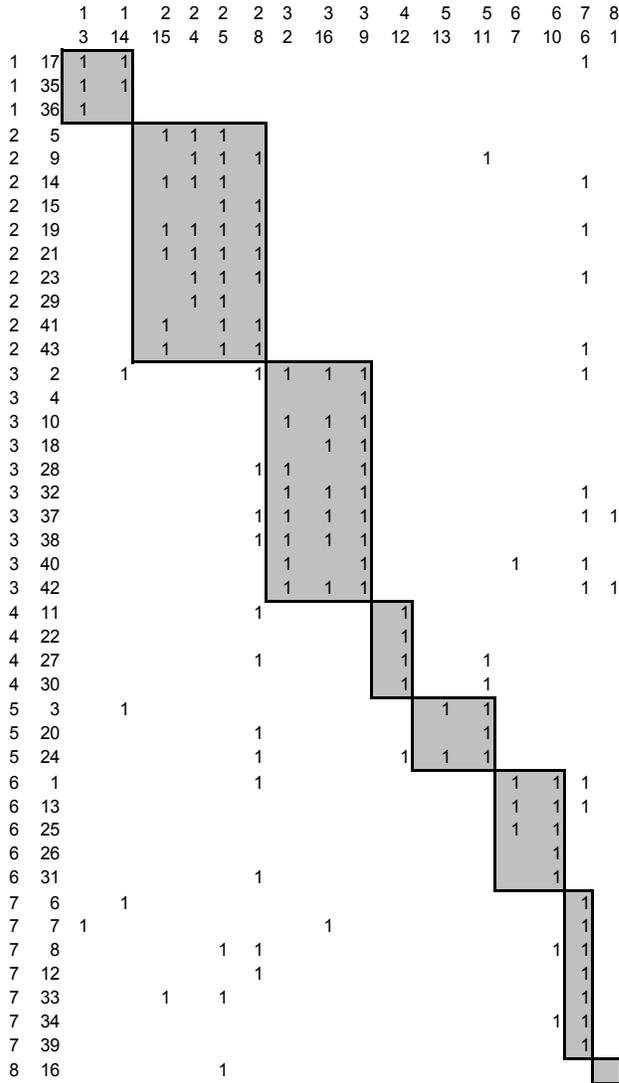
Instance 15



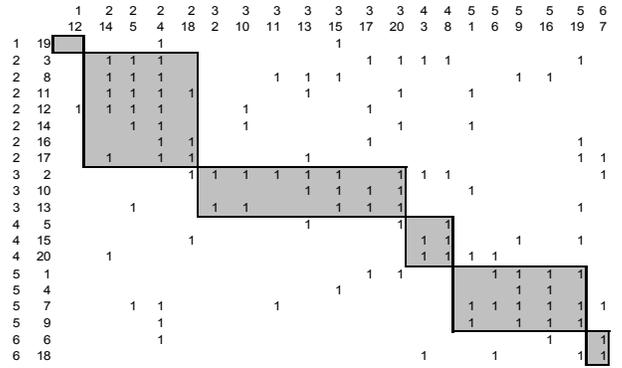
Instance 14



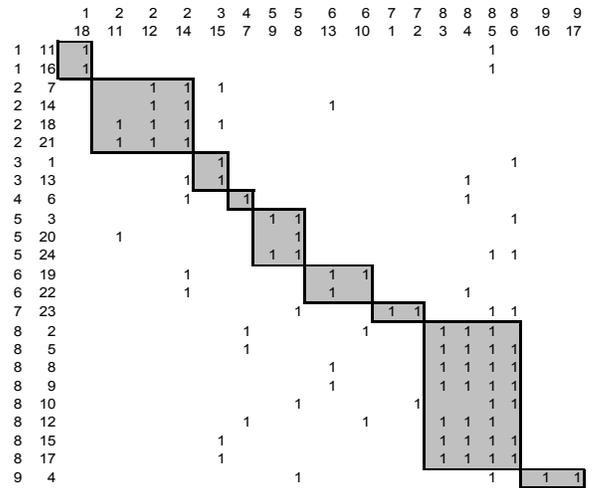
Instance 16



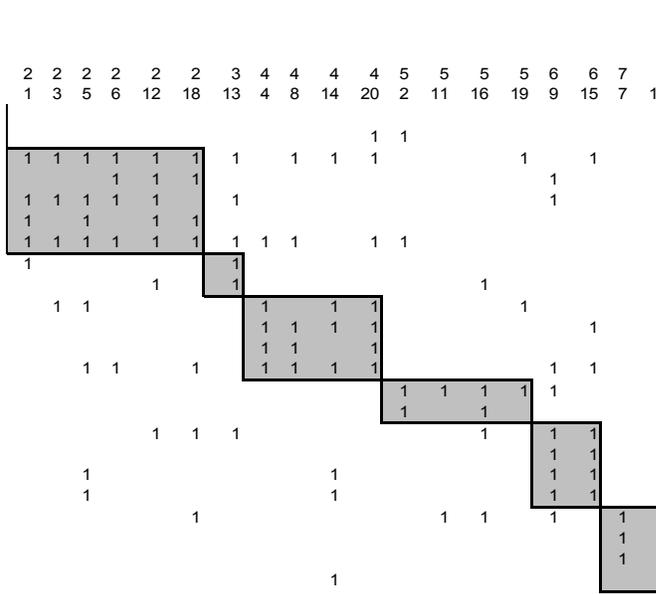
Instance 17



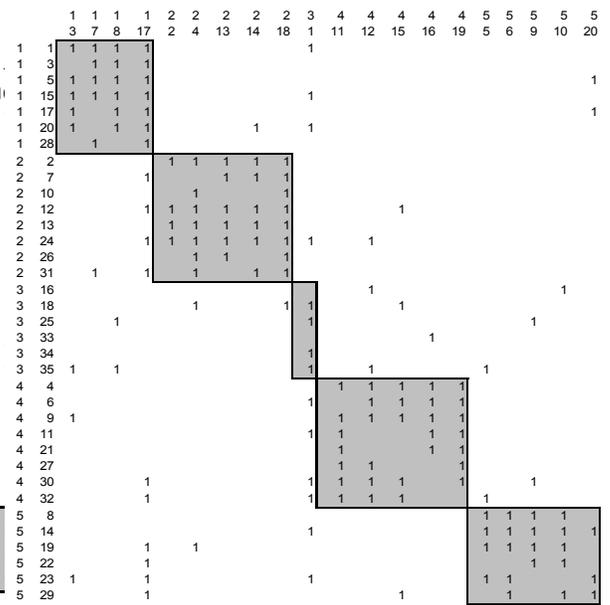
Instance 18



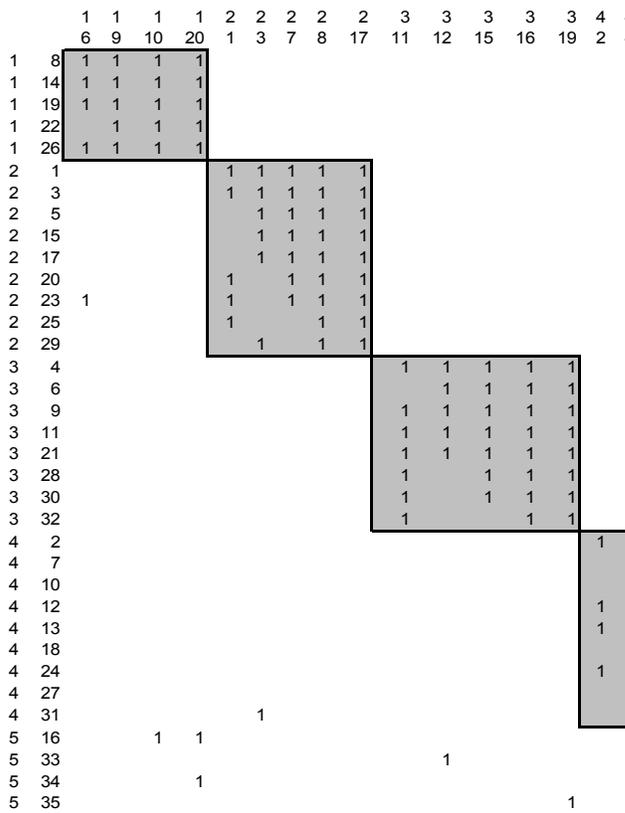
Instance 19



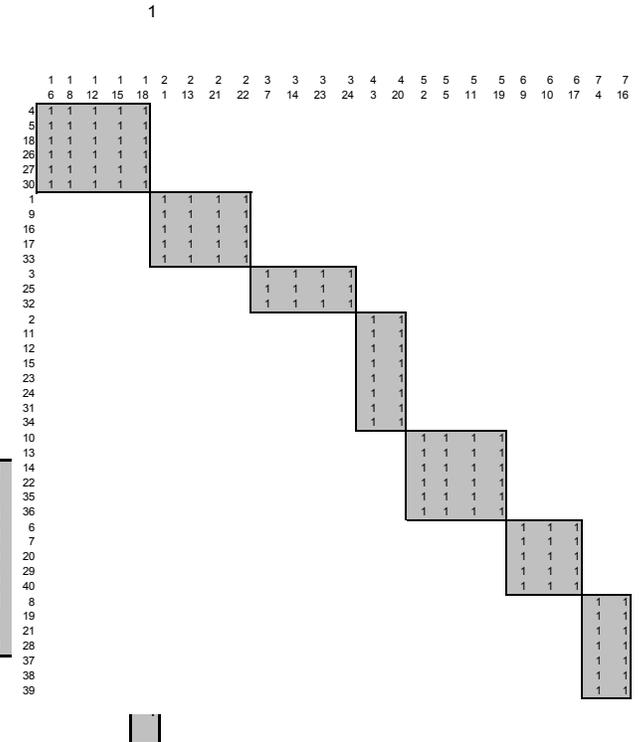
Instance 21



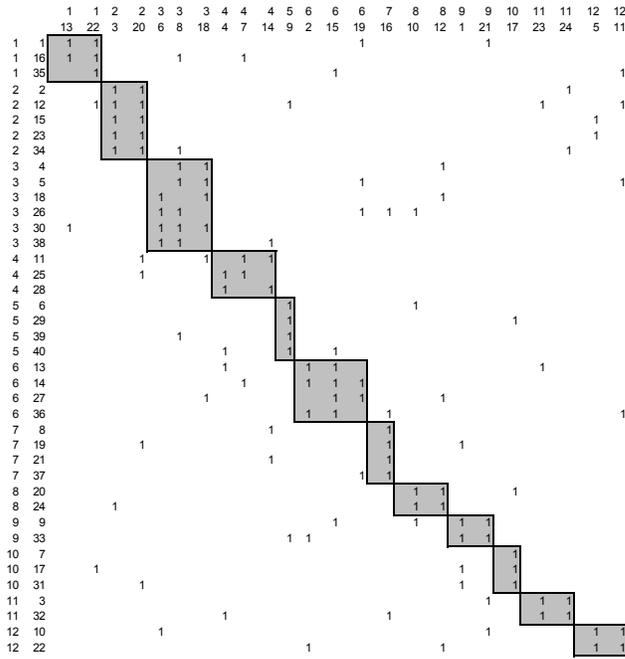
Instance 20



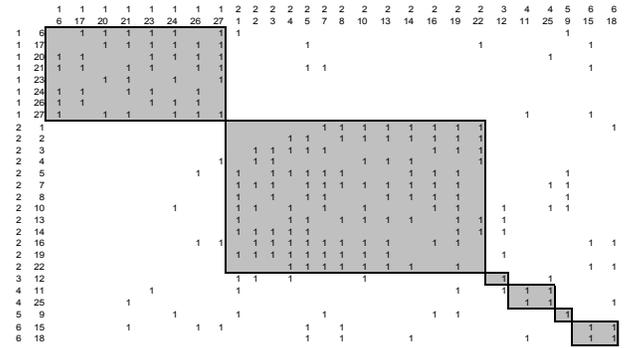
Instance 22



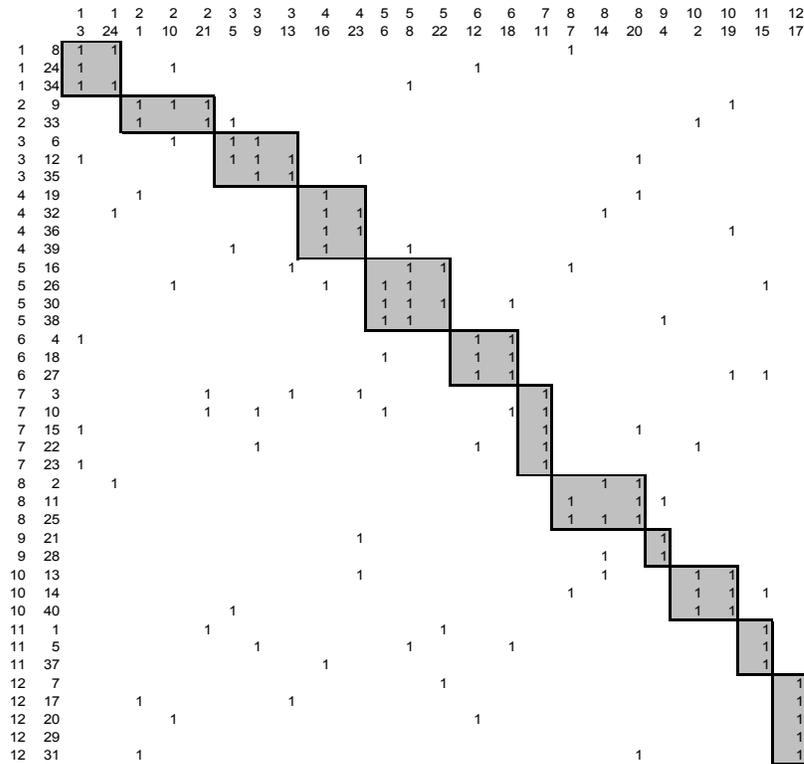
Instance 26



Instance 28



Instance 27



Instance 29

	1	2	2	2	2	3	3	4	4	5	5	5	6	6	6	6	7	7	7	7	8	8	8	8	9	9	10
1 38	1																										
2 33		1																									
3 17			1																								
4 44				1																							
4 45					1																						
5 14						1																					
5 18							1																				
5 19								1																			
5 20									1																		
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5 28														1													
5 30															1												
5 31																1											
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7 39																											1
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7 43																											
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8 9																											
8 10																											
8 11																											
8 32																											
8 36																											
9 13																											
9 26																											
9 27																											
9 29																											
9 37																											
10 34																											
10 35																											
10 46																											

Instance 32

	1	2	2	3	3	4	4	4	4	5	5	5	6	6	6	6	7	7	8	8	8	9	9	10	10	11	12	13	14	14
	6	7	28	13	20	8	9	23	30	1	4	14	10	25	26	27	16	21	17	18	22	5	29	19	24	15	2	11	3	12
1	31	1				1		1								1														
1	32	1														1														1
1	44	1																	1		1		1							
1	48	1																												1
2	10		1	1													1													
2	12			1	1																									
2	14		1								1											1				1				
2	18		1	1																										
2	40		1	1																										
3	1				1	1																								1
3	4				1	1																								1
3	29				1	1																								1
3	33				1	1																								1
3	42				1	1																								1
3	45		1			1	1																							1
4	35						1	1	1																					1
4	39						1	1	1	1																				1
5	8									1	1	1																		1
5	9										1	1																		1
5	21					1		1				1	1																	1
5	36					1							1	1																1
5	41													1	1															1
6	13															1	1	1	1											1
6	15																1	1	1	1										1
6	34							1					1																	1
7	2																													1
7	3																													1
7	11																													1
8	28																													1
8	30																													1
8	50		1																											1
9	23																													1
9	24																													1
9	25																													1
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10	7																													1
10	26																													1
10	27																													1
11	37																													1
11	46		1																											1
11	47																													1
12	19	1																												1
12	20	1																												1
12	38																													1
13	16					1		1																						1
13	49																													1
14	17																													1
14	22																													1
14	43																													1

Instance 33

	1	1	2	3	4	5	5	6	7	7	7	8	9	10	11	12	12	12	13	13	13	13	13	13	13	13	14	15	16	16	16	17								
	32	34	18	13	15	7	20	36	17	16	22	25	27	30	1	26	35	28	11	31	33	2	3	4	8	10	12	14	24	29	6	9	5	19	21	23				
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11 APPENDIX D – Diagonal Matrices Obtained Using the Similarity Measure as the Fitness Score

Instance3

	1	1	1	2	2
	2	3	5	1	4
1	4	1	1	1	
1	7		1	1	
1	9	1			
1	10	1	1	1	
1	15	1	1	1	
1	18	1	1	1	
2	1			1	1
2	2				1
2	3			1	1
2	5				1
2	6			1	1
2	8			1	1
2	11			1	1
2	12			1	1
2	13			1	1
2	14				1
2	16				1
2	17				1

Instance 5

	1	2	3	4	4	5	5
	6	5	4	2	3	1	7
1	4						1
1	9						1
1	10			1			
2	5					1	
2	8			1			
3	1						1
3	6						1
4	11				1	1	
5	2						1
5	3			1			1
5	7						1

Instance 1

	1	1	1	2	2
	2	3	5	1	4
1	1	1	1	1	
1	3		1	1	
1	7	1			
2	2			1	1
2	4			1	1
2	5				1
2	6				1

Instance 2

	1	1	1	1	2
	2	3	4	5	1
1	2	1	1	1	
1	3	1		1	
1	4	1	1	1	
1	5	1	1	1	
2	1				1
2	6	1	1		1
2	7				1

Instance 4

	1	1	1	2	2	2
	2	3	5	1	4	6
1	1	1	1			
1	3	1	1	1		
1	5		1	1		
1	6	1	1	1		
1	8	1	1	1		
2	2				1	
2	4				1	1
2	7				1	1

Instance 6

	1	2	2	3	3	4	4
	6	4	7	2	3	1	5
1	4						1
1	11						1
2	5			1	1		
2	8			1			
2	10			1	1		
3	2				1	1	
3	6				1	1	
3	9				1		
4	1						1
4	3	1					1
4	7						1

Instance 7

	1	1	2	2	2	3	3	4
	7	8	4	5	6	2	3	1
1	11	1	1					1
1	12	1	1					1
2	7		1	1	1		1	1
2	8		1	1	1		1	
2	9			1	1		1	
2	10			1	1	1		1
3	3					1	1	1
3	4					1	1	1
3	5					1	1	
3	6				1	1	1	
4	1							1
4	2							1

Instance 8

	1	1	2	2	3	3	3	3
	5	6	1	3	2	4	7	8
1	1	1						
1	5	1	1					
1	10	1	1					1
1	12	1	1					1
1	15	1	1					
2	2			1	1			
2	8			1	1			
2	9	1		1	1			
2	11			1	1			1
2	13			1	1			
2	14			1	1			1
2	16			1	1			
2	17	1		1	1			
2	19			1	1			
3	3			1	1	1	1	1
3	4			1	1	1	1	1
3	6	1		1	1	1	1	1
3	7			1	1	1	1	1
3	18			1	1	1	1	1
3	20	1		1	1	1	1	1

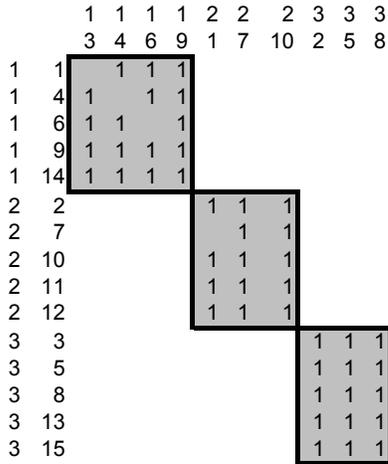
Instance 10

	1	1	1	1	2	2	2	3	3	3
	3	4	6	9	1	7	10	2	5	8
1	1	1	1	1						
1	4	1	1	1						
1	6	1	1	1						
1	9	1	1	1	1					
1	14	1	1	1	1					
2	2				1	1	1			
2	7				1	1	1			
2	10				1	1	1			
2	11				1	1	1			
2	12				1	1	1			
3	3							1	1	1
3	5							1	1	1
3	8							1	1	1
3	13							1	1	1
3	15							1	1	1

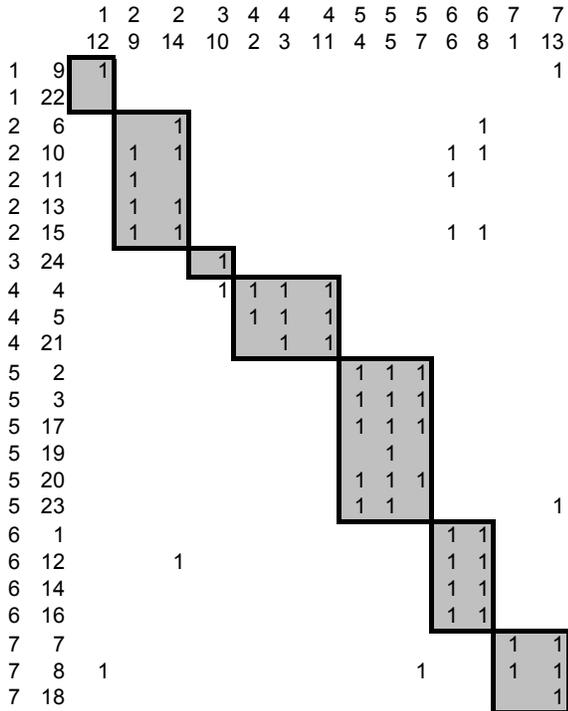
Instance 9

	1	1	2	2	2	2	2	2
	3	7	1	2	4	5	6	8
1	5	1	1					1
1	6	1	1					1
1	7	1	1	1	1			1
1	8	1	1	1	1			1
1	11	1	1			1		1
1	12	1	1					1
1	13	1	1					1
1	17	1	1					1
1	20	1	1					1
2	1				1	1	1	1
2	2				1	1	1	1
2	3				1	1	1	1
2	4				1	1	1	1
2	9				1	1	1	1
2	10				1	1	1	1
2	14				1	1	1	1
2	15				1	1	1	1
2	16	1	1		1	1	1	1
2	18				1	1	1	1
2	19	1	1		1	1	1	1

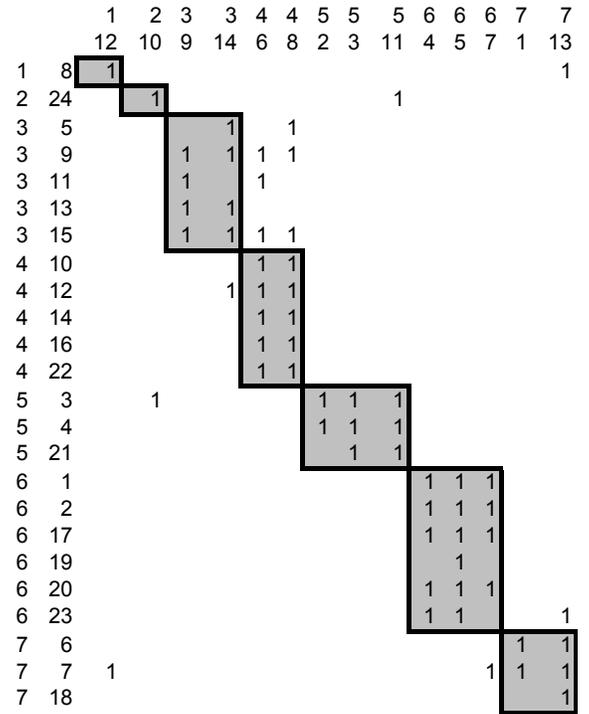
Instance 11



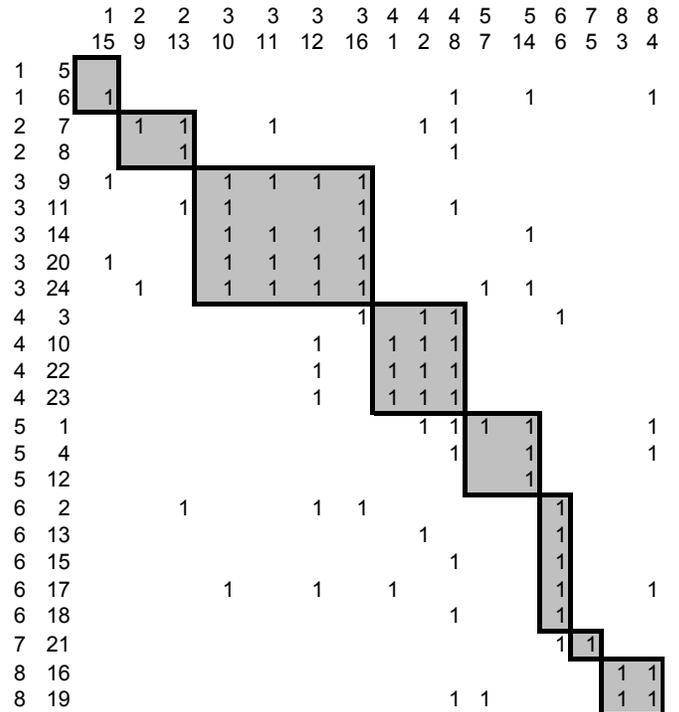
Instance 12



Instance 13



Instance 14



Instance 15

	1	2	3	3	3	3	3	3	4	4	4	5	5	5	5	6
	13	9	1	4	7	8	11	12	3	6	15	5	10	14	16	2
1	3	1													1	
1	10	1														1
1	13	1														1
2	5		1	1						1						
2	17												1			
2	19		1		1											
2	28		1							1						
3	2			1	1	1	1	1	1							
3	4			1	1	1	1	1	1							1
3	7			1	1	1	1	1	1							
3	9			1	1			1	1						1	
3	12			1	1	1	1		1							
3	18			1	1	1	1	1	1						1	
3	22			1		1	1	1	1			1				1
3	30	1		1	1	1	1	1	1							
4	23		1					1	1	1	1					
4	25		1			1			1	1	1					
4	27		1						1	1	1					
4	29	1							1	1	1					
5	6									1	1	1	1			
5	8									1	1	1	1			
5	11			1						1	1	1	1			
5	14									1	1	1	1			
5	15									1	1	1	1			
5	21									1	1	1	1			
5	24									1		1	1			
5	26							1		1	1	1	1			
6	1															1
6	16															1
6	20	1			1											1

Instance 16

	1	2	2	3	3	3	4	4	5	5	6	7	7	7	8	8	
	13	7	10	4	5	15	11	12	6	8	1	2	9	16	3	14	
1	3	1															1
2	1		1	1							1	1					
2	13		1	1								1					
2	25		1	1													
2	26			1													
2	31			1								1					
2	34			1												1	
3	5			1	1	1											
3	9			1	1	1					1	1					
3	14			1	1	1										1	
3	16			1	1	1											
3	19			1	1	1								1	1		
3	21			1	1	1								1			
3	29			1	1	1											
3	33			1	1	1										1	
3	41			1	1	1											
4	11							1				1					
4	20								1			1					
4	22								1			1					
4	24	1							1	1	1						
4	27								1	1	1						
4	30								1	1							
5	8			1			1					1	1				
5	12											1	1				
5	15							1				1					
5	23						1	1				1	1				
5	39											1					
5	43						1	1				1	1				
6	4																1
7	2										1	1		1	1	1	
7	10													1	1	1	
7	18													1	1	1	
7	28										1				1	1	1
7	32											1			1	1	1
7	37											1	1	1		1	1
7	38											1			1	1	1
7	40						1						1		1	1	1
7	42												1	1		1	1
8	6																1
8	7															1	1
8	17												1			1	1
8	35															1	1
8	36															1	1

Instance 17

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	11	12	14	15	18	13	16	17	8	9	1	2	7	10	3	4	5	6	
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1	14	1	1			1													
1	18	1	1	1	1														
1	21	1	1	1															
2	1			1															1
2	13			1	1														1
3	11				1														1
3	16				1														1
4	19			1															1
4	22			1															1
5	4																		1
6	3																		1
6	20	1																	1
6	24																		1
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7	23																		1
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9	2																		1
9	5																		1
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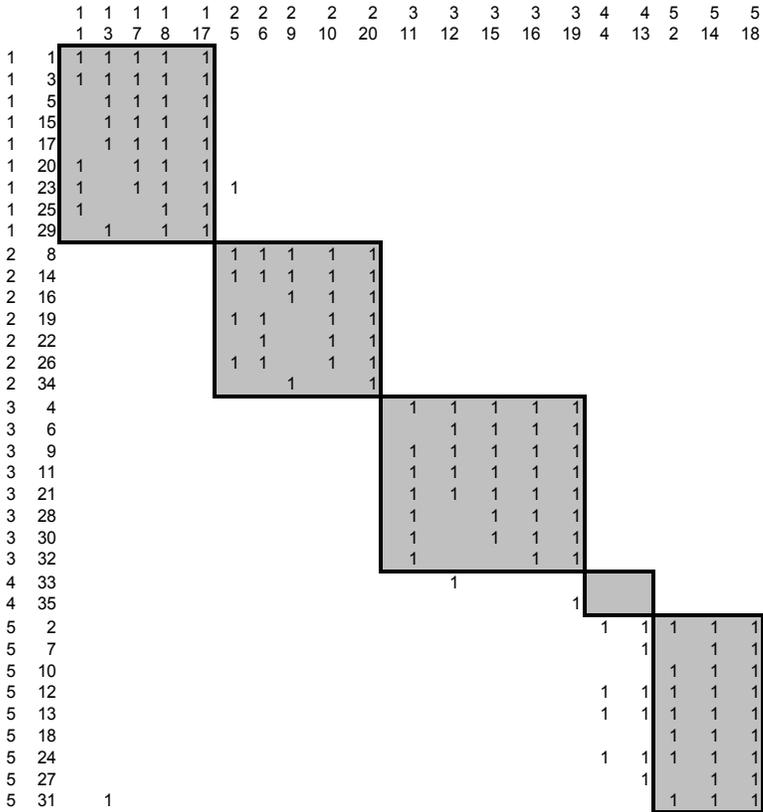
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1	15	1	1																			
1	20	1	1																			
2	2	1	1	1	1	1																
2	17	1	1	1	1																	
3	1																					
3	4																					
3	7																					
3	9																					
3	18	1																				
4	3	1	1																			
4	8																					
4	11																					
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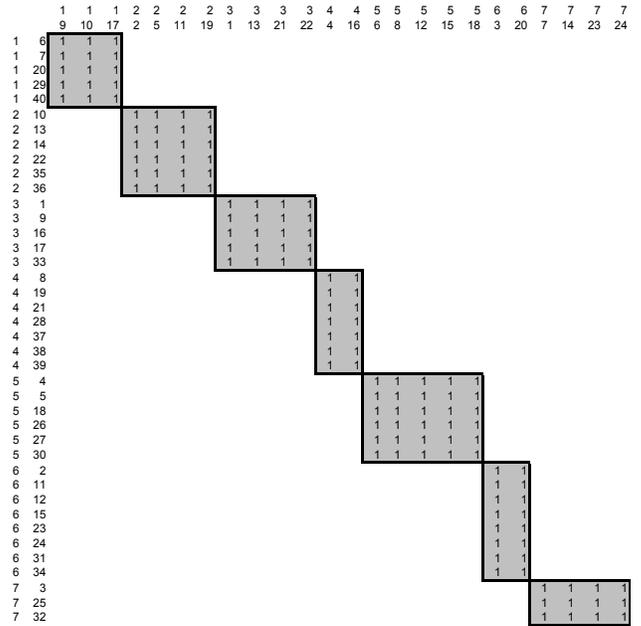
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1	7	1	1																			
1	8	1	1																			
1	9	1	1																			
1	17	1	1																			
2	12																					
2	16																					
3	3																					
4	1																					
4	2																					
4	4																					
4	10																					
4	11																					
4	15																					
4	18																					
5	5																					
5	14																					
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6	22																					
6	23																					
7	6																					
7	13																					

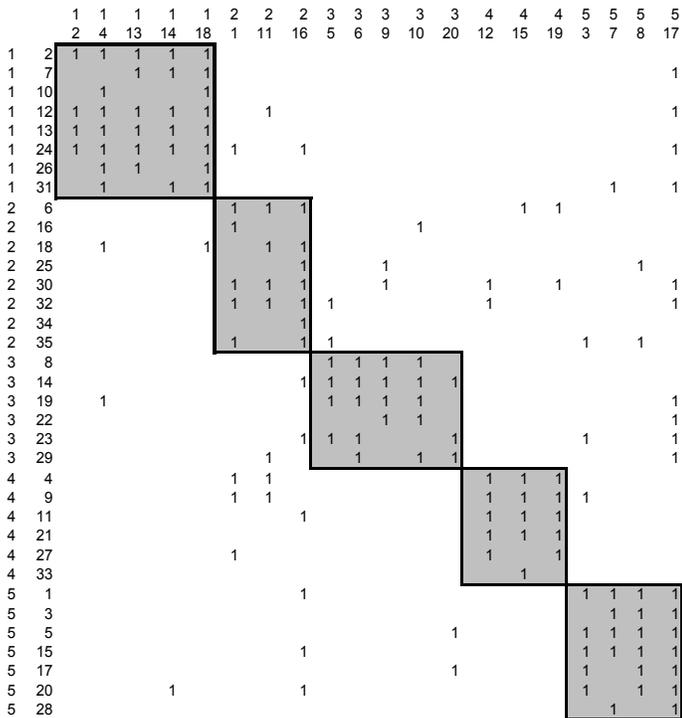
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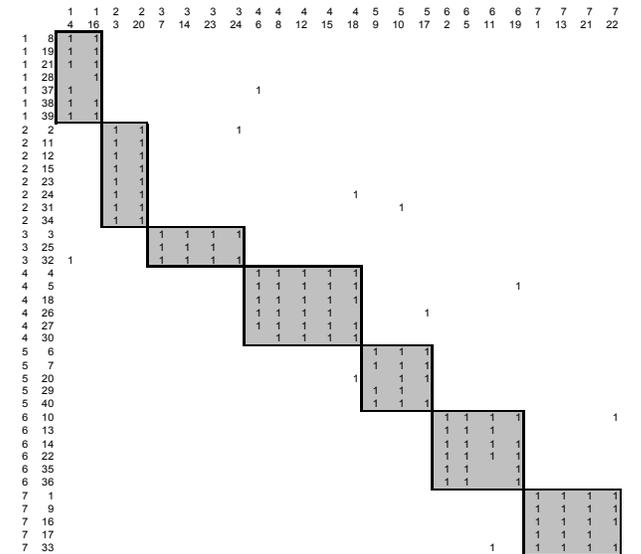
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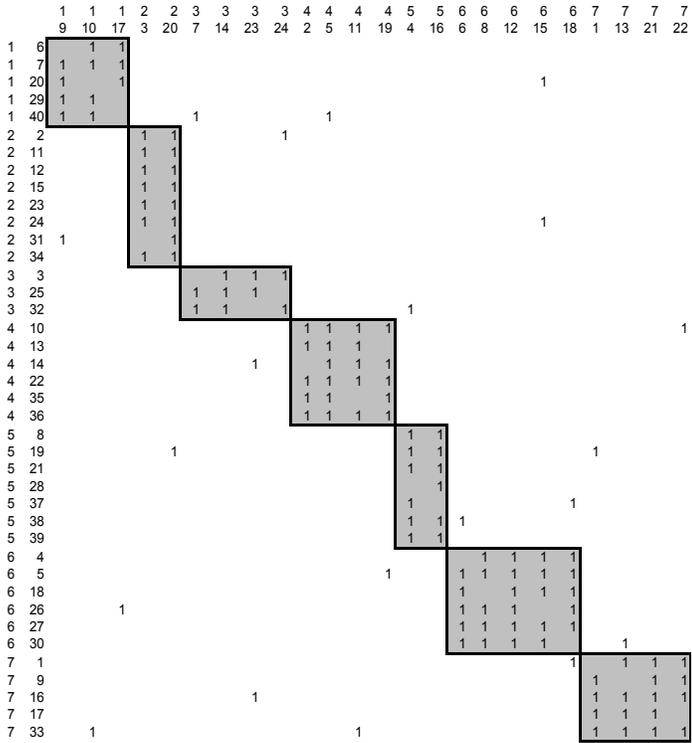
Instance 21



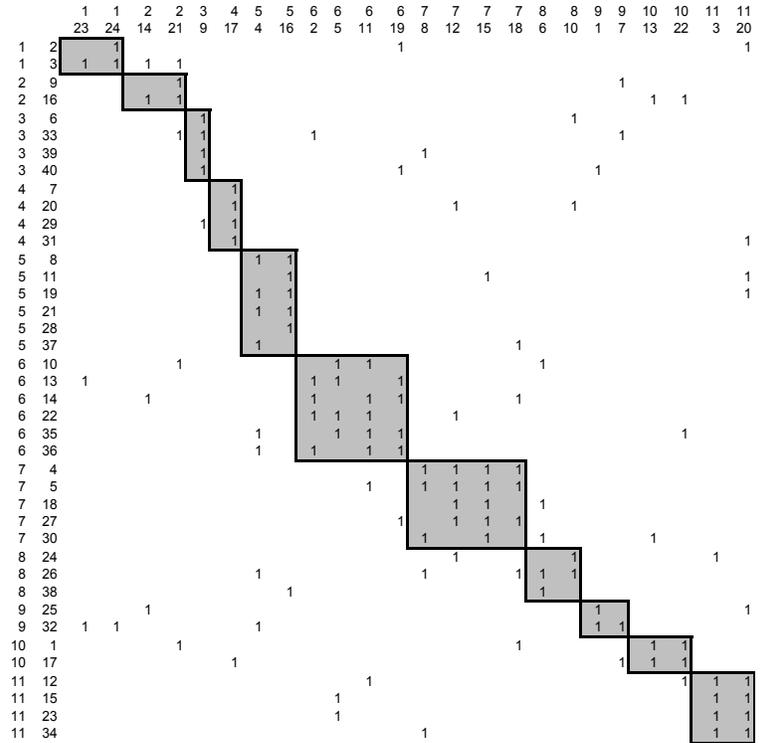
Instance 23



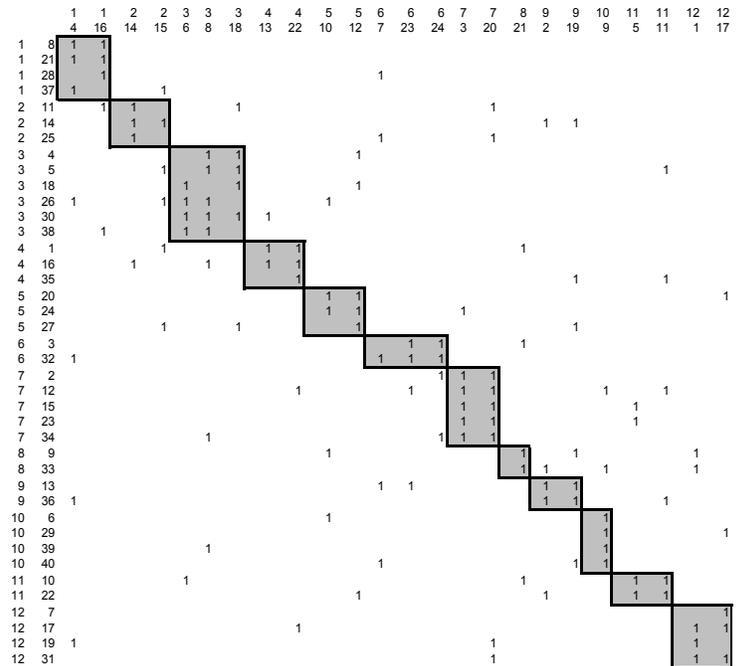
Instance 24



Instance 25



Instance 26



Instance 31

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	6	8	12	1	13	4	11	19	21	23	7	14	16	2	5	9	18	20	22	15	17	3	10	24	30	26	28	25	27	29	
1	13	1	1								1																				
1	14	1	1	1																											
1	15	1	1	1																											
1	16	1	1	1																											
2	5	1	1		1	1																									
2	6				1	1											1						1	1							
2	8				1	1																		1							
3	1				1	1	1	1									1	1													
3	7	1	1			1	1	1								1								1							
3	18				1	1	1	1																1							
4	29								1	1										1											
4	31								1	1	1																				
4	33								1	1	1																				
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6	19											1	1																		
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6	23												1	1	1								1								
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6	27														1	1	1														
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7	3		1													1	1	1													
7	17		1													1	1	1													
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8	37																1	1	1	1											
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9	22																		1												
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10	4																														
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10	11																														
11	39																														
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11	44																														
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12	43																														
12	46																														
12	47																														
13	40																														
13	41																														
13	45																														
13	49																														
13	50																														

Instance 32

	1	1	1	2	2	3	3	3	4	5	5	6	7	7	7	8	8	9	9	10	10	11	11	12	12	13	13	13	14	14					
	25	26	27	9	23	2	6	10	15	7	28	22	1	4	14	19	24	16	21	8	30	17	18	5	29	11	13	20	3	12					
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1	15	1	1	1																															
1	34	1	1	1					1						1												1			1					
2	21		1	1	1									1	1								1												
2	31		1	1	1	1			1														1												
2	32		1	1	1	1																								1					
2	39		1	1	1	1			1											1	1						1			1		1			
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13	42																																		
13	45																																		
14	17																																		
14	22																																		
14	43																																		
14	48																																		

12 APPENDIX E – Case Results

MERCAN

Cell-1		Cell-2		Cell-3		Cell-4					
Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts				
7	12	1	1	4	6	208	2	3	77	130	192
9	16	5	2	10	9	209	3	4	78	131	193
11		6	10	12	11	210		5	79	132	194
		8	124	13	13	211		7	80	134	195
			133		15	213		8	81	135	196
			145		17			14	82	136	197
			207		20			18	83	137	198
					22			19	84	140	199
					24			21	85	142	200
					25			23	86	146	202
					26			28	87	147	212
					27			29	88	150	
					32			30	89	151	
					33			31	93	152	
					34			43	94	153	
					35			44	95	154	
					36			45	96	156	
					37			46	97	159	
					38			47	98	162	
					39			48	99	163	
					40			49	100	164	
					41			50	101	165	
					42			51	102	167	
					71			52	103	168	
					90			53	104	169	
					91			54	105	170	
					92			55	106	171	
					128			56	107	172	
					129			57	108	173	
					138			58	109	174	
					139			59	110	175	
					141			60	111	176	
					143			61	112	177	
					144			62	113	178	
					148			63	114	179	
					149			64	115	180	
					155			65	116	181	
					157			66	117	182	
					158			67	118	183	
					160			68	119	184	
					161			69	120	185	
					166			70	121	186	
					201			72	122	187	
					203			73	123	188	
					204			74	125	189	
					205			75	126	190	
					206			76	127	191	

KONVEYOR

Cell-1		Cell-2		Cell-3		Cell-4		Cell-5		Cell-6			Cell-7			Cell-8				Cell-9												
Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts	Machines	Parts			
10	156	5	102	7	248	1	1	8	5	12	28	736	6	2	379	3	14	170	485	2	7	99	225	311	392	448	528	584	639	693	747	
18		14		20	266	9	3	19	6			39	737	23	59	604	4	21	176	487	11	8	104	226	312	393	449	530	587	640	694	748
		15		21	467	13	4	22	12			41			63	644	25	23	177	489	17	9	105	228	313	394	450	531	588	642	695	749
					641	16	48		13			65			64	655		25	178	492	26	10	109	230	315	395	451	532	589	643	696	750
						24	53		29			71			106			26	181	493	11	110	231	316	396	452	533	590	645	697	751	
							331		30			131			107			31	183	498	15	111	233	318	397	454	534	591	646	698	752	
							336		38			154			108			32	185	506	16	112	234	319	398	462	535	595	647	699	753	
							406		44			168			122			34	192	508	17	116	235	321	399	469	536	597	648	700	754	
							546		45			171			136			35	194	509	18	117	236	322	400	470	537	598	649	701	755	
							583		55			172			148			36	197	518	19	118	237	323	401	471	538	599	650	702	756	
							658		62			174			155			42	201	519	20	119	238	324	403	472	539	601	652	703	757	
									70			175			169			43	203	524	22	120	239	325	405	476	540	602	653	704		
									72			179			173			57	206	547	24	121	240	326	407	478	541	603	654	705		
									75			186			267			58	207	548	27	123	242	328	408	479	542	605	656	706		
									76			195			268			61	208	549	33	130	244	329	409	480	543	606	657	707		
									91			196			289			66	210	573	37	132	245	330	410	481	544	607	659	708		
									127			205			291			68	212	574	40	133	249	334	411	482	545	608	661	709		
									139			232			292			69	213	585	46	134	250	335	413	483	550	609	662	710		
									140			275			293			73	217	586	47	137	251	337	414	486	551	610	663	711		
									141			278			294			80	219	592	49	138	252	340	415	488	552	611	664	712		
									161			279			295			82	220	593	50	146	253	341	417	490	553	612	665	713		
									167			280			296			100	227	594	51	150	254	343	418	491	554	613	666	714		
									180			283			297			101	229	596	52	159	255	345	419	494	555	614	667	715		
									182			286			298			103	241	600	54	162	256	355	420	495	556	615	668	716		
									216			305			300			113	243	660	56	163	257	356	421	496	557	616	669	717		
									287			306			301			114	246		60	164	258	361	422	497	558	617	670	718		
									288			344			302			115	247		67	184	259	362	423	499	559	618	671	719		
									351			347			303			124	310		74	187	260	363	424	500	560	619	672	720		
									352			348			304			125	402		77	188	261	364	426	501	561	620	673	721		
									353			349			307			126	412		78	189	262	366	429	502	563	621	674	722		
									357			404			308			128	416		79	190	263	367	430	503	564	622	675	724		
									358			456			309			129	425		81	191	264	371	431	504	565	623	676	727		
									360			458			314			135	427		83	193	265	373	432	505	566	624	677	728		
									368			460			317			142	428		84	198	269	376	433	507	567	625	678	730		
									369			464			320			143	443		85	199	270	377	434	510	568	626	679	731		
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									463			562			339			151	461		90	211	276	384	439	515	575	631	684	739		
									651			342			342			152	466		92	214	277	385	440	516	576	632	685	740		
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									725			354			354			158	474		95	221	284	388	444	521	579	635	688	743		
									726			359			359			160	475		96	222	285	389	445	522	580	636	689	744		
									729			365			365			165	477		97	223	290	390	446	523	581	637	691	745		
									732			378			378			166	484		98	224	299	391	447	526	582	638	692	746		