A Sequence-Pair and Mixed Integer Programming Based Methodology for the Facility Layout Problem

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Dissertation Submitted to the Faculty of the
Virginia Polytechnic Institute and State University
in Partial Fulfillment of the Requirements for the Degree of

Doctor of Philosophy

in

Industrial & Systems Engineering

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November 22, 2004
Blacksburg, Virginia

Keywords: Facility Layout Problem, Sequence-Pair Representation, Mixed Integer Programming, Aisle Structure, Rectangular-Shaped and Non-Rectangular-Shaped Departments

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(ABSTRACT)

The facility layout problem (FLP) is one of the most important and challenging problems in both the operations research and industrial engineering research domains. In FLP research, the continuous-representation-based FLP can consider all possible all-rectangular-department solutions. Given this flexibility, this representation has become the representation-of-choice in FLP research. Much of this research is based on a methodology of mixed integer programming (MIP) models. However, these MIP-FLP models can only solve problems with a limited number of departments to optimality due to a large number of binary variables used in the models to prevent departments from overlapping. Our research centers around the sequence-pair representation, a concept that originated in the Very Large Scale Integration (VLSI) design literature. We show that an exhaustive search of the sequence-pair solution space will result in finding the optimal layout of the MIP-FLP and that every sequence-pair solution is binary-feasible in the MIP-FLP. Based on this fact, we propose a methodology that combines the sequence-pair and MIP-FLP model to efficiently solve large continuous-representation-based FLPs. Our heuristic approach searches the sequence-pair solution space and then use the sequence-pair representation to simplify and solve the MIP-FLP model. Based on this methodology, we systematically study the different aspects of the FLP throughout this dissertation.

As the first contribution of this dissertation, we present a genetic algorithm based heuristic, SEQUENCE, that combines the sequence-pair representation and the most recent MIP-FLP model to solve the all-rectangular-department continuous-representation-based FLP. Numerical experiments based on different sized test problems from both the literature and industrial applications are provided and the solutions are compared with both the optimal solutions and the solutions from other heuristics to show the effectiveness and efficiency of

our heuristic. For eleven data sets from the literature, we provide solutions better than those previously found.

For the FLP with fixed departments, many sequence-pairs become infeasible with respect to the fixed department location and dimension restrictions. As our second contribution, to address this difficulty, we present a repair operator to filter the infeasible sequence-pairs with respect to the fixed departments. This repair operator is integrated into SEQUENCE to solve the FLP with fixed departments more efficiently. The effectiveness of combining SEQUENCE and the repair operator for solving the FLP with fixed departments is illustrated through a series of numerical experiments where the SEQUENCE solutions are compared with other heuristics' solutions.

The third contribution of this dissertation is to formulate and solve the FLP with an existing aisle structure (FLPAL). In many industrial layout designs, the existing aisle structure must be taken into account. However, there is very little research that has been conducted in this area. We extend our research to further address the FLPAL. We first present an MIP model for the FLPAL (MIP-FLPAL) and run numerical experiments to test the performance of the MIP-FLPAL. These experiments illustrate that the MIP-FLPAL can only solve very limited sized FLPAL problems. Therefore, we present a genetic algorithm based heuristic, SEQUENCE-AL, to combine the sequence-pair representation and MIP-FLPAL to solve larger-sized FLPAL problems. Different sized data sets are solved by SEQUENCE-AL and the solutions are compared with both the optimal solutions and other heuristics' solutions to show the effectiveness of SEQUENCE-AL.

The fourth contribution of this dissertation is to formulate and solve the FLP with non-rectangular-shaped departments. Most FLP research focuses on layout design with all-rectangular-shaped departments, while in industry there are many FLP applications with non-rectangular-shaped departments. We extend our research to solve the FLP with non-rectangular-shaped departments. We first formulate the FLP with non-rectangular-shaped departments (FLPNR) to a MIP model (MIP-FLPNR), where each non-rectangular de-

partment is partitioned into rectangular-shaped sub-departments and the sub-departments from the same department are connected according to the department's orientation. The effect of different factors on the performance of the MIP-FLPNR is explored through a series of numerical tests, which also shows that MIP-FLPNR can only solve limited-sized FLPNR problems. To solve larger-sized FLPNR problems, we present a genetic algorithm based heuristic, SEQUENCE-NR, along with two repair operators based on the mathematical properties of the MIP-FLPNR to solve the larger-sized FLPNR. A series of numerical tests are conducted on SEQUENCE-NR to compare the SEQUENCE-NR solutions with both the optimal solutions and another heuristic's solutions to illustrate the effectiveness of SEQUENCE-NR.

As the first systematic research study on a methodology that combines the sequence-pair representation and the MIP-based FLP, this dissertation addresses different types of continuous-representation based facility layout design problems: from block layout design with and without fixed departments to re-layout design with an existing aisle structure, and from layout design with all-rectangular-shaped departments to layout design with arbitrary non-rectangular-shaped departments. For each type of layout design problem, numerical experiments are conducted to illustrate the effectiveness of our specifically designed family of sequence-pair and MIP-based heuristics. As a result, better solutions than those previously found are provided for some widely used data sets from the literature and some new data sets based on both the literature and industrial applications are proposed for the first time. Furthermore, future research that continues to combine the sequence-pair representation and the MIP-FLP model to solve the FLP is also discussed, indicating the richness of this research domain.

Note: This work received support from the National Science Foundation, the Center for High Performance Manufacturing at Virginia Tech, and Ingersoll-Rand (Steelcraft).

Acknowledgement

First and foremost, the author would like to heartily thank Dr. Russell D. Meller for his consistent guidance, encouragement and patience, and for his invaluable professional and personal assistance. The completion of this dissertation would not have been possible without his support and advisory. The author has learned so much from him as a model of teaching and research excellence.

In a similar way, the author would like to express his appreciation for the other committee members for their insightful advice, encouragement and support throughout the process. Specifically, the author would like to thank Dr. Fraticelli for her support and advice in the mathematical modeling area, Dr. Deisenroth for his advice and support in the modeling and numerical experiment design, Dr. Barkhi for his advice in the meta-heuristic design and his considerations for scheduling the final defense, and Dr. Chen for his insightful suggestions and encouragement. The author also would like to specially thank Dr. Yossi Bukchin for his advice, cooperation and support for this dissertation.

Finally, the author would like to thank his parents and friends for helping him throughout this dissertation research. The author sincerely thanks his parents, Qunzhang and Shujuan, for supporting all of his educational endeavors. The author also would like to specially thank his girl friend, Huaiying, for her dedicated love, heartwarming encouragement, and consistent help and support.

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Chapter 1

Introduction

The effective utilization of a company's facility is one of the key challenges facing plant managers today. Facility utilization encompasses not only the utilization of facility space, but also the challenge of providing support for an efficient facility flow network. The cornerstone to both of these challenges is the facility layout. As such, solving the facility layout problem is a critical component to the competitiveness of a company.

The research outlined in this dissertation aims to provide a methodology to help companies solve the critical problem of the facility layout problem. In Section 1.1 we discuss the motivation for this dissertation topic. In Section 1.2 we provide background on facility layout problem approaches, including Very Large Scale Integration (VLSI) design. In Section 1.3 we describe the facility layout problem in more detail, including objective functions that are commonly used (see Section 1.3.1) and one of the key aspects of any facility layout approach, the layout representation (see Section 1.3.2). We then discuss our research objectives in Section 1.4. Finally, in Section 1.5 we discuss the organization of this dissertation.

1.1 Motivation

In the past 10 years, with rapidly increased global competition, elimination of waste and continuous productivity improvement have become more and more critical for manufacturing companies to run their business effectively and efficiently. Most of the business concepts and strategies arising recently, like Enterprise Resource Planning (ERP), Supply Chain Management (SCM), Just-In-Time (JIT) Manufacturing, Flexible Manufacturing Systems (FMS) and Lean Manufacturing, consider eliminating waste and continuous productivity improvement as their foundation.

The productivity and efficiency of an organization greatly depends on how people plan, organize and utilize the facilities in that organization. Facilities planning "determines how an activity's tangible fixed assets best support achieving the activity's objective" [66]. Thus, facilities planning has a great impact on the productivity and efficiency of running an organization.

As stated in [66, pg. 9], "since 1955, approximately 8% of the gross national product (GNP) has been spent annually on new facilities in the United States." Adding to this figure is the realization that many existing facilities are renovated each year, which yields an estimate of $250B spent each year on facilities planning and replanning [66, pg. 10]. Thus, from an upfront investment and recurring project expense, facilities planning is a critical issue in today's competitive manufacturing and service sectors.

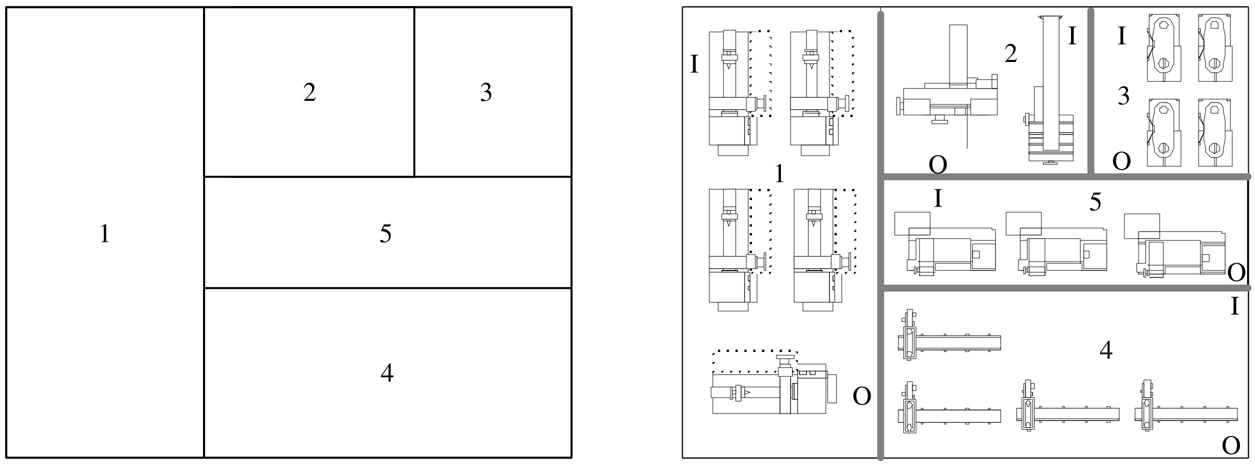
In addition to the upfront investment involved in facilities planning, there are operational issues that make facilities planning a critical issue. The most obvious impact is on material handling expenses. As suggested in [66, pg. 10], "effective facilities planning can reduce [material handling] costs by 10 to 30%."

However, the impact of the facility layout goes beyond material handling costs (which are likely to be a rather small cost in the facility). An effective facility layout implies that departments with high flow are close together. In addition to reducing material handling costs, this is also likely to reduce the material handling batch size. By reducing the material handling batch size, work-in-process inventory (WIP) will also decrease. Decreasing WIP has a direct cost implication (likely a large one) and is also likely to improve the lead time and quality of the product being moved (since feedback due to poor quality is shortened along with lead time). Finally, companies that are able to simultaneously shorten lead time, improve quality, and reduce their costs are much more likely to have increased opportunities for their product. Thus, the impact of facilities planning goes significantly beyond the impact on material handling expenses (e.g., productivity ratios concerning manufacturing cycle, aisle space, and energy [62, pp. 259–261]). In summary, facilities planning has an impact on many aspects of the company, either directly or indirectly.

The main components of facilities planning include facility location, facility system design, facility layout design, and material handling system design. As one of the critical steps in facilities planning, the facility layout design is "concerned with determining the 'most efficient' arrangement of interacting departments within a designated section of a building subject to constraints imposed by the site plan, the building, the departmental area, service requirements, and the decision-maker" [11].

The facility layout problem (FLP) has broad applications, from a new hospital to an assembly line, from an existing warehouse to the baggage department in an airport, from an office to a retail store. In manufacturing, the facility layout design involves the determination of how to design the physical layout of manufacturing facility systems to provide the best support for production.

More specifically, the facility layout procedure traditionally includes two phases: the block layout phase and the detailed layout phase. The block layout phase specifies the relative location and size of each department (see Figure 1.1(a)). Based on the block layout output, the detailed layout phase determines exact department locations, aisle structures, input/output (I/O) point locations, and the layout within each department (see Figure 1.1(b)).



(a) (b)

Figure 1.1: Facility Layout Solutions in (a) Block Layout and (b) Detailed Layout.

1.2 Background

There is a significant amount of research activity to support facility layout design. The research can be classified in one of two directions: exact algorithms and heuristic approaches. We will discuss these two research directions next.

1.2.1 Exact Algorithms

Exact algorithms for the FLP represent those algorithms developed to obtain, in theory, an optimal solution to the facility layout problem. The major advantage of an exact algorithm is that it considers the whole solution space and the optimality of the final layout solution can be guaranteed. Unfortunately, these models are not necessarily of practical value. This is because they can only consider very small sized problems (less than 10 unequal sized departments), which are far from the size of common industry-practical problems (30–40 departments). When the size of the problem increases, the algorithms become impossible to solve in a practical sense because of the computational complexity of the FLP.

The well-known exact algorithms for the FLP include the quadratic assignment problem (QAP) model and the mixed integer programming (MIP) model. The QAP [35], as a special case of distance-based FLP with discrete representation, assumes that every department has equal area and that all locations (grids) are fixed and known *a priori*. The QAP formulation assigns every department to one location and at most one department to each location, which means a one-to-one matching between departments and locations. The cost of placing a department at a particular location is dependent on the location of the interacting departments. Although the QAP formulation greatly simplifies the FLP and cannot describe the reality of the industrial applications, the QAP is still one of the most challenging optimization problems—recently, a 30-facility QAP required 1000 computers in a massive parallelization effort over a seven-day period that lead to an equivalent 6.9 years of computational effort [1]. The size of the QAP that can be solved in a reasonable computational effort is around 20 departments [17].

A MIP-based formulation for the facility layout problem (MIP-FLP) was presented by Montreuil [51]. He formulates the FLP as a 0-1 mixed integer programming model with a distance-based objective function. Because the MIP-FLP model utilizes a continuous representation, it is more accurate and realistic than the traditional QAP model [45, 51]. The MIP-FLP has become one of the main focus areas in FLP research in recent years [6, 37, 38, 39, 45, 50]. However, since the MIP-FLP is very difficult to solve to optimality (less than 10 departments), an efficient heuristic that is based on the MIP-FLP needs to be developed.

1.2.2 Heuristic Approaches

Due to the difficulty of obtaining an exact solution to a FLP, many heuristics have been developed. Construction and improvement heuristics intend to find a "good" solution by implementing a certain layout representation. Construction-type heuristics build a single solution in an open space from scratch by alternatively selecting and locating new departments until the layout is complete. Improvement-type heuristics require an initial layout as input and the program improves the initial layout by making use of some improvement mechanism, such as pair-wise or multi-pair-wise exchanges, within a heuristic framework. A comprehensive survey of FLP research, including construction and improvement heuristics, can be found in [48].

1.2.3 Very Large Scale Integration (VLSI) Design

A problem related to the FLP is the Very Large Scale Integration (VLSI) systems design problem from the electronics industry. Within the VLSI problem, components correspond to departments and the chip corresponds to the facility. Within the VLSI problem, the "departments" typically have fixed dimensions (unlike in the FLP), and the objective function is typically different than the objective function in the FLP, which will be discussed in the next section.

1.3 Facility Layout Problem

1.3.1 Facility Layout Problem Objective Functions

In the facility layout problem (FLP) we are to find an efficient non-overlapping planar arrangement of n departments within a given facility. The efficiency of the facility layout is typically measured in terms of material handling costs. In the literature, two common surrogate objectives widely used to approximate material handling costs are given as follows [48]:

1. Closeness Rating Function: A department adjacency-based objective is defined as follows:

$$\max \sum_i \sum_j (r_{ij}) x_{ij}, \tag{1.1}$$

where x_{ij} equals 1 if departments i and j are adjacent, and 0 otherwise. The reward r_{ij} is a numerical value to represent a closeness rating between departments i and j. Such an objective is based on the material handling principle that material handling costs are reduced significantly when two departments are adjacent.

2. Flow Cost Function: An interdepartmental distance-based objective is defined as follows:

$$\min \sum_i \sum_j (f_{ij} c_{ij}) d_{ij}, \tag{1.2}$$

where f_{ij} is the material flow from department i to department j, c_{ij} is the cost to move one unit load one distance unit from department i to department j, and d_{ij} is the distance from department i to department j. This objective is based on the material handling principle that material handling costs increase with the distance the unit load must travel.

There are a variety of ways to measure the distance between a pair of departments (d_{ij}). The following represents commonly-used distance measures for the FLP.

Centroid-to-Centroid (CTC) Distance: During the block layout phase where the input/output point and aisle structure are unknown, the distance between two departments is often measured with respect to their centroid locations. The main shortcomings of CTC distance include: the mathematically optimal layout may be one with departments represented as concentric rectangles; an algorithm based on CTC attempts to align the department centroids as close as possible, which may make the departments very long and narrow; and L-shaped departments may have a centroid that falls outside of the department [48]. There are some variations to CTC distance measure; e.g., distributed centroid-to-centroid distances (DCTC) and expected distances (EDIST) [10].

Contour Distance: Distance may be measured along the aisles between the input/output points of a pair of departments (e.g., see [3, 57]). The positive aspect of this measure is that the measured distance is accurate. The major drawback of this accurate measure is that during the block layout design phase one does not know the exact location of input/output points and the aisles, which are to specified during the detailed layout design.

3. Weighted Cost Function: A weighted cost function represents a trade-off between adjacency-based and distance-based objectives. Because there are advantages and disadvantages to adjacency-based and distance-based objectives and the optimal solution under one objective may not be optimal, or even good, under the other objective, some researchers [58, 18] have combined these two objectives in a weighted criteria approach. One kind of weighted model is given as follows:

$$\min \alpha \sum_i \sum_j (f_{ij} c_{ij}) d_{ij} - (1-\alpha) \sum_i \sum_j (r_{ij}) x_{ij}, \tag{1.3}$$

where α is a weight with a value between 0 and 1. Such an objective leads to research in the area of the multiple objective facility layout problem [19, 67, 33, 63]. One of the drawbacks of (1.3) is that adjacency-based and distance-based objectives have different scales (mostly since $d_{ij} \gg x_{ij}$). Thus, it is difficult to relate the value of the weighing factor α to some physical aspect of the problem. For example, even $\alpha = 0.5$ does not mean that the adjacency-based and distance-based objectives are weighted equally because they are in different scales. Meller and Gau [47] present a revised objective function to solve this difficulty, which is given as follows:

$$\min \sum_i \sum_j (f_{ij} c_{ij}) d_{ij} + \sum_i \sum_j (w_{ij} r_{ij})(1 - x_{ij}), \tag{1.4}$$

where the parameter w_{ij} replaces the weighting factor α in (1.3). In order to minimize the impact of setting the weighting factor w_{ij} correctly, a robust layout method is also presented in [47].

1.3.2 Facility Layout Problem Representation

The representation of an FLP solution forms the basis for a mathematical model and greatly impacts the structure and efficiency of the applied optimization algorithms. There are a variety of FLP representation methods, but most of them fall into two main categories: discrete representation and continuous representation.

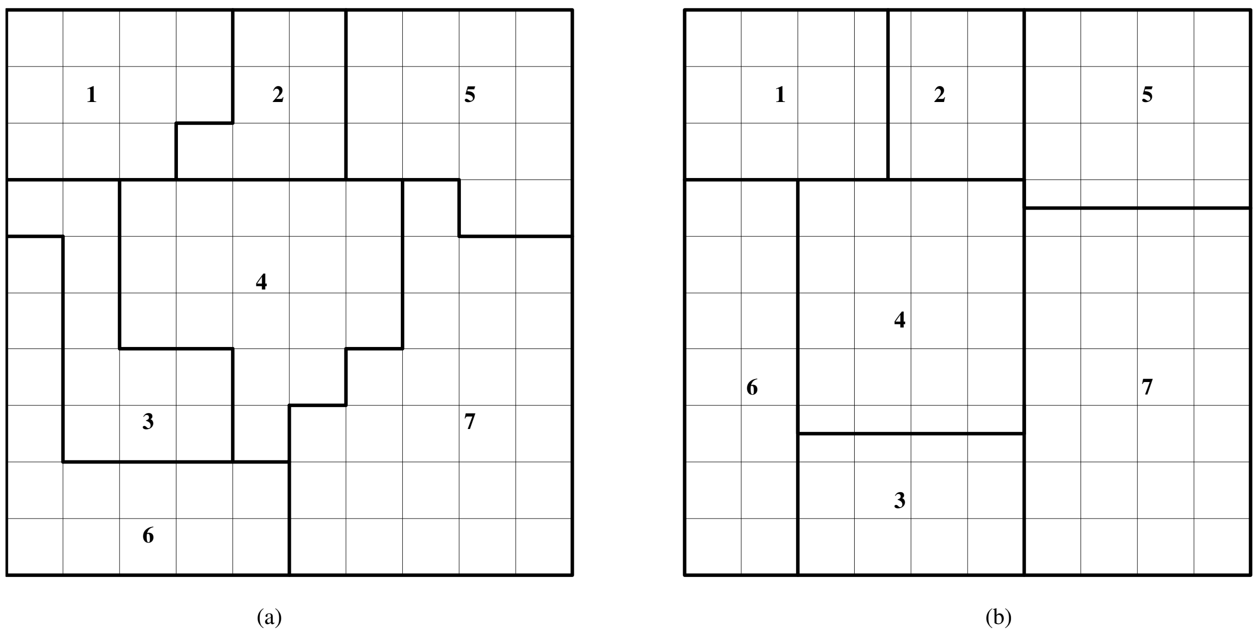


Figure 1.2: Layout Solutions with (a) Discrete Representation and (b) Continuous Representation.

Discrete Representation: With a discrete representation, the facility is represented by an underlying grid structure with fixed dimensions and all departments are composed of an integer number of grids (see Figure 1.2(a)). By representing the FLP in a discrete fashion, the FLP is simplified, but at the penalty of eliminating many solutions from consideration. Of course, the grid size can be chosen sufficiently small such that this penalty is minimized. However, a smaller grid size (i.e., increasing the resolution) will increase the computational effort as well. Most research on the FLP utilizes a discrete representation.

Continuous Representation: In a continuous representation, department dimensions are not restricted to an underlying grid structure, but rather, represented continuously (i.e., department dimensions may take on non-integer values). For example, the discrete layout in Figure 1.2(a) could be modeled with a continuous representation as shown in Figure 1.2(b). A continuous representation is more accurate and realistic than a discrete representation, and thus, is capable of finding the "real optimal" final layout solution. However, the continuous representation also increases the complexity of the FLP. As a result, most algorithms based on a continuous representation assume that departments are rectangular in shape. Thus, the "real optimal" layout is restricted as well with most algorithms that utilize a continuous representation.

A mixed-integer programming (MIP) formulation based on a continuous representation was presented by Montreuil [51]. This model uses a distance-based objective with a continuous representation of a layout and considers departments with unequal areas. Both locations and dimensions of departments are decision variables. A number of binary integer variables are used to avoid department overlapping.

1.4 Research Objectives

We state the objectives of our research in this section.

Our primary research objective is to develop the most elegant and powerful facility layout methodology. We represent solutions with a continuous representation and utilize the elegant and powerful modeling framework provided by the MIP for the FLP. The resulting model and heuristic algorithm consider every all-rectangular-department solution. As we show further later, the uniqueness of our methodology will be based on the sequence-pair representation from VLSI design, which fits naturally with the MIP-FLP model. Thus, we will create a methodology to find the "optimal" sequence-pair.

Our secondary research objective is to extend the above approach to consider the continuous-representation-based FLP with fixed departments, where additional considerations should be given with respect to the locations and dimensions of the fixed departments.

Our third research objective is to extend the above approach to explicitly consider the continuous-representation-based FLP with an existing aisle network structure. Since there are many constraints with respect to the main-aisle network, there is the need for a methodology to incorporate it into the facility layout problem explicitly.

Our final research objective is to extend the above approach to consider the continuous-representation-based FLP with non-rectangular-shaped departments. This research objective has only been considered in a very limited sense in past research. However, given that department shapes like L-shaped and U-shaped manufacturing and assembly cells are quite common in industry, this extension would greatly impact the applicability of the above approach.

1.5 Organization of the Dissertation

The remainder of this dissertation is organized as follows. In Chapter 2 we review the literature relevant to the research contained in this dissertation. It starts with a literature review on the FLP, which classifies the research on the FLP into two categories: exact algorithms and heuristics. In each category, some well-known research approaches are reviewed with emphasis on their layout representation and their advantages and disadvantages. Literature on the sequence-pair representation, taken from VLSI design, is then reviewed in Chapter 2 as a precursor to consideration in the facility layout design.

The problem statement for our research is presented in Chapter 3. First, we give the detailed mathematical description of Montreuil's MIP-FLP model. The limitation of solving this model is also discussed. We then describe the sequence-pair representation and the translation between the sequence-pair representation and the MIP-FLP model. We also summarize the properties of the sequence-pair representation with respect to the MIP-FLP. Based on these properties, we present our methodology for combining the sequence-pair representation and the MIP-FLP. In this chapter we also provide a discussion on the benefits of combining the sequence-pair representation with the MIP-FLP model.

In Chapter 4 we present our heuristic approach for combining the sequence-pair representation and the MIP-FLP to solve the continuous-representation-based FLP. Different design issues are discussed in detailed and numerical experiments are used to illustrate the effectiveness and efficiency of our heuristic.

In Chapter 5 we extend our heuristic approach for combining the sequence-pair representation and the MIP-FLP to further consider the FLP with fixed departments. Based on an analysis of the impact of the locations and dimensions of the fixed departments on the sequence-pair representation, we present our specially designed operator for the FLP with fixed departments. Numerical experiments are provided to illustrate the effectiveness of the combination of our heuristic and the specially designed operator to solve the FLP with fixed departments.

In Chapter 6 we further extend the MIP-FLP model and our heuristic approach for combining the sequence-pair representation to consider the FLP with an existing aisle structure. We first present our MIP model for the FLP with an existing aisle structure and run numerical experiments to test the performance of our proposed MIP model. Based on the sequence-pair representation and this MIP model for the FLP with an aisle structure, we then present our specially designed heuristic to solve the FLP with an aisle structure and illustrate the effectiveness of the proposed heuristic by numerical experiments.

In Chapter 7 we focus our research on the FLP with non-rectangular-shaped departments, which is rarely studied in the FLP research domain. We first present an MIP model for this type of FLP followed by an analysis on the performance of the MIP model. We then extend our heuristic approach on combining the sequence-pair representation and the proposed MIP model to solve the FLP with non-rectangular departments. Numerical experiments are provided to illustrate the effectiveness of our proposed heuristic.

In Chapter 8 we summarize our research contributions in this dissertation and provide our perspectives on the future research in the research domain of applying the sequence-pair representation to the facility layout problem.

Chapter 2

Literature Review

Since an efficient facility layout is critical for high productivity and quality manufacturing, a lot of research has been performed — and is still being performed — in this area. However, the extremely complicated nature underlying the FLP, various application and implementation issues, as well as the continuously increasing requirements from industry, lead us to the conclusion that the research in the FLP is still far from being "well done." As a result, research related to the FLP continues to be one of the academic focus areas in industrial engineering and operations research. Developing some cutting-edge algorithms for the FLP is not only important to academia, but also to industry.

In the FLP research literature, a variety of approaches are proposed to solve this combinatorial optimization problem. These approaches are different in terms of layout representation, objective functions, constraints, algorithm search strategies, etc. One of the most widely used classification methods for these approaches is to divide them into two categories: exact algorithms and heuristics. Another important classification is based on layout representation: discrete or continuous. In this chapter we give a detailed literature review of FLP research based on this two-level classification. First, we classify the literature into exact algorithms and heuristics. Second, in each of these two categories, the literature is further classified and reviewed with respect to their layout representation.

2.1 Exact Algorithms

Exact algorithms in FLP research represent those algorithms developed to obtain, in theory, an optimal solution to the facility layout problem with respect to their formulation framework.

2.1.1 Exact Algorithms with Discrete Representation

The QAP was the first exact approach in FLP research. The QAP was first proposed by Koopmans and Beckman in 1957 [35], which was introduced to model interacting plants of equal areas. A typical QAP model is given as follows:

$$\min \quad \sum_{i=1}^{n}\sum_{j=1}^{n}\sum_{k=1}^{n}\sum_{l=1}^{n} c_{ijkl}x_{ik}x_{jl} \tag{2.1}$$

$$\text{s.t.} \quad \sum_{i=1}^{n} x_{ik} = 1, \quad k = 1, \dots, n \tag{2.2}$$

$$\sum_{j=1}^{n} x_{jl} = 1, \quad l = 1, \dots, n \tag{2.3}$$

$$x_{ik} = \begin{cases} 1 & \text{if department } x \text{ is assigned to location } k, \\ 0 & \text{otherwise} \end{cases} \quad i, k = 1, \dots, n \tag{2.4}$$

where c_{ijkl} is the cost incurred by assigning department i in location k and department j in location l. The binary decision variable, x_{ik}, is equal to 1 if department i is assigned to location k and 0 otherwise.

As we discussed in Chapter 1, the QAP assumptions include equal-area departments and fixed and known locations to place the departments. Utilizing a discrete representation, the QAP formulation takes fixed locations as "giant grids" and assigns every department to exactly one grid (see (2.2) and (2.3)). The cost of such a one-to-one assignment between departments and grid locations depends on the location of the interacting departments (see (2.1)). An alternative formulation of the QAP considers assigning interdepartmental distances to department pairs [59]. The QAP has been proven to be NP-complete [22]. Optimal solutions for the QAP model in general cases can only be found for problems with less than 18 departments [32].

Some modified QAP models [36, 41] were presented to solve the unequal-area FLP by breaking departments into small grids with equal area, assigning large artificial flows between those grids of the same department to ensure that the departments are not split, and solving the resulting QAP. Such approaches actually increase the discrete representation resolution (i.e., smaller grids underlying the facility), allowing each department to be assigned to more than one grid. However, due to the increase in the number of "departments," it is not possible to solve even small-sized problems with a few unequal-area departments. Moreover, it is shown in [10] that such an approach is not effective because it implicitly adds a department shape constraint. Such a constraint limits the solution space in a manner that cannot be known beforehand.

Some researchers have used QAP in a modified form to solve a specific facility layout problem. For example, Bozer and Rim [12] developed a QAP model to address the bidirectional circular layout problem (Bi-CLP), where the departments are arranged along a simple closed-loop aisle and the flow between departments can occur either in the clockwise or counterclockwise direction based on whichever is shorter along the aisle.

Another discrete representation based exact algorithm is the MIP-FLP model represented by Michael *et al.* [23] to solve the process plant layout problem in the chemical industry. This model is different from the QAP in the following ways: (1) considering the equipment size and orientation; (2) considering both the two-dimension and the three-dimension layout solutions; and (3) developing a multi-objective function that includes not only material handling cost, but also land, piping and floor construction costs. However, this model still suffers from the discrete representation weaknesses discussed in Section 1.3.2.

2.1.2 Exact Algorithms with Continuous Representation

Graph Theoretic Approaches

Graph theoretic approaches assume that the closeness ratings between departments are known *a priori*. Each department is represented as a node and adjacency relationships between departments are represented by an arc connecting the two adjacent nodes (departments) in the adjacency graph [48]. There are no underlying grids in such a representation, so usually graph theoretic approaches are considered as continuous representation based approaches.

The optimization objective used in graph theoretic approaches is the closeness rating function in (1.1). This objective function is first translated to obtain a maximal weighted planar graph (MWPG)[1]. Secondly, the MWPG is transformed into a dual graph. Finally, a block layout is generated through the dual graph. Giffin [24] showed that MWPG is a NP-complete problem. Like the QAP approach, even small-sized problems cannot be solved to optimality. As a result, many construction heuristics based on graph theoretic models are developed. Some of them are reviewed in the following section. A thorough review of such heuristics can be found in [26].

Mixed Integer Programming Approaches

A MIP formulation for the FLP was originally presented in 1990 by Montreuil [51]. This model uses a distance-based objective, but is not based on the traditional QAP framework. Instead, it utilizes a continuous representation of a layout and considers departments with unequal areas. In this model, the locations of, and dimensions of, departments are decision variables. A number of binary integer variables are used to avoid overlapping departments.

[1] A graph is planar if it can be drawn in the plane and each arc intersects no other arcs and passes through no other nodes. A planar subgraph of an adjacency graph is called a maximal planar graph if no arcs can be added without destroying the planarity of the graph.

This model is commonly referred to as FLP0.

One of the problems in FLP0 is that in lieu of the exact nonlinear (specifically nonconvex and hyperbolic) area constraint, a *bounded perimeter constraint* is used to linearize the model. However, using a bounded perimeter constraint instead of an exact area constraint can lead to errors in the final area of each department. For the maximum aspect ratio[2] of departments equal to 2, 3, 4, and 5, the boundary perimeter constraint used in FLP0 is satisfied even if the final area of a department is less than its actual required department by 11%, 25%, 36% and 44%, respectively.

A modified MIP-FLP model based on FLP0 was presented in 1999 by Meller, Narayanan and Vance [45] to improve the model accuracy and approach efficiency. This model is commonly referred to as FLP1. The bounded perimeter constraint in FLP1 is modified, which results in final department areas that are no less than their actual area requirements by 2.5%, 2.5%, 6.3% and 14.3% for an aspect ratio equal to 2, 3, 4, and 5, respectively. More importantly, this modified MIP-FLP model also adds some valid inequalities in order to eliminate some infeasible solutions from the solution space and to improve the algorithm's efficiency. Numerical results from that literature show that FLP1 is more accurate and effective than FLP0 in terms of solution quality and computational efforts.

This MIP-based model has advantages over the QAP and graphic theoretic approaches, especially in terms of department shapes and problem representation. However, because of the added complications of unequal areas, varying department horizontal and vertical dimensions, and overlapping prohibition constraints, it is extremely difficult to solve such MIP-based models to optimality. The literature shows that for FLP0 it can only solve very small sized problems ($n \approx 5$). For FLP1, even though the authors introduced a number of valid inequalities to the model, the increased problem size that can be solved ($n \approx 7$) is still far from the size of common industry practical problems (30–40 departments).

[2]The aspect ratio of a department is the ratio of its longest side length over its shortest side length.

In order to further improve the performance of the MIP-FLP model and algorithm, a series of enhancements were presented in 2003 by Sherali, Fraticelli and Meller [61]. Those new enhancements are based on FLP1, including a novel polyhedral outer approximation scheme for the nonlinear area constraints, symmetry-avoiding valid inequalities, several surrogate constraints and inequalities to prevent the department overlapping, and a well-designed branching variable selection priority scheme. The computation results from [61] show that the efforts and accuracy of final solutions are increased ($n \approx 9$) and some difficult test cases are solved for the first time in the literature. However, the problem size is still limited and not applicable for most industrial applications.

One of the major difficulties that arises in solving the MIP-FLP is from the disjunctive constraints and the large quantity of binary integer variables that prevent departmental overlap. Hence, many researchers [6, 50, 37, 39, 38] have attempted to solve such MIP-FLP models by heuristically fixing a subset of those binary integer variables and then solving the resulting simplified model. Some of the literature in studying the heuristics for the MIP-FLP model is reviewed in the Section 2.2.2.

2.2 Heuristic Approaches

Because of the computational difficulty in solving the QAP, graph theory models, or the MIP-FLP to optimality, a great deal of research has centered on finding "good" solutions by implementing heuristic approaches. There are two types of heuristics: construction heuristics and improvement heuristics. Construction-type heuristics build a single solution from scratch (typically in an open space) by successively selecting and locating a new department until the layout is completed. Alternatively, improvement-type heuristics require an initial layout as input, and the algorithm improves the initial layout by making use of some improvement mechanism, such as pair-wise or multi-pair-wise exchanges, until no further improvements can be found. Many improvement routines have been applied (e.g., steepest-descent, simulated annealing, genetic algorithms, etc.) to improvement-type heuristics.

In addition to the above classification on the basis of search mechanism, we also classify and review the heuristic literature according to the layout solution representation (discrete or continuous). We do so because the focus of this chapter is the layout representation used in previous research instead of search strategy.

2.2.1 Heuristics with Discrete Representation

Montreuil, Ratliff, and Goetschalckx [52] presented an interactive construction-type heuristic, MATCH, which utilizes a discrete representation and integer programming to solve a b-matching model. A b-matching problem is to find a maximum weighted matching in a edge-weighted graph that each edge has its lower and upper bounds to restrict the number of times the edge can be used and each vertex has a integer parameter to specify the number of the vertex must be matched with all other vertexes. Their approach tries to find a matching that maximizes the adjacency score while satisfying the constraints for number of matches in the adjacency graph.

SHAPE [27] is a construction-type heuristic based on a discrete representation and distance-based objective. The department entry sequence is determined by each department's flows and a user-defined critical flow value. The first department is placed at the center of the layout. Subsequent departments are placed based on the objective function value increase if placed on each of the four sides of current layout.

CRAFT [4] is one of the first improvement-type heuristics. CRAFT searches for the improvements by implementing two-way or three-way exchanges of the centroids of non-fixed departments. Due to the primitive exchange routine, only departments that are either of the same size or adjacent in the current layout may be exchanged.

The spacefilling curve representation is another example of a discrete representation. A spacefilling curve is a curve visiting the underlying grids contiguously to avoid the presence of split departments. MULTIPLE [11] and SABLE [43] are two algorithms based on the spacefilling curve representation. MULTIPLE utilizes a two-way exchange to improve the initial layout. SABLE applies a simulated annealing (SA) algorithm to search for “good” layout solutions. Both algorithms are capable of solving single-floor and multiple-floor layout problems.

Some researchers combine meta-heuristics with CRAFT to provide randomness mechanism to allow CRAFT to explore additional two-way local optimal solutions. One of the newest research results is presented by DePuy, Usher and Miles [16], named Meta-RaPS CRAFT, which is based on a discrete representation and a distance-based objective. Meta-RaPS is a strategy used to change the priority rules based on the insertion of a random element. In Meta-RaPS CRAFT, the decision of department exchange is based on the priority rule, which is determined by Meta-RaPS under a random mechanism.

2.2.2 Heuristics with Continuous Representation

The deltahedron approach (DA) [20] is one of the most widely cited construction-type heuristics. As a graph-based approach, DA uses the adjacency-based objective and generates a layout by determining the entry sequence of nodes (departments) into the graph. At each stage, a node (department) enters the graph to maximize the adjacency benefits with the other nodes (departments) in the graph. A great deal of research has been conducted to improve DA’s performance [2, 9, 40]. Another construction-type heuristic based on graph theoretic approaches and the adjacency-based objective is SPIRAL [25], which utilizes the concept of “relationship tuples” to construct an adjacency graph.

LOGIC [64] is an improvement-type heuristic based on a collection of rectangular partitions called a *slicing tree*. Based on the slicing tree structure, the given facility is recursively partitioned. LOGIC can consider fixed and non-fixed departments.

NLT [68] is an approach based on nonlinear programming and the distance-based objective. NLT utilizes a continuous representation and solves the constrained nonlinear programming model by transforming the model into an unconstrained form by an exterior point quadratic penalty function method. The resulting department shapes are all rectangular.

Some heuristics have been developed to improve the performance of Montreuil's MIP-FLP model. Banerjee *et al.* [6] and Montreuil, Venkatadri and Ratliff [50] applied qualitative layout anomalies (QLAs) and design skeletons to Montreuil's MIP-FLP model. The heuristics utilize context-based information to reduce the solution tree. Lacksonen [37] proposed an approach that combines the QAP model with Montreuil's MIP-FLP model. First, a QAP model is solved by applying a cutting plane heuristic. The result of the QAP is used as an input of approximate location information of departments, which is used to reduce the number of binary variables in the MIP model.

Langevin, Montreuil and Riopel [39] proposed a heuristic approach based on Montreuil's MIP-FLP model to solve the spine layout problem, where a main aisle is used for material handling and all departments are located along the both sides of the aisle. This approach first generates an ordered list of departments based on a heuristic proposed by Heragu and Kusiak [28] to solve a single row layout problem. Then, it applies the ordered list to the Montreuil's MIP-FLP model to fix the binary variables and transforms Montreuil's model from an MIP model to a linear programming model. The maximum size of test problems presented in [39] is 22 departments. This approach uses a heuristically-fixed ordered list as initial input and cannot consider all the possible solutions. It is also specifically designed for the spine layout problem. As such, it is not suitable for the general FLP.

Lacksonen [38] proposed a pre-processing heuristic to fix a subset of the total binary variables according to a regression formula based on the area of each department and material flows associated with each department. The maximum size of test problems in [38] is 12 departments.

Montreuil *et al.* [53] presented an AntZone meta-heuristic based on a continuous representation, where an ant colony approach is used to generate the layout code, and given a layout code, a zone-based linear programming model is solved to optimize the zone-based layout solution.

Another type of continuous-representation-based heuristic design is focused on studying the FLP with fixed-shaped departments and fixed input/output locations, where the locations of the departments are represented continuously. One of the most recent research is presented by Kim and Kim [34], where an MIP model is formulated and a construction-improvement heuristic is presented based on the MIP model to minimize the distance-based objective function for the FLP with pre-specified-shaped departments and fixed input/output locations. However, the department shapes are restricted to rectangular-shaped only.

Irohara and Yamada [29] present a location matrix based heuristic to solve the FLP with aisle structure where there are three alternatives for the input/output locations. One main limitation for this research is that the approach assigns departments within a zone in a sequential-order along either the horizontal direction or vertical direction. Therefore, it cannot consider all-possible layout solutions.

2.3 Sequence-Pair Representation

A great deal of research has been conducted in the VLSI layout design domain, which is similar to the FLP. In VLSI layout design problems, there are three kinds of modules: modules with specified placement ("pre-placed" modules), modules with specified dimensions, but no specified placement ("hard" modules), and modules with specified area, but no specified dimensions ("soft" modules). Correspondingly, in the FLP, each department is either a "pre-placed" department (department with fixed dimensions and location), a "hard" department (department with fixed dimensions; e.g., assembly lines) or a "soft" department (department with non-fixed dimensions and location). Therefore, although the objective function of a VLSI problem (usually to minimize the size of the chip that includes all of the modules) is different than a facility layout problem, the problem structure and physical representation are very similar.

Sequence-pair representation based algorithms are one of the most recent research approaches in the VLSI layout design area [54, 56, 55, 60]. A sequence-pair is a pair of module sequences that is used for a layout solution. A layout solution in a sequence-pair based layout problem is a set of the positioning relationship information of every module to that of every other module. Some of the research literature in applying the sequence-pair representation to solve VLSI layout design problems is reviewed next and the details about the sequence-pair representation are discussed in Chapter 3.

The sequence-pair representation was first presented to solve the rectangle packing problem (RP)[3] by Murata *et al.* [54]. The objective function in RP problem is typically to minimize the total bounding area. Murata *et al.* [54] showed in their paper that for every sequence-pair, there is a set of corresponding layout solutions and for every layout solution there is a single corresponding sequence-pair. In that paper, they assumed all of the modules are of fixed and known dimensions (known as "hard modules") and developed a simulated annealing algorithm to search for the sequence-pair that can generate the layout with the minimum bounding area. Given the sequence-pair, a longest path algorithm was used to find the "optimal" layout under the given sequence-pair.

Murata, Fujiyoshi and Kaneko [56] extended their previous model to include pre-placed modules (both the location and the dimensions of the modules are fixed and known *a priori*). When there is a pre-placed module, the input sequence-pair may be infeasible. To address these difficulties, they proposed a procedure called "adaptation" that changes an inconsistent sequence pair to a consistent one with the utmost consideration for minimizing the impact of the modification on the objective function. By a simulated annealing search that includes the "adaptation" procedure, the output of their algorithm is guaranteed to be a feasible sequence pair (i.e., a sequence that is consistent with any pre-placed module constraints).

[3] Rectangle packing (RP) problem: Let Ω be a set of m rectangular modules whose height and width are given in real numbers (orientation is fixed). A packing of Ω is a non-overlapping placement of the modules. The minimum bounding rectangle of a packing is called the chip. The RP problem is to find a packing of Ω in a chip with the minimum area.

Murata and Kuh [55] further extended the above research on sequence-pair based methods by including hard modules, pre-placed modules and soft modules (both dimensions and locations are flexible). They presented a two-phase approach to find a good packing under a given sequence-pair.

Some research has been conducted to consider the non-rectangular-shaped modules in a sequence-pair representation. Fujiyoshi and Murata [21] presented a method to represent the packing of a set of rectilinear blocks, including arbitrarily-concave rectilinear blocks. Since some sequence-pairs of rectanglar blocks with such constraints may not be feasible (i.e., there is no corresponding packing), necessary and sufficient conditions of feasible sequence-pairs are also given in [21].

Kang and Dai [31] presented a partitioning-compacting method based on the sequence-pair representation to solve the VLSI layout design problem with arbitrarily-shaped rectilinear modules. The non-rectangular modules are first partitioned into rectangular sub-modules, then the sequence-pair representation is applied to those sub-modules. An "alignment" operation is then conducted on both the $x-$ and y-coordinates to compact the sub-modules into the non-rectangular original modules. They utilize a stochastic search algorithm to find the optimal sequence-pair in the solution space.

Xu, Guo and Cheng [69] presented another partitioning-compacting method that partitions the non-rectangular module into L-shaped sub-modules instead of rectangular-shaped ones. Based on the properties explored in [69] for L-shaped sub-modules, the feasibility of any sequence-pair for arbitrary rectilinear modules can be checked. They utilized a simulated annealing algorithm to search in the sequence-pair solution space. The infeasible sequence-pairs are tested and eliminated by adding a penalty item into the evaluation function in the simulated annealing algorithm.

2.4 Summary

From our review of the literature, we observe that developing a heuristic that utilizes the MIP-FLP is of considerable interest. This is due mainly to both the continuous representation and the powerful MIP framework. We also observe that there is a correspondence between the FLP and VLSI design problems, especially with respect to the sequence-pair continuous representation. In the next chapter we detail the problem statement of our research based on these two observations.

Chapter 3

Sequence-Pair Representation and the MIP-FLP Model

In this chapter we first discuss the MIP-FLP model and then introduce the basic concepts and properties of the sequence-pair representation. We then discuss our proposed methodology to combine the MIP-FLP model and the sequence-pair representation.

3.1 MIP-FLP Model

The first MIP-FLP model in the literature is due to Montreuil [51]. Referred to as FLP0 in the literature, this model is used to formulate the FLP with unequal area departments under a continuous representation. The parameters, decision variables and the general formulation of FLP0 follow.

Parameters:

s	Direction index ($s = x, y$).
L^x, L^y	Side length of the facility in the x- and y-directions.
N	The total number of departments.
i, j	Department indices ($i, j = 1, \ldots, N$).
a_i	Area requirements for department i.
α_i	Maximum aspect ratio requirement for department i, which denotes the maximum permissible ratio between its longest and shortest sides ($\alpha_i \geq 1$).
ub_i, lb_i	Upper and lower limits on the side length of department i.
P_i, p_i	Upper and lower limits on the perimeter of department i.
f_{ij}	Material flow between department i and department j ($f_{ij} > 0, \forall i < j$).

Decision Variables:

d_{ij}	Rectilinear distance between department i and j, which is expressed as the sum of the distances in the x-direction, d^x_{ij}, and the y-direction, d^y_{ij} ($d_{ij} = d^x_{ij} + d^y_{ij}$).
c^x_i, c^y_i	Location of centroid of department with respect to x- and y-coordinates.
l^x_i, l^y_i	Half of side length of department i in x- and y-directions.

z^x_{ij}, z^y_{ij}	Binary decision variables, which denote relative locations of departments with respect to x- and y-coordinates and are used to prevent the overlapping of departments. The definition of z^x_{ij} and z^y_{ij} are as follows:

$$z^x_{ij} = \begin{cases} 0 & \text{if } i \text{ must proceed } j \text{ in the } x\text{-direction,} \\ 1 & \text{otherwise} \end{cases} .$$

$$z_{ij}^{y} = \begin{cases} 0 & \text{if } i \text{ must proceed } j \text{ in the } y\text{-direction,} \\ 1 & \text{otherwise} \end{cases} .$$

For example, if department i is to the southwest of department j, then $z_{ij}^{x} = 0$ and $z_{ij}^{y} = 0$.

FLP0 Formulation:

$$\min \quad \sum_{i} \sum_{j>i} f_{ij}(d_{ij}^{x} + d_{ij}^{y}) \tag{3.1}$$

$$\begin{aligned}
\text{s.t.} \quad & d_{ij}^{s} = |c_i^s - c_j^s|, && \forall i < j; \forall s && (3.2)\\
& l_i^s \leq c_i^s \leq L^s - l_i^s, && \forall i; \forall s && (3.3)\\
& lb_i \leq 2l_i^s \leq ub_i, && \forall i && (3.4)\\
& 2 \leq z_{ij}^{x} + z_{ji}^{x} + z_{ij}^{y} + z_{ji}^{y} \leq 3, && \forall i, j; i < j && (3.5)\\
& c_i^s + l_i^s \leq c_j^s - l_j^s + L^s z_{ij}^{s}, && \forall i, j; \forall s && (3.6)\\
& c_j^s + l_j^s \leq c_i^s - l_i^s + L^s z_{ji}^{s}, && \forall i, j; \forall s && (3.7)\\
& p_i \leq 4(l_i^x + l_i^y) \leq P_i, && \forall i && (3.8)\\
& z_{ij}^{s} \in [0, 1] && \forall i, j; \forall s && (3.9)
\end{aligned}$$

The objective, (3.1), is a distance-based objective function, which is equal to the product of the flow and rectilinear distance between department centroids. The absolute values in the distance function (3.2) can be linearized as $d_{ij}^{s} \geq c_i^s - c_j^s$ and $d_{ij}^{s} \geq c_j^s - c_i^s$ since $f_{ij} > 0$. In (3.3), each department is constrained to be within the facility. The side length is constrained in (3.4) by using upper and lower limits $ub_i = \min\left\{\sqrt{a_i \alpha_i}, \max_s\{L^s\}\right\}/2$ and $lb_i = a_i/4ub_i$. In (3.5)–(3.7), the relative location decision variables are utilized to ensure that departments do not overlap. In lieu of the exact nonlinear area constraint, $a_i = 4l_i^x l_i^y$, a *bounded perimeter constraint* is used in (3.8), where $p_i = 4\sqrt{a_i}$ and $P_i = 2\sqrt{a_i}(1 + \alpha_i)/\sqrt{a_i}$. The formulation of FLP0 is easily extended to model fixed departments and other linear side constraints.

FLP0, (3.1)–(3.9), considers every all-rectangular-department layout solution, but becomes difficult to solve even for instance of $n \approx 5$. Furthermore, as discussed in Section 2.1.2, the bounded perimeter constraint, (3.8), used in FLP0 is not accurate.

To improve the solvability of FLP0, a modified MIP-FLP model based on FLP0 was developed by Meller, Narayanan and Vance [45]. We refer to the MIP-FLP in [45] as FLP1. FLP1 is essentially a two-dimensional version of the well-known linear ordering model for single machine scheduling problems. Based on the acyclic subgraph structure underlying FLP1, some general classes of valid inequalities are incorporated into FLP1 to improve its LP lower bounds. These valid inequalities (named *T3*, d^{min}, *B2, V2, B3a,b, V3a,b, BV3a,b, S3a,b*), which comprise one of the two most important differences between FLP0 and FLP1, are intended to tighten the solution space of FLP0, and in turn, lead to faster computation speed. Another advantage of FLP1 is that it utilizes a more accurate surrogate area constraint as follows:

$$4(l_i^x + l_i^y) \geq 3\sqrt{a_i} + f \times 2l_i^{max}, \tag{3.10}$$

where $l_i^{max} \geq l_i^s, \forall s$ and the constant f is typically assigned as 0.95. The bounded perimeter constraint, (3.10), in FLP1 results in final department areas that are constrained to be greater than 97.5%, 97.5%, 93.7% and 85.7% of their actual area requirements for the maximum aspect ratio equal to 2, 3, 4, and 5, respectively.

Furthermore, FLP1 defines the binary variables, z_{ij}^s, in a different way than in FLP0:

$$z_{ij}^x = \begin{cases} 1 & \text{if } i \text{ must proceed } j \text{ in the } x\text{-direction,} \\ 0 & \text{otherwise} \end{cases}.$$

$$z_{ij}^y = \begin{cases} 1 & \text{if } i \text{ must proceed } j \text{ in the } y\text{-direction,} \\ 0 & \text{otherwise} \end{cases}.$$

Based on the algorithm performance provided in [45], we see that FLP1 improves the tractable problem size ($n \approx 7$).

A further enhanced MIP-FLP model based on FLP1 was presented by Sherali, Fraticelli and Meller [61], which we refer to as FLP2. The first enhancement is an improved representation of the nonlinear area constraint based on a novel polyhedral outer approximation scheme, which is given in the following:

$$a_i l_i^x + 4\bar{x}^2 l_i^y \geq 2a_i\bar{x}, \quad \forall lb_i^x \leq \bar{x} \leq ub_i^x, \tag{3.11}$$

$$\bar{x} = lb_i^x + \frac{\lambda}{\Delta - 1}(ub_i^x - lb_i^x), \forall\lambda = 0, 1, \ldots, \Delta - 1, \text{for any selected integer } \Delta \geq 2. \tag{3.12}$$

The new surrogate constraint, (3.11–3.12), provides as tight a representation as desired — unlike the approximation used in FLP0 and FLP1 — by using a large enough number of discretization points, Δ, for the tangential supports. From the comparison of computation results between FLP1 and FLP2 in [61], the FLP1 model produced an average maximum error of 6.74% while FLP2 reduced this average maximum error to 0.42%, 0.20%, and 0.03% when using $\Delta = 10$, 20, and 50 supports, respectively.

Another important enhancement in FLP2 concerns preventing department overlapping by two alternative formulations, DJ1 and DJ2. In addition, a new class of valid inequalities, called *UB inequalities*, is revealed by exploring DJ2. DJ1 and DJ2 possess certain partial convex hull properties and provide increased tightness for the MIP-FLP model, but they also lead to a substantial increase in solution time as compared with FLP1 because of their size. Thus, three different strategies were implemented in [61] to impart the tightness from DJ1 and DJ2, while limiting the increase in problem size. These strategies include: (1) applying DJ1 to one pair of selected departments; (2) applying DJ2 to one pair of selected departments; and (3) incorporating UB equalities regardless of whether DJ2 is used or not. Strategy (1) was deemed to be the most successful.

Other enhancements in FLP2 consist of a symmetry-breaking constraint and some branching priorities for the branch-and-bound search. Combing all of these enhancements leads to greatly reduced algorithm runtime and improves the tractable problem size ($n \approx 9$). Thus, some challenging test problems from the literature were solved for the first time by FLP2.

In our following discussion, we use the definition of binary decision variables, z_{ij}^s, first presented in FLP1, since it seems more intuitively appealing.

3.2 Sequence-Pair Representation

In this section we discuss the sequence-pair representation in detail. The sequence-pair representation was originally presented by Murata [54] to solve the Rectangle Packing (RP) problem based on the concept of a *P-admissible* solution space. We first give the definitions of the RP problem and a P-admissible solution space.

Definition 1 (Rectangle Packing problem) [54]*: Let Ω be a set of m rectangular modules whose height and width are given in real numbers (orientation is fixed). A packing of Ω is a non-overlapping placement of the modules. The minimum bounding rectangle of a packing is called a chip. The RP problem is to find a packing of Ω in a chip with the minimum area.*

It is known that the RP problem is NP-hard [54]. Therefore, several heuristics are presented in the literature to solve the RP problem, one of which is called "combinatorial search" [60]. Combinatorial search represents a solution space for a given RP problem as a set of "codes." Each code represents a packing or placement for the given RP problem. A code is said to be feasible if the corresponding packing is feasible; i.e., for the given RP problem there exists a feasible packing corresponding to that code. The performance measure of a code is the evaluation of the corresponding packing. The objective is to search for a feasible code that yields the best packing. For the search to be effective, then the following are the minimum requirements of the solution space [54]:

1. The solution space is finite;
2. Every solution is feasible;
3. Evaluation for each code is possible in polynomial time, and so is the translation from the code to its corresponding packing;
4. The packing corresponding to the best-evaluated code in the space relates to an optimal solution to RP.

A solution space that satisfies the above four requirements is called P-admissible.

It is shown in [54] that the sequence-pair solution space is a P-admissible solution space, in which each code is a pair of module sequences.

3.2.1 Encoding a Layout to a Sequence-Pair

In this section we describe the two-step procedure presented in [54] to encode a given layout to a sequence-pair. Throughout this section we use the layout in Figure 3.1 as an example.

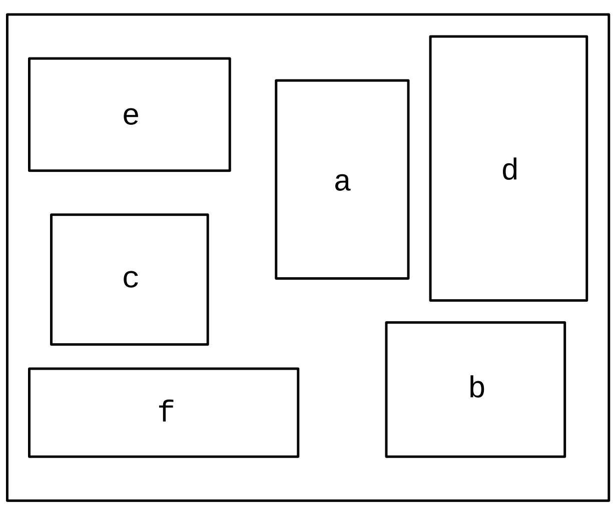


Figure 3.1: A Six-Department Block Layout.

Step 1: Draw the positive step-line.

For each department i, a line is drawn from its center to the department's right edge. The line's direction is then turned up, right, up, right, whenever it encounters one of three types of objects: (i) the boundary of a department, (ii) the boundary of the facility, or (iii) a previously drawn line. The line stops when it reaches the upper right corner of the facility. The drawn line is called the *right-up step-line* of the department i. Similarly, a *left-down step-line* is drawn. The union of these two step-lines is called the *positive step-line* of department i, since it tends to go inside the first and third quadrants. Given the department order to draw the positive step-line, one positive step-line is uniquely defined for each department. These lines are referred to by the corresponding department names. For example, Figure 3.2 is obtained if we draw positive step-lines for each department in the order of a, b, c, d, e, f.

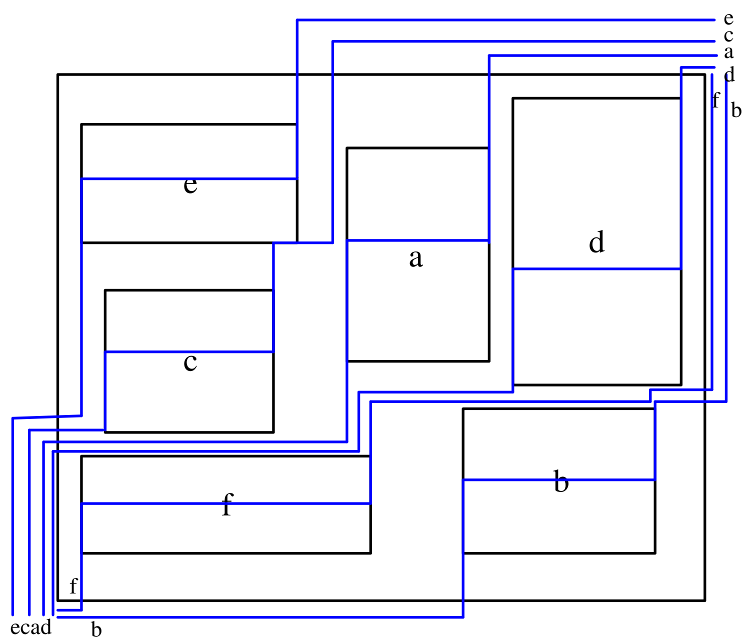


Figure 3.2: The Positive Step-Line for the Given Layout.

From construction, no two positive step-lines cross each other. This implies that the departments are linearly ordered. Here we order the positive step-lines from the upper left. Let Γ_+ be the department name sequence in the order. From the above figure, the step-line $\Gamma_+ = ecadfb$ is obtained.

Step 2: Draw the negative step-line.

Negative step-lines are drawn similarly to the positive step-lines. The main difference is that the negative step-line is the union of the *up-left step-line* and the *down-right step-line*, whose direction changing policies are "up, left, up, left," and "down, right, down, right," respectively. The negative step-lines are ordered from lower left. Let Γ_- be the department name sequence in the order. From Figure 3.3, the step-line $\Gamma_- = fcbead$ is obtained.

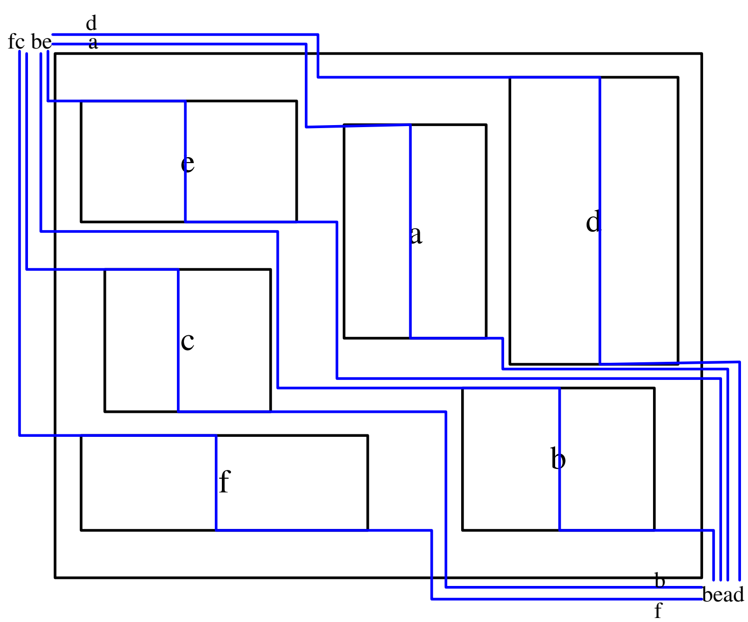


Figure 3.3: The Negative Step-Line for the Given Layout.

The ordered pair (Γ_+, Γ_-) is called the sequence-pair for a layout. For this example, $(\Gamma_+, \Gamma_-) = (ecadfb, fcbead)$ is the resultant sequence-pair for this layout.

Thus, by implementing the procedures described above, we can find a corresponding sequence-pair for any feasible layout.

3.2.2 Properties of the Sequence-Pair Representation

We discuss some important properties of the sequence-pair representation in this section. The detailed proofs for the following theorems can be found in [54].

1. **Horizonal/Vertical Relationship Property**

   Given a sequence-pair, (Γ_+, Γ_-), for a department x, any other department x' is uniquely constrained in one of four classes, which are defined in [54] as follows:

$$M^{aa}(x) = \{x' | x' \text{ is after } x \text{ in both } \Gamma_+ \text{ and } \Gamma_-\}, \tag{3.13}$$

$$M^{bb}(x) = \{x' | x' \text{ is before } x \text{ in both } \Gamma_+ \text{ and } \Gamma_-\}, \tag{3.14}$$

$$M^{ba}(x) = \{x' | x' \text{ is before } x \text{ in } \Gamma_+ \text{ and after } x \text{ in } \Gamma_-\}, \tag{3.15}$$

$$M^{ab}(x) = \{x' | x' \text{ is after } x \text{ in } \Gamma_+ \text{ and before } x \text{ in } \Gamma_-\}. \tag{3.16}$$

   Theorem 1 *Given a sequence-pair, (Γ_+, Γ_-), and x and x' as two different departments in (Γ_+, Γ_-), then x and x' satisfy the following horizontal/vertical relationship in a facility layout* [54]*:*
   If $x' \in M_{aa}(x)$, then department x' is to the right of department x.
   If $x' \in M_{bb}(x)$, then department x' is to the left of department x.
   If $x' \in M_{ba}(x)$, then department x' is above department x.
   If $x' \in M_{ab}(x)$, then department x' is below department x.

   Based on Theorem 1, each layout represented by a sequence-pair is guaranteed to be feasible with respect to the overlap constraints (obviously if there are other constraints a particular layout may be infeasible). This also means there is no sequence-pair that corresponds to an infeasible layout with respect to the overlap constraints. Thus, such an infeasible layout is automatically excluded from sequence-pair solution space.

2. **Dual Property**

   Theorem 2 *Given a sequence-pair,* (Γ_+, Γ_-)*, and* x *and* x' *as two different departments in* (Γ_+, Γ_-)*, then departments* x *and* x' *are in a dual relationship as shown in* [54] *through* $x \longleftrightarrow x'$*, and* $a \longleftrightarrow b$ *as follows:*
   $x' \in M_{aa}(x) \Longleftrightarrow x \in M_{bb}(x')$,
   $x' \in M_{ba}(x) \Longleftrightarrow x \in M_{ab}(x')$.

3.3 Combination of the Sequence-Pair Representation and the MIP-FLP Model

3.3.1 Sequence-Pair Representation with Respect to the MIP-FLP Model

Before we consider how to combine the sequence-pair representation and the MIP-FLP model, we first provide two theorems regarding the properties of the sequence-pair representation with respect to the MIP-FLP model.

Theorem 3 (Binary Variable Specifying Theorem) *Given a sequence-pair,* (Γ_+, Γ_-)*, and departments* i *and* j *as two different departments in* (Γ_+, Γ_-)*, then the corresponding binary variables in FLP1 are specified as follows:*

$i \in M_{aa}(j) \Longrightarrow z^x_{ij} = 0, z^x_{ji} = 1.$

$i \in M_{bb}(j) \Longrightarrow z^x_{ij} = 1, z^x_{ji} = 0.$

$i \in M_{ba}(j) \Longrightarrow z^y_{ij} = 0, z^y_{ji} = 1.$

$i \in M_{ab}(j) \Longrightarrow z^y_{ij} = 1, z^y_{ji} = 0.$

Considering the sequence-pair representation in the MIP-FLP framework, we provide the following definitions with respect to sequence-pair feasibility. Recall that the FLP is different than the RP problem since the "chip" size is typically constrained in the FLP.

Definition 2 (Sequence-Pair Feasibility) *A sequence-pair is classified as* ***feasible*** *with respect to the MIP-FLP if setting the binary variables of the MIP-FLP as specified in Theorem 3 results in a feasible layout. Likewise, a sequence-pair is classified as* ***infeasible*** *with respect to the MIP-FLP if setting the binary variables of the MIP-FLP as specified in Theorem 3 will not result in a feasible layout.*

Definition 3 (Sequence-Pair Optimal-Layout) *A feasible sequence-pair may yield multiple feasible layouts in the MIP-FLP. For a feasible sequence-pair, the layout that achieves the best objective function value for the MIP-FLP is denoted as the* ***sequence-pair optimal-layout*** *(there is no sequence-pair optimal-layout for an infeasible sequence-pair).*

Definition 4 (Optimal Sequence-Pair) *A sequence-pair is denoted as* ***optimal*** *with respect to the MIP-FLP if the sequence-pair optimal layout for this sequence pair corresponds to the optimal facility layout of the MIP-FLP.*

Theorem 4 *An exhaustive search of the sequence-pair solution space will result in finding the optimal layout of the MIP-FLP.*

Proof: For any feasible layout solution of the MIP-FLP (including the optimal MIP-FLP layout), there must exist a corresponding feasible sequence-pair, (Γ_+, Γ_-), which can be obtained by applying the procedures presented in Section 3.2.1. For any feasible sequence-pair, there must be one or multiple corresponding feasible layout solutions of the MIP-FLP by specifying the binary variables according to Theorem 3 and solving the resulting model. Furthermore, a sequence-pair optimal layout is the best layout we can obtain from all the feasible layouts represented by that sequence-pair. Therefore, the optimal layout for the MIP-FLP must correspond to the best layout from the set of all sequence-pair optimal layout solutions. By an exhaustive search of the sequence-pair solution space, every sequence-pair optimal solution can be obtained. Thus, we can choose the best layout solution from the set of all sequence-pair optimal layout solutions, which is also the optimal layout of the MIP-FLP. In addition, the corresponding sequence-pair for that optimal layout solution is the optimal sequence-pair. ∎

3.3.2 Potential Benefits of Combining the Sequence-Pair with the MIP-FLP Model

One of the major difficulties in MIP-FLP models is that there are a large number of binary integer variables and constraints used for preventing infeasible solutions with departments overlapping. These binary variables and constraints greatly impact the performance of optimization algorithms applied to solve this problem. The reason is that the different settings of these binary variables represent both feasible and infeasible layout solutions and searching through the solution space to exclude the infeasible solutions contributes a great deal to the computational difficulty in solving such MIP-FLP models. Thus, heuristics intended to solve the MIP-FLP model efficiently can be assisted by placing emphasis on decreasing or eliminating the need for the binary variables and the associated constraints.

In this regard, the reasons why a sequence-pair representation is of potential interest are as follows:

1. The sequence-pair representation avoids department overlapping and eliminates all binary-feasible variable settings that lead to infeasible layouts. Every layout under a given sequence-pair is feasible in terms of representing a feasible relative location relationship between departments and preventing departments from overlapping. So by combining the sequence-pair representation with a MIP-FLP model, the difficulty of ensuring feasibility with respect to department overlap in the MIP solutions becomes trivial. More specifically, we show the power of the sequence-pair representation in terms of eliminating all binary-feasible variable settings that lead to infeasible layouts mathematically below.

For the MIP-FLP with n departments, there are $2n(n-1)$ binary variables, so there are $2^{2n(n-1)}$ possible binary variable settings. Among all these binary variable settings, the number of binary variable settings satisfying $\sum_s (z_{ij}^s + z_{ji}^s) = 1$ is equal to $2^{n(n-1)}$. That is, for each pair of departments, we have four different binary variables: z_{ij}^x, z_{ij}^y, z_{ji}^x, and z_{ji}^y. The number of possible combinations of randomly picking one variable from the four binary variables to make it equal to 1 is equal to $C_4^1 = 4$. By doing so, the other three binary variables are determined to be 0. So actually, for each pair of departments there are four possible binary variable settings that satisfy the constraint $\sum_s (z_{ij}^s + z_{ji}^s) = 1$. Given n departments, the number of possible combinations of a pair of departments is equal to $C_n^2 = \frac{n(n-1)}{2}$. So the total number of binary variable settings that satisfy $\sum_s (z_{ij}^s + z_{ji}^s) = 1$ is equal to $4^{\frac{n(n-1)}{2}} = 2^{n(n-1)}$.

However, the binary variable settings satisfying $\sum_s (z_{ij}^s + z_{ji}^s) = 1$ do not ensure that the binary variable settings will lead to a feasible layout. For example, a binary variable setting of $z_{ij}^x = 1$, $z_{ij}^y = z_{ji}^x = z_{ji}^y = 0$, $z_{jk}^x = 1$, $z_{jk}^y = z_{kj}^x = z_{kj}^y = 0$, $z_{ki}^x = 1$, and $z_{ki}^y = z_{ik}^x = z_{ik}^y = 0$ satisfies $\sum_s (z_{ij}^s + z_{ji}^s) = 1$, but these binary variable values are not layout feasible since this setting cannot represent a feasible relative location relationship between the three departments (i.e., this setting implies that Department i is to the left of j, j is to the left of k and k is to the left of i). Such a "cycling" conflict is just one example of feasible binary variable settings satisfying $\sum_s (z_{ij}^s + z_{ji}^s) = 1$ that lead to an infeasible layout.

On the other hand, the sequence-pair representation represents the "true" feasible binary variable settings since given any sequence-pair there is a series of corresponding feasible layouts. As an example, consider how the sequence-pair representation can filter such a "cycling" conflict since the sequence-pair representation does not allow i to be before j in both sequences (i is to the left of j), j to be before k in both sequences (j is to the left of k), and k to be before i in both sequences (k is to the left of i) simultaneously. Therefore, the number of possible combinations of the sequence-pair representation for a FLP with n departments is equal to $(n!)^2$, which represents the number of feasible binary variable settings.

Table 3.1 illustrates the percentage of MIP-FLP binary-feasible, but not layout-feasible, solutions correctly eliminated with the sequence-pair representation.

Table 3.1: The Percentage of MIP-FLP Binary-Feasible, but not Layout-Feasible, Solutions Correctly Eliminated with the Sequence-Pair Representation.

Number of Departments (n)	Number of Binary Variable Settings		% of Eliminated Binary Variable Settings
	MIP-FLP ($2^{n(n-1)}$)	SP ($(n!)^2$)	
2	4	4	0.0
3	64	36	43.8
4	4,096	576	85.9
5	1,048,576	14,400	98.6
6	1,073,741,824	518,400	99.9
7	4.398E+12	25,401,600	$\approx$ 100

2. The sequence-pair representation is capable of representing every all-rectangular-department layout solution. Searching the sequence-pair solution space is equivalent to searching the all-rectangular-department space. Every possible all-rectangular-department solution can be reached by searching the corresponding sequence-pair solution space.

3. The sequence-pair representation is a relative-position-based representation and appears to be one that will permit the integration of detailed layout issues like aisle structure. As of yet, there is no research on creating a new sequence-pair representation specifically for the FLP.

3.3.3 How to Combine the Sequence-Pair with the MIP-FLP Model

Since the optimal layout for the MIP-FLP is the sequence-pair optimal layout under the optimal sequence-pair, theoretically, the optimal layout can be obtained by searching for the optimal sequence-pair in the sequence-pair solution space and then solving the resulting model to obtain the sequence-pair optimal layout.

The sequence-pair representation can be used to generate feasible settings of the binary overlap variables in the FLP-MIP model. By doing so, the FLP-MIP model is greatly simplified. As we show in Theorem 3, half of the binary variables are set to a particular value, while the other binary variables are free to be set by the MIP without affecting the feasibility (and thus are eliminated). Clearly, this makes the model much easier to solve. A layout heuristic based on these results will take experimentation to determine how to search within the sequence-pair representation solution space; i.e., a heuristic will need to be developed to search for the "optimal" sequence-pair.

The following example illustrates how the sequence-pair representation and the MIP-FLP model are combined. The problem data used is from a data set with 9 departments [45]. A summary of the layout data is provided as follows:

1. Facility Size: $L^x = 12$, $L^y = 13$.

2. Department Data:

Department (i)	1	2	3	4	5	6	7	8	9
Area (a_i)	14.4	14.4	14.4	32.4	32.4	8.1	8.1	8.1	8.1
Maximum Aspect Ratio (α_i)	3	3	3	3	3	3	3	3	3

3. Inter-Departmental Flow Data:

From-To Flow (f_{ij})	1	2	3	4	5	6	7	8	9
1	-			5	5				1
2		-		3	3				1
3			-	2	2				1
4				-		4	4		
5					-	3			4
6						-			2
7							-		1
8								-	
9									-

Given an arbitrary sequence-pair, $(\Gamma_+, \Gamma_-) = (3\,6\,8\,5\,4\,2\,9\,7\,1,\ 4\,2\,3\,5\,6\,7\,1\,9\,8)$, we correspondingly set the binary variables of the MIP-FLP as follows:

z_{ij}^x	1	2	3	4	5	6	7	8	9	z_{ij}^y	1	2	3	4	5	6	7	8	9
1	-	0	0	0	0	0	0	0	0	1	-	0	0	0	0	0	0	1	1
2	1	-	0	0	0	0	1	0	1	2	0	-	1	0	1	1	0	1	0
3	1	0	-	0	1	1	1	1	1	3	0	0	-	0	0	0	0	0	0
4	1	1	0	-	0	0	1	0	1	4	0	0	1	-	1	1	0	1	0
5	1	0	0	0	-	0	1	0	1	5	0	0	0	0	-	1	0	1	0
6	1	0	0	0	0	-	1	1	1	6	0	0	0	0	0	-	0	0	0
7	1	0	0	0	0	0	-	0	0	7	0	0	0	0	0	0	-	1	1
8	0	0	0	0	0	0	0	-	0	8	0	0	0	0	0	0	0	-	0
9	0	0	0	0	0	0	0	0	-	9	0	0	0	0	0	0	0	1	-

Thus, the MIP-FLP model is simplified to a linear programming model. Solving the linear programming model to optimality yields the optimal layout under the given sequence-pair (i.e., the sequence-pair optimal layout), which is shown in Table 3.2 and Figure 3.4.

Table 3.2: Results of the Sequence-Pair Optimal Layout of the Example Problem Under the Given Sequence-Pair.

Department (i)		1	2	3	4	5	6	7	8	9
Centroid (c_i^s)	$s = x$	10.90	6.83	1.17	2.75	5.26	4.76	8.98	9.59	9.09
	$s = y$	3.33	2.89	8.96	2.89	8.52	12.13	2.89	12.13	8.96
Half Side Length (l_i^s)	$s = x$	1.10	1.33	1.17	2.75	2.91	2.41	0.82	2.41	0.93
	$s = y$	3.33	2.89	3.18	2.89	2.74	0.87	2.89	0.87	2.30
Side length ($2l_i^s$)	$s = x$	2.19	2.66	2.35	5.50	5.81	4.83	1.64	4.83	1.85
	$s = y$	6.66	5.78	6.37	5.78	5.49	1.74	5.78	1.74	4.60

The layout objective function value for the layout given in Figure 3.4 is 299.591. Since this layout is obtained from an arbitrary sequence-pair, we did not investigate its quality. Our research will develop an algorithm to search efficiently for the layout with the lowest objective function value.

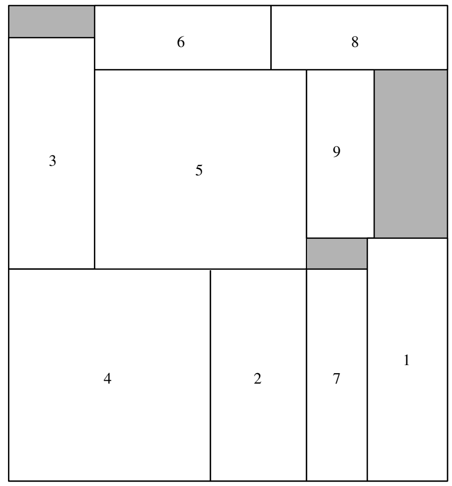


Figure 3.4: Sequence-Pair Optimal Layout of the Example Problem Under the Given Sequence-Pair.

Also note the “gaps” in the layout due to the area approximation employed in FLP1. We incorporate the area constraint approach of FLP2 in our subsequent work in this dissertation to minimize area errors.

3.4 Summary

In this chapter we outlined our problem statement and included our preliminary findings as the foundation for this dissertation research. First, we introduced the MIP-FLP model and the sequence-pair representation. We then discussed the properties of the sequence-pair representation with respect to the MIP-FLP. Based on these properties, we presented our methodology of combining the sequence-pair representation and the MIP-FLP model and discussed the potential benefits that can be obtained by implementing this methodology. In the next chapter we present our heuristic for the sequence-pair based MIP-FLP with all rectangular-shaped departments.

Chapter 4

A Heuristic for the FLP with All Rectangular-Shaped Departments

One of our primary research objectives is to design a heuristic algorithm utilizing the sequence-pair representation and the MIP-FLP model to solve the FLP with all rectangular-shaped departments. The research necessary for this objective includes: (1) the combination of the sequence-pair representation and the MIP-FLP model; and (2) the design of the search algorithm in the sequence-pair solution space. The methodology for the combination of the sequence-pair representation and the MIP-FLP model has been presented in Section 3.3.3. For the heuristic design, we propose a genetic algorithm (GA) based heuristic to search in the sequence-pair solution space for the optimal sequence-pair, where different operators are developed and applied based on the specific encoding scheme.

In this chapter we first provide a flow diagram of the overall methodology of our algorithm in Section 4.1. We then present a genetic algorithm based heuristic to solve the sequence-pair-representation-based MIP-FLP in Section 4.2, where the different GA design issues, like fitness function, selection rule, GA operator design and GA parameter settings, are discussed in detail. The effectiveness and efficiency of our heuristic is illustrated in Section 4.3 via numerical experiments on a variety of data sets from the literature and industrial applications. The comparisons in the numerical experiments are with both optimal solutions and other heuristic solutions. Finally, a summary of this chapter is provided in Section 4.4.

4.1 Overall Methodology

In Section 3.3.3 we presented how to combine the sequence-pair representation with the MIP-FLP model. We implemented this approach with a program combining a search heuristic and an MIP-FLP model. The program utilizes a GA-based heuristic to search the sequence-pair solution space and then to set the corresponding binary variable values for use in the MIP-FLP model. The MIP-FLP model is then simplified to be an LP model by utilizing those binary variable settings (every binary variable set to a value) and is solved to optimality. The optimal objective function value of the simplified MIP-FLP model corresponds to the sequence-pair optimal layout of the sequence-pair given by the search heuristic. The search heuristic continues searching in the sequence-pair solution space for the optimal sequence-pair until the stopping criteria is satisfied. A flow diagram of our heuristic is given in Figure 4.1.

4.2 SEQUENCE: A Genetic Algorithm Based Heuristic for the Sequence-Pair Based MIP-FLP

A sequence-pair is represented as a pair of ordered department sequences, where the relative positions of each department in the pair of department sequences are the critical information to determine the relative location relationship of departments in the layout. Such a permutation characteristic implies that an algorithm based on a permutation encoding scheme may be a good choice for the sequence-pair based MIP-FLP.

GA is one of the most widely utilized global optimization meta-heuristics, especially for permutation-encoding-scheme-based problems. There has been a lot of research in ap-

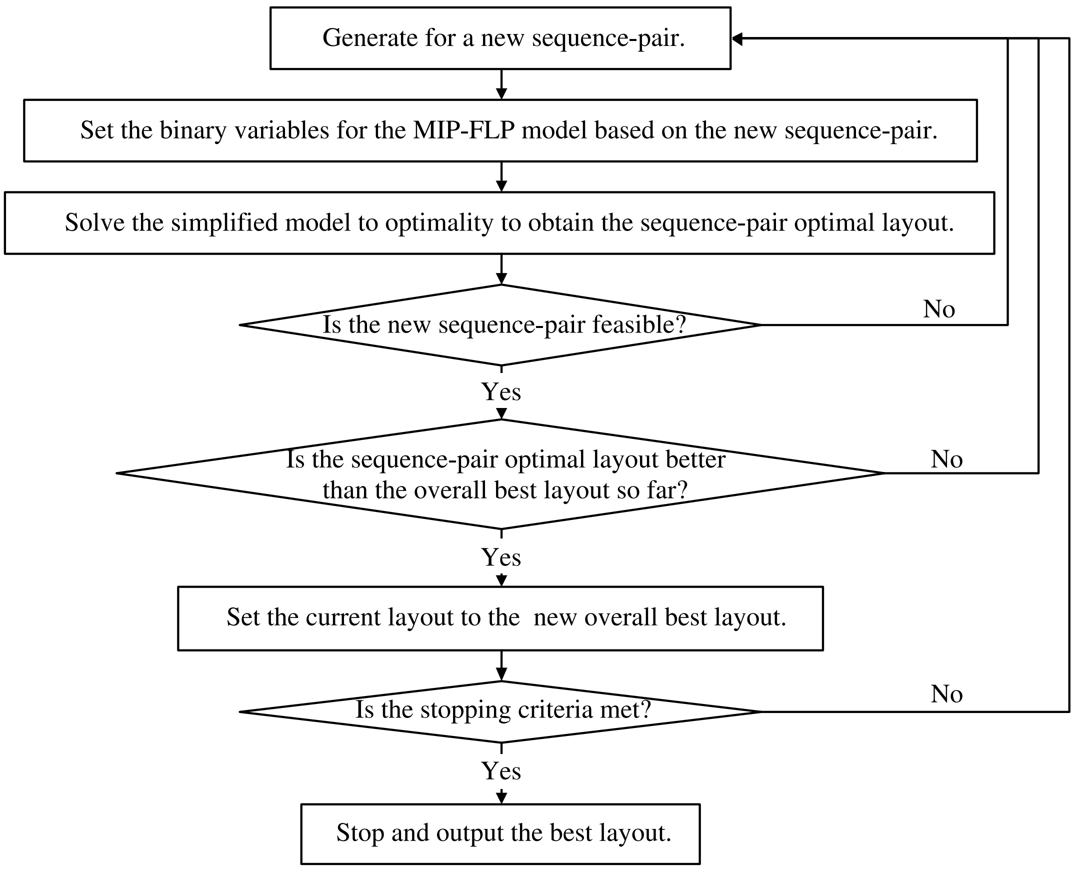


Figure 4.1: The Flow Diagram for the Sequence-Pair Based MIP-FLP Algorithm.

plying GA to solve the FLP [42]. We present a genetic algorithm based heuristic named SEQUENCE to solve the sequence-pair based MIP-FLP. Although there is no proof that GA will perform better than other meta-heuristics, such as Simulated Annealing (SA) and Tabu Search (TS), in solving the sequence-pair based MIP-FLP, there are some potential advantages we expect from utilizing a GA scheme. One main potential advantage in using a GA-based heuristic is that, unlike most other meta-heuristics that utilize random mutation as the main instrument for variation and evolution, GA utilizes a crossover operator instead. The ability of a crossover operator to recombine highly fit chromosome patterns makes us believe that GA is more powerful in keeping, recombining and further strengthening some good “combination patterns” (relative location patterns between departments in the FLP) with respect to the permutation encoding scheme. (In fact, we have tested a simulated annealing version of SEQUENCE, but found that the GA version outperforms it.)

For the design of our GA, some important issues need to be considered, such as the encoding scheme, fitness function, chromosome selection rule and genetic operator design. To encode sequence-pair solutions, it is clear that a permutation structure can be adopted. However, the simple permutation structure cannot be applied directly because a sequence-pair is not a single permutation, but a pair of interacting permutations. Therefore, a specially designed encoding scheme is required. A fitness function is a function that assigns a score (called "fitness" in GA) to each chromosome in the population. The fitness of a chromosome is determined by how well that chromosome scores on an objective function; i.e., the better the chromosome scores on an objective function, the fitter the chromosome. A chromosome selection rule is a rule to select the parent chromosomes from the current generation, and the parent chromosomes are used to generate the offspring in the new generation. The most common genetic operators include a reproduction operator, a crossover operator, and a mutation operator. These operators are applied to parent chromosomes to generate the offspring in the new generation. In the remainder of this chapter we address these issues respectively in detail.

4.2.1 Encoding Scheme Design

An encoding scheme is the basis of a GA, so we first present our encoding scheme for SEQUENCE. There are a variety of encoding schemes in GA [5]; e.g., binary strings, real-valued vectors, permutations, finite-state representations, etc. Here we consider utilizing a permutation encoding scheme because of the nature of the order-based structure in the sequence-pair representation. However, a sequence-pair includes a pair of permutations (ordered departments), so simple permutation encoding schemes are not suitable for our problem. We next present our encoding scheme, which we refer to as a *position-pair-based* encoding scheme.

To represent a sequence-pair, (Γ_+, Γ_-), a chromosome in a position-pair-based encoding scheme is a string with a pair of values assigned to each gene in the string. The first value represents the position of the corresponding department in the first department sequence, Γ_+. Correspondingly, the second value represents the position of the same department in the second department sequence, Γ_-. For the example sequence-pair in Section 3.2.1, $(\Gamma_+, \Gamma_-) = (ecadfb, fcbead)$, the corresponding position-pair based chromosome is shown in Figure 4.2.

a	*b*	*c*	*d*	*e*	*f*
(3, 5)	(6, 3)	(2, 2)	(4, 6)	(1, 4)	(5, 1)

Figure 4.2: The Position-Pair-Based Chromosome for a Sequence-Pair $(ecadfb, fcbead)$.

The reason that the position-pair-based encoding scheme is of potential benefit is that it establishes some "links" between the two positions of each department in a sequence-pair by including them in the same gene. That is, in a sequence-pair, the location of a department is determined by both of its positions in Γ_+ and Γ_-. Such "links" may be useful for keeping a "good" pattern after crossover and mutation operations. For example, if Department a at (3, 5) and Department b at (6, 3) is a "good" pattern to some extent, then in a position-pair-based encoding scheme, such a good pattern in a chromosome will be more likely to survive than we would expect in a single-valued-string-based chromosome.

4.2.2 Fitness Function and the Selection Rule Design

After the encoding scheme is determined, the second decision to make in designing a GA is how to perform selection; i.e., how to select the chromosomes in the current population that are used to create offspring for the next generation. For the MIP-FLP, the objective is to minimize the total material handling travel distances, so the smaller the objective function value, the higher the fitness score corresponding to the chromosome. In SEQUENCE, we use the following fitness function:

$$F(g, m) = f_g^0 - f_{gm}, \qquad \forall g \in \{1, \ldots, G\}, \forall m \in \{1, \ldots, M\}, \tag{4.1}$$

where $F(g, m)$ is the fitness score function for Chromosome m in Generation g, f_{gm} is the objective function value of the sequence-pair optimal solution from Generation g, using Chromosome m, and $f_g^0 = \max_m \{f_{gm}\}$. Parameter G is the total number of generations and M is the size of the population in each generation.

Given the above fitness score function, one of the most widely applied selection rules, the "roulette wheel," is used in SEQUENCE. Roulette wheel selection is a fitness-proportionate selection, where each chromosome is assigned a slice of a circular "roulette wheel," the size of the slice being proportional to the individual's fitness score in comparison with the fitness scores of the other chromosomes in the population. The probability that a chromosome is selected on a particular spin is given as follows:

$$p_{gm} = \frac{F(g, m)}{\sum_{k=1}^{M} F(g, k)}, \qquad \forall g \in \{1, \ldots, G\}, m \in \{1, \ldots, M\}. \tag{4.2}$$

4.2.3 A Revised Elitism Operator

In addition to roulette wheel selection, we also consider applying an additional operator termed "Elitism," which was first introduced by Kenneth De Jong [15]. An elitism operator is an addition to the selection operator, where the elitism operator forces the GA to retain some number of the best individuals at each generation. Such individuals can be lost if they are not selected to reproduce or if they are destroyed by crossover or mutation. Many researchers have found that elitism significantly improves the GA's performance [49].

The best two-way exchange is shown to be an effective method to improve FLP solutions in some heuristics; e.g., CRAFT [4] and MULTIPLE [11]. In each iteration, the best two-way exchange method first tests all possible two-way exchanges of department positions based on the current layout and then makes the actual two-way exchange of department positions that results in the largest improvement to the current layout solution. The process continues until there is not any two-way exchange of department positions that can improve the current layout solution. The resulting layout solution is called a two-way optimal layout solution. However, there are also some disadvantages associated with the best two-way exchange operator. First, the two-way exchange stops at a two-way optimal solution instead of the globally optimal solution. Second, the computational time for the two-way exchange increases exponentially as the department number increases.

In SEQUENCE, we designed a revised elitism operator, which combines an elitism operator and a best two-way exchange operator for the sequence-pair. In order to describe the best two-way exchange operator, we first give the following definition:

Definition 5 (Two-Way Optimal Sequence-Pair) *A sequence-pair is defined as a two-way optimal sequence-pair if the exchange of the positions of any pair of departments in the sequence-pair cannot generate a better sequence-pair optimal solution.*

In each iteration, the best two-way exchange operator tests the possible improvement by exchanging the positions of any pair of departments in the two sequences of the sequence-pair. It then accepts the exchange that can provide the largest improvement in terms of the sequence-pair optimal solution and proceeds to the next iteration. The best two-way exchange operator stops when there is no two-way exchange of department positions that can provide a better sequence-pair optimal solution. Therefore, the resulting sequence-pair from a best two-way exchange operator must be a two-way optimal sequence-pair.

Our revised elitism operator first selects the best K chromosomes from the last generation and then applies the best two-way exchange operator to the best chromosome of the

K selected chromosomes before copying the K chromosomes to the new generation. The reasons why we only apply the best two-way exchange operator to the best chromosome of the last generation are because: (1) the best chromosome has the greatest impact on the performance of the new generation since it has the highest probability to be selected for the GA operators, and we want to facilitate the convergence of SEQUENCE by further emphasizing the superiority of the best chromosome in each generation; (2) the time for the best two-way exchange operator increases exponentially as the number of departments increases, so only applying the best two-way exchange operator to the best chromosome of the last generation is time efficient; (3) by applying the best two-way exchange operator only to the best chromosome of the last generation there are not too many two-way optimal sequence-pairs carried over to the next generation, which might lead SEQUENCE to prematurely terminate.

4.2.4 GA Operator Design

Operator design is one of the core phases and the most "tricky" part in designing a GA. The operators vary from encoding scheme to encoding scheme and from problem to problem. There are a variety of operators designed for specific GA programs, but generally speaking, most of them belong to one of the following categories: reproduction, crossover and mutation. We discuss them separately next.

Reproduction is a simple operator that merely copies the parents without any modification to the next generation. This permits some amount of overlap between the generations and has shown to be effective by Davis [13].

As the major instrument of variation and innovation in GA, a crossover operator exchanges sub-chromosomes between two parent chromosomes, which results in two new offspring chromosomes. An obvious attribute of permutation problems is that simple crossover operators fail to generate offspring that are valid permutations. Therefore, Davis [13] defined some of the first crossover operators for permutation problems. After that, a variety of permutation crossover operators were designed for different purposes. One of the most commonly used crossover operators is the uniform order-based crossover proposed by Davis [14].

To implement a uniform order-based crossover operator, a binary bit string is generated to denote the selection of positions. Offspring 1 copies the genes directly from Parent 1 in those positions in the bit string marked by "1" bits. Offspring 2 copies the genes from Parent 2 in those positions marked by "0" bits. Both offspring then copy remaining genes from the other parent in the relative order of the genes in the other parent's code. An example is illustrated in Figure 4.3.

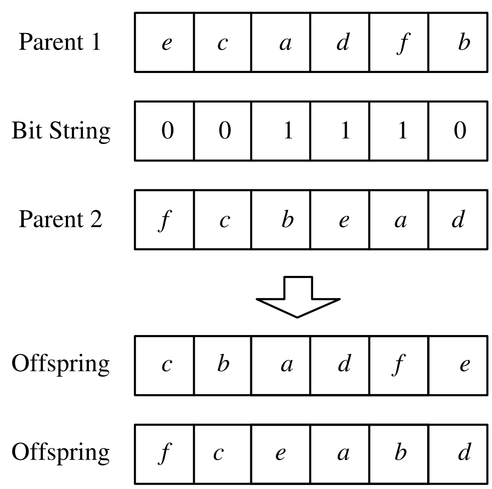


Figure 4.3: Uniformed Order-Based Crossover Operator.

Although useful with a normal single string permutation, the uniform order-based crossover cannot be directly applied to a position-pair-based encoding scheme because a position-pair-based chromosome is not a pure permutation of department positions, but rather a list of position pairs corresponding to each department. Therefore, we consider a modified order-based crossover specifically designed for the position-pair-based encoding scheme.

In Stage 1, like in the uniform order-based crossover, our modified crossover first generates a bit string to indicate the selection of positions. Then Offspring 1 copies the position pair directly from Parent 1 in those positions in the bit string marked by "1" bits. Offspring 2 copies the elements from Parent 2 in those positions marked by "0" bits. Until this step, it is similar to the uniform order-based crossover. An illustration of Stage 1 of our modified order-based crossover operator is provided in Figure 4.4.

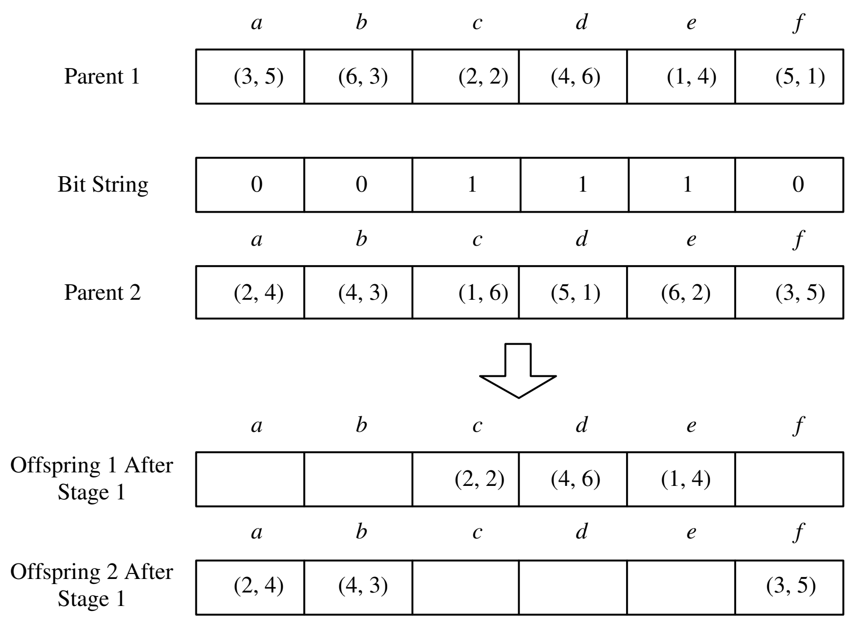


Figure 4.4: Modified Order-Based Crossover Operator–Stage 1.

Our primary modification is apparent in Stage 2 in how both offspring calculate the new position-pairs for the remaining elements based on the relative order in the other parent. Instead of simply copying the remaining elements in the relative order from another parent, both offspring replicate the remaining elements in the relative orders of the elements according to the sequence-pair corresponding to the other parent (the two relative orders in Γ_+ and Γ_-, separately). An illustration of Stage 2 of our modified order-based crossover operator is provided in Figure 4.5.

Another important operator, mutation, provides insurance that the population will evolve to other regions of the solution space. Any form of a mutation operator applied to a permutation structured code must yield a valid string, which also represents a feasible permutation. Most mutation operators for permutations are related to operators that have also been used

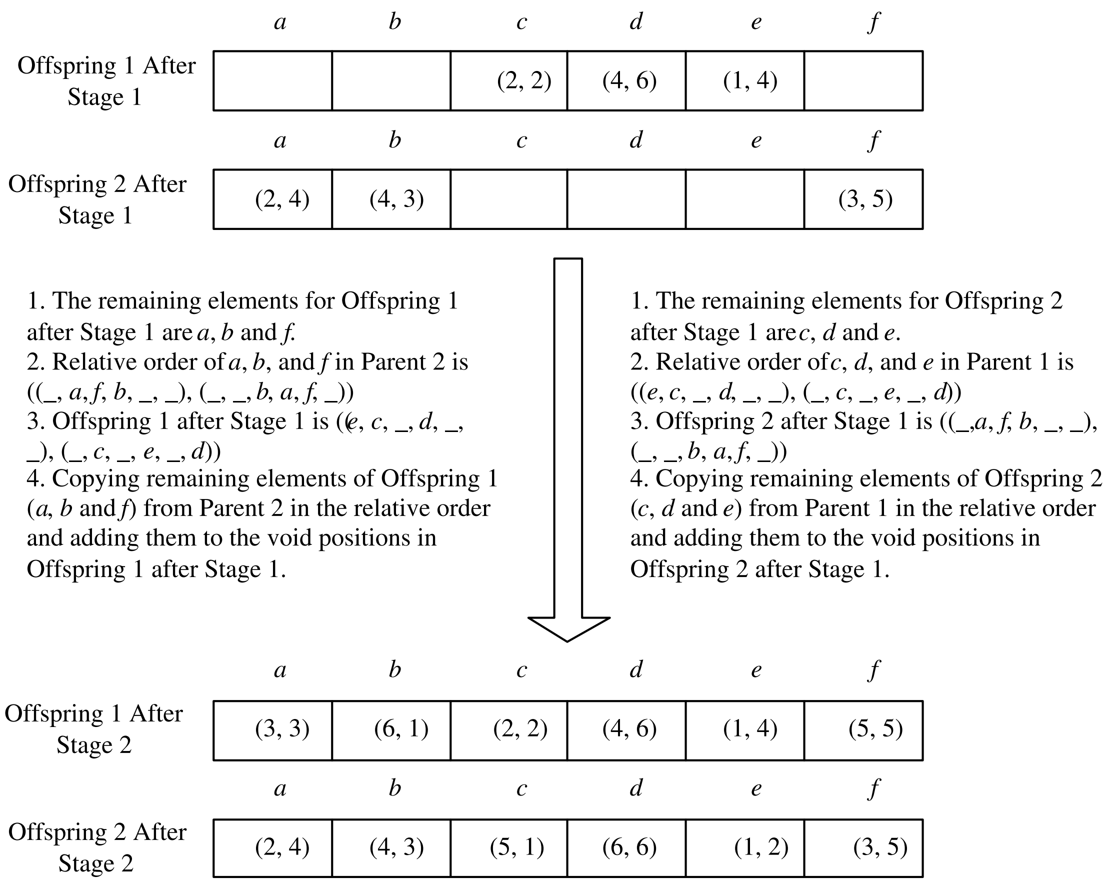


Figure 4.5: Modified Order-Based Crossover Operator–Stage 2.

in neighborhood local search strategies. Those mutation operators include: position-based mutation operators, which randomly select one gene and insert it at some other position in the chromosome; order-based operators, which select two genes and swap the position of these two genes; and scramble mutation operators, which select a segment of the string and randomly reorder it.

In SEQUENCE, we consider utilizing the random 2-way exchange mutation operator, which simply mutates the chosen chromosome by exchanging two randomly picked genes. The random 2-way exchange mutation operator can improve the diversity of the population and prevent the algorithm from premature termination.

4.2.5 Algorithm Scheme of SEQUENCE

The following notation is used to describe the algorithm SEQUENCE:

G	Maximum number of generations.
M	Population size of each generation.
m	Counter of the number of the chromosomes in the new population.
i	Generation index.
j, k	Chromosome indices.
$F(i, j)$	Fitness function value of Chromosome j in Generation i.
p_{ij}	Selection probability of chromosome j in Generation i based on the roulette selection rule.
$\bar{F}_i$	The average fitness function value of Generation i.
g_i^*	The fittest chromosome in Generation i.
f_i^*	The objective function value of the sequence-pair optimal solution corresponding to g_i^*.
g^*	The overall best chromosome.
f^*	The objective function value of the sequence-pair optimal solution corresponding to g^*.
K	The number of the best chromosomes to be copied to the next generation in the elitism operator.
PC	The probability of applying the crossover operator to the selected chromosomes.
PM	The probability of applying the mutation operator to the selected chromosomes.
S	The maximum number of successive generations without producing a new g^*.
ϵ	The tolerance value for the percentage difference between $\bar{F}_i$ and $\bar{F}_{i+1}$.

The genetic procedures of SEQUENCE to solve the sequence-pair based MIP-FLP are given as follows:

1. Generate the initial generation, Generation 0, of size M. Each chromosome in Generation 0 corresponds to a feasible sequence-pair and has an objective function value of f_{0j}. Calculate $F(0, j)$ by using (4.1) and p_{0j} by using (4.2). Record the fittest chromosome, g_0^*, and its corresponding objective function value, f_0^*. Set $i = 0$, $g^* = g_0^*$ and $f^* = f_0^*$.

2. Apply the revised elitism operator to Generation i as follows:

   (a) Select the fittest K chromosomes from Generation i, which include the best chromosome of Generation i, g_i^*.

   (b) If g_i^* is not a chromosome that represents a two-way optimal sequence-pair, apply the best two-way exchange operator to g_i^*. The result, g_i^*, represents a two-way optimal sequence-pair.

   (c) Copy the K chromosomes to Generation $i + 1$ and set $m = K$.

3. To fill the remaining $M - m$ chromosomes in the new generation, randomly select two different parent chromosomes, j_1 and j_2, from Generation i based on the roulette wheel selection rule.

4. With the probability of PC and PM, where $PC + PM = 1$, apply crossover and mutation operators as shown below to Chromosomes j_1 and j_2 to generate two offspring chromosomes, k_1 and k_2, for Generation $i + 1$.

   (a) Generate a random number, r, from a standard uniform distribution $U(0, 1)$.

   (b) If $r \leq PC$, apply crossover operator to Chromosomes j_1 and j_2 to generate Chromosomes k_1 and k_2.

   (c) If $r > PC$, apply the random 2-way exchange mutation operator to j_1 and j_2 to generate Chromosomes k_1 and k_2.

5. Translate Chromosomes k_1 and k_2 into sequence-pairs, set the corresponding binary variables in the MIP-FLP model, and then solve the simplified MIP-FLP model to

optimality. If Chromosome k_i ($i = 1, 2$) corresponds to a feasible sequence-pair, add Chromosome k_i into the new population. Update the value of m as appropriate.

6. If $m < M$, go to Step 3. Otherwise, set the new generation as the current generation by $i = i + 1$ and $m = 0$.

7. In Generation i, calculate $F(i, j)$ using (4.1) and p_{ij} using (4.2) for each chromosome. Record the fittest chromosome, g_i^*, and its corresponding objective function value, f_i^*. If $f_i^* < f^*$, set $g^* = g_i^*$ and $f^* = f_i^*$.

8. If at least one of the following two stopping criteria is satisfied, go to Step 10: (1) $i \geq G$; (2) $\dfrac{\|\bar{F}(i) - \bar{F}(i-1)\|}{\bar{F}(i-1)} \leq \epsilon$ and g^* has not been updated for S generations. Otherwise, go to Step 2.

9. Apply the best two-way exchange operator to the best T chromosomes of the last generation. If the best chromosome of the T chromosomes after applying the best two-way exchange operator is better than g^*, update g^* and f^*. Stop SEQUENCE and output g^* and f^*.

4.2.6 Parameter Setting and Sensitivity Analysis

Parameter setting is another important aspect in GA design since it has a great impact on the performance of the GA. However, these parameters typically interact with each other and their effects cannot be isolated, so it is extremely difficult to optimize them one at a time. Although parameter settings have been discussed extensively in the GA literature, no conclusive results with respect to parameter settings have been presented. So, in most cases, researchers either conduct experimental tests to find "good" parameter settings or they set the parameters according to experience or knowledge about the specific problems where GA is applied. Through an experimental design, we set the parameters for SEQUENCE as follows: $G = 200$, $M = 50$, $K = 10$, $PC = 0.90$, $PM = 0.10$, $S = 10$, $\epsilon = 0.1\%$ and $T = 5$.

4.2.7 Usage of a Penalty Function in the MIP model

Through our initial research, we found that the main constraints that affect the feasibility of a sequence-pair are the aspect ratio constraint and the facility dimension constraint, especially when the facility area is 100% utilized. That is, when a relatively small departmental aspect ratio is used along with a very high area utilization of a facility, it is difficult to generate feasible sequence-pairs in SEQUENCE (especially in generating the initial feasible sequence-pairs).

This difficulty can be addressed by adding some extra area to the facility, which relaxes the facility area constraint and decreases the area utilization. Based on our research, even just a very limited relaxation (e.g., 5% – 10% of the total facility size) permits many of the sequence-pairs to be declared feasible, which greatly reduces the heuristic solution time. An additional benefit of a small relaxation is that the algorithm can provide better chromosome variety in the first several generations with some additional chromosomes that may not be exactly feasible, but are close to feasible under the small relaxation.

To relax the facility dimensions, we fix the left-bottom corner of the facility and increase the width and height of the facility with the same proportion (e.g., a 5% increase in the height and width simultaneously). To implement such a relaxation in the MIP-FLP, we modify the MIP-FLP model as follows (only the modified expressions are shown):

1. Objective Function:

$$\min \quad \sum_i \sum_{j>i} f_{ij}(d_{ij}^x + d_{ij}^y) + (\sum_i \sum_j f_{ij})(L^x + L^y) \sum_i \sum_s t_i^{s-}; \tag{4.3}$$

2. Facility Boundary Constraints:

$$L^s - l_i^s - c_i^s = t_i^{s+} - t_i^{s-} \qquad \forall i; \forall s, \tag{4.4}$$

$$t_i^{s-} \leq (r-1)L^s, \qquad \forall i; \forall s; \tag{4.5}$$

Table 4.1: Impact of 5% Relaxation of the Facility Dimensions on SEQUENCE Performance.

Problem	Without Relaxation		With Relaxation	
	Number of SPs	CPU Time (sec.)	Number of SPs	CPU Time (sec.)
O9	746	79	74	9
M15	2816	348	75	11
M25	100000[a]	8929	3393	323

[a]SEQUENCE has reached the maximum number of sequence-pairs without generating any feasible sequence-pair.

3. Overlapping Constraints:

$$c_i^s + l_i^s \leq c_j^s - l_j^s + rL^s(1 - z_{ij}^s), \qquad \forall i, j; \forall s; \tag{4.6}$$

where t_i^{s-} and t_i^{s+} measure the distance from the right or above side of department i to the right or above side of the facility as defined in (4.4), and t_i^{s-} is greater than 0 if i exceeds the actual dimension of the facility in the s-direction (t_i^{s+} is used to ensure an equality in (4.4) when the solution is feasible). The relaxation of the facility dimensions is constrained by (4.5), where r is a relaxation factor ($r > 1$) to determine how much relaxation is applied to the facility dimensions. We use an upper bound of the layout objective function value, $(\sum_i \sum_j f_{ij})(L_x + L_y)$, in (4.3) as the penalty multiplier. Furthermore, we also modify the overlapping constraint (4.6) by changing the constant parameter L to rL, which means that if $z_{ij} = 0$ (i does not proceed j in s direction) the distance from the left side of j to the right side of i is no more than rL^s.

Table 4.1 illustrates the effectiveness of our relaxation method on the efficiency of the generating feasible sequence-pairs (SPs) in SEQUENCE. A 5% relaxation of the facility dimensions ($r = 1.05$) is applied to three test data sets. We then compared the total number of sequence-pairs and CPU time required to generate 50 initial feasible sequence-pairs with and without the relaxation. Data sets O9, M15 and M25, are of 9, 15 and 25 departments, respectively.

It is obvious that the application of the relaxation of the facility dimensions to SEQUENCE greatly improves the efficiency of SEQUENCE to generate the feasible sequence-pairs. To guarantee the feasibility of the sequence-pair in the final solution, the relaxation parameter, r ($r \geq 1$) is reduced exponentially as shown in (4.7) as the generations evolve.

$$r = 1.0 + r_0 \frac{1}{\sqrt{e^g}}, \tag{4.7}$$

where r_0 is the initial relaxation and g is the generation index of the genetic algorithm. So, after just a few generations, all chromosomes become feasible. The following table gives the percentage of the relaxation of the facility dimensions in the first twenty generations.

Generation	Percentage of Relaxation	Generation	Percentage of Relaxation
1	5.00%	11	0.03%
2	3.03%	12	0.02%
3	1.84%	13	0.01%
4	1.12%	14	0.01%
5	0.68%	15	0.00%
6	0.41%	16	0.00%
7	0.25%	17	0.00%
8	0.15%	18	0.00%
9	0.09%	19	0.00%
10	0.06%	20	0.00%

4.3 Numerical Experiments

To illustrate the effectiveness and efficiency of SEQUENCE for solving the continuous-representation-based FLP, a series of numerical experiments based on different sized test problems from both the literature and industrial applications are conducted. The following numerical tests are conducted in two phases: (1) optimality comparison test; and (2) heuristic comparison test. All numerical tests are conducted on a computer with a Pentium IV 3.2M Hz CPU and 2.0 GB of physical memory.

4.3.1 Optimality Comparison Test

In the optimality comparison test, our purpose is to compare SEQUENCE solutions with optimal solutions to show the quality of SEQUENCE solutions. The data sets we use for the optimality comparison test are the 15 test problems delineated by Sherali, Fraticelli, and Meller [61], which, to our knowledge, represent all of the continuous-representation-based FLPs that have been solved to global optimality in the framework of MIP-FLP.

The properties of the test data sets for the optimality comparison test are summarized in Table 4.2. Here the *flow density* is defined as a percentage of the number of departmental pairs with positive flow interactions over the maximum possible number of pairs. The *area utilization* is defined as the sum of the department areas divided by the available area.

Table 4.2: Properties of the Test Problems for the Optimality Comparison Test.

Problem Name	# of Depts	Aspect Ratio	Flow Density (%)	Area Utilization (%)
M6	6	4	26.67	98.67
M7	6	4	23.81	99.00
FO7	7	4	28.57	99.98
FO7-1	7	4	28.57	97.48
FO7-2	7	5	28.57	99.98
FO8	8	4	25.00	99.98
FO9	9	4	22.22	100.00
NO7	7	4	42.86	99.98
NO7-1	7	4	42.86	97.48
NO7-2	7	5	42.86	99.98
O7	7	4	47.62	99.98
O7-1	7	4	47.62	97.48
O7-2	7	5	47.62	99.98
O8	8	4	53.57	99.98
O9	9	4	41.67	100.00

For each test problem, we run SEQUENCE until the optimal solution reported in [61] is found. The maximum number of runs of SEQUENCE for the test problems is 8; i.e., if SEQUENCE cannot achieve the optimal solution in 8 runs, we stop SEQUENCE and report the optimality gap between the best SEQUENCE solution and the optimal solution. Correspondingly, the reported SEQUENCE solution time is the total run time for SEQUENCE to find the optimal solution or the total run time of 8 runs if SEQUENCE fails to find the optimal solution in 8 runs.

The results of the optimality comparison test are summarized in Table 4.3. Here the optimality gap represents the percentage of the difference between the objective function value of the best SEQUENCE solution and the objective function value of the optimal solution [61] for each test problem.

Table 4.3: Comparison Between SEQUENCE Solutions and the Optimal Solutions.

Problem Name	Optimal Solution		SEQUENCE Solution			Optimality Gap
	Objective	Time (sec.)[a]	Objective	Num. of Runs	Time (sec.)	
M6	82.26	0.04	82.26	1	562	0.00%
M7	106.76	0.07	106.76	1	607	0.00%
FO7	20.73	29	20.73	8	3615	0.00%
FO7-1	19.56	17	19.56	1	243	0.00%
FO7-2	17.75	6	17.75	7	2825	0.00%
FO8	22.31	29	22.31	4	1985	0.00%
FO9	23.46	56	23.46	6	2403	0.00%
NO7	98.49	244	98.49	1	360	0.00%
NO7-1	90.73	71	90.73	2	1134	0.00%
NO7-2	90.50	80	90.50	1	417	0.00%
O7	131.63	790	131.63	6	1644	0.00%
O7-1	120.99	691	120.99	1	358	0.00%
O7-2	116.94	619	116.94	1	238	0.00%
O8	242.88	3860	245.41	8	3056	1.03%
O9	235.95	5384	246.26	8	3879	4.10%

[a]The solution time for the optimal solutions is revised from the literature based on the same computer where we run SEQUENCE.

From Table 4.3 we can see that SEQUENCE achieves the optimal solution for 13 of the 15 test problems in 8 runs and the optimality gaps for the two problems that SEQUENCE does not solve to optimality in 8 runs are small. Therefore, according to the results for the optimality comparison test, the best solution from 8 runs of SEQUENCE is equal to or at least very close to the global optimal layout solution for each test problem and the solution times for the relatively larger test problems are reduced. The detailed best SEQUENCE solutions for all data sets used in the optimality comparison test are summarized in Appendix A.1.

We also run SEQUENCE and the MIP-FLP model to solve a larger test problem with 10 departments [68]. The MIP-FLP takes 18377 seconds and exceeds 2.0 GB of physical memory without finding the optimal solution. The best solution found by the MIP-FLP is 21580, which is worse than the best solution (19997) found by SEQUENCE in much less time (6652 seconds).

4.3.2 Heuristic Comparison Test

In the heuristic comparison test, we use SEQUENCE to solve larger data sets from the literature that are widely used in FLP heuristic research. We compare the results from SEQUENCE to the results published in the literature. These test data sets, to our knowledge, have only been solved to sub-optimality by some existing heuristics and through the comparison of our results with the best reported results from these heuristics, we can show the advantages of SEQUENCE versus other algorithms. Additionally, in order to test the effectiveness of our heuristic for even larger and more practical data sets, we also provide some new data sets based on a recent industrial project.

Data Set Description

Because different researchers often use different data sets to conduct their numerical experiments, we tried to find as many as possible applicable data sets to compare SEQUENCE solutions. Table 4.4 shows the properties of the data sets used in the heuristic comparison test, where the "Reference" column provides the sources that have referred to the corresponding data sets in their research (in chronological order). Data Sets Ba12 and Ba14 are two data sets with 12 and 14 departments, respectively, which were first presented by Bazaraa [8]. There is a small dummy department in Data Set Ba14, which has no flow in and out. Some researchers [8, 27, 68, 30] refer to Ba14 in their research without considering the dummy department, so we refer to the revised Ba14 without the dummy department

Table 4.4: Properties of the Test Problems for the Heuristic Comparison Test.

Problem	Dept Number	Flow Density	Area Utilization	Reference
BM9	9	41.67%	100.00%	[10]
v10	10	26.67%	100.00%	[68, 65, 7, 30, 57]
M11*	11	32.73%	100.00%	[11, 43, 47]
BM12	12	25.76%	100.00%	[10]
Ba12	12	89.39%	88.33%	[8, 27, 68, 65, 7, 30, 57]
Ba13	13	73.08%	95.24%	[8, 27, 68, 30]
Ba14	14	62.64%	96.83%	[8, 65, 7, 57]
M15*	15	20.00%	100.00%	[11, 43, 47]
AB20	20	64.74%	100.00%	[4, 11, 47, 65, 7]
M25*	25	11.33%	100.00%	[11, 43, 47]

as Ba13. Data Sets M11*, M15* and M25* are three data sets first presented by Bozer *et al.* [11]. There is a fixed department in each of the original data sets of M11, M15 and M25, and we modified the original data sets by relaxing the fixed department restrictions in our heuristic test and named the revised data sets as M11*, M15* and M25*, respectively.

In the heuristic comparison test, as appears to be the standard, we run SEQUENCE 10 times and compare the best SEQUENCE solution of 10 runs with the best solution from different heuristics.

Heuristic Comparison Test 1

In Heuristic Comparison Test 1 we compare the best SEQUENCE solutions with other heuristic solutions based on 5 widely used data sets with the best solution found by continuous-representation-based heuristics. To make our solutions comparable to the results from other heuristics, we use the same aspect ratio value as used in the best solutions of other heuristics. For Data Set v10, we use a minimum side length equal to 5. For Data Sets Ba12 and Ba13, we use a minimum side length equal to 1. For Data Sets Ba14, we use a minimum side length equal to 1, except for the dummy department, where we place no shape restriction on it (as other researchers [65, 7]). For AB20, we use the common aspect ratio of 4 for each department.

Table 4.5 presents the numerical test results for Heuristic Comparison Test 1. For each data set, the solutions from different heuristics are given. The improvement column shows the percentage of the improvements compared with the best solution found by other heuristics.

Table 4.5: Results of Objective Function Value Comparison for Heuristic Comparison Test 1.

Data Set	CRAFT [4]	Bazaraa [8]	SHAPE [27]	NLT [68]	Tate & Smith [65]	Kamoun & Yano [30]	Banerjee, *et al.* [7]	SEQU-ENCE	Imp. (%)
v10	–	–	28119	–	23671	24085	22395	19997	10.71
Ba12	–	14079	11910	10578	8768	11470	–	8702	0.76
Ba13	–	–	6875	6339	–	6671	–	4852	23.46
Ba14	–	8171	–	–	5080	–	5052	5004	0.94
AB20	7862	–	–	–	5743	–	5833	5668	1.31

From Table 4.5, it is obvious that SEQUENCE performs better than all compared heuristics in all test data sets in terms of the best objective function value. The improvements over the best solutions we found in literature for the five test data sets are: v10 (10.71%), Ba12 (0.76%), Ba13 (23.46%), Ba14 (0.94%) and AB20 (1.31%), respectively.

Heuristic Comparison Test 2

In Heuristic Comparison Test 2 we compare the SEQUENCE solutions with two discrete-representation-based heuristics, MULTIPLE [11] and SABLE [43] (as implemented in LayoutSFC 1.0 [44]). For a discrete-representation, it is difficult to control and measure the department shapes through an aspect ratio. We therefore utilize a shape factor defined by Bozer, Meller and Erlebacher [11] as follows:

$$\Omega_i = \frac{P_i}{4\sqrt{a_i}}, \tag{4.8}$$

where P_i and a_i are the perimeter and area of department i, respectively. The smaller the shape factor, Ω_i, the more squared the department shape. The purpose for Heuristic Comparison Test 2 is that it shows not only the relative advantage of SEQUENCE in terms of solution quality, but also the potential benefits that can be obtained from a continuous-representation-based heuristic, specifically, in terms of shape factor as measured by (4.8). We run MULTIPLE, SABLE and SEQUENCE 10 times for the discrete-representation-based data sets and compare both the best solutions and the maximum shape factor in the best solutions to illustrate that SEQUENCE can provide the overall better solutions in terms of both the material handling distances and the resulting department shapes.

For the data sets used in Heuristic Comparison Test 2, we use the common aspect ratio values of 4, 4, 4, 5, and 5 for Data Sets BM9, BM12, M11*, M15* and M25*, respectively, even though no shape control is used by MULTIPLE and SABLE. Table 4.6 shows the results of Heuristic Comparison Test 2.

Table 4.6: Results of Comparison for Heuristic Comparison Test 2.

Problem	Best Layout Solutions				Maximum Shape Factor		
	MULTIPLE	SABLE	SEQUENCE	Imp.[a]	MULTIPLE	SABLE	SEQUENCE
BM9	252	252	246	2%	1.67	1.67	1.25
M11*	1344	1373	1171	13%	1.34	1.34	1.24
BM12	149	149	142	4%	1.25	1.25	1.25
M15*	32359	31936	28526	11%	1.42	1.55	1.31
M25*	1596	1588	1371	14%	1.34	1.34	1.34

[a]The improvement is calculated between the SEQUENCE solution and the better solution between MULTIPLE and SABLE solutions.

From Table 4.6, it is clear that SEQUENCE performs better than MULTIPLE and SABLE in terms of both the best objective function value and the department shape factor in all test data sets.

Heuristic Comparison Test 3

In Heuristic Comparison Test 3 we explore the capability of SEQUENCE to solve larger-scale industry-based facility layout problems. We provide two new data sets for relatively large problems based on some real industrial applications, SC30, SC35, where there are 30 and 35 departments, respectively. These two problems, to our knowledge, are the largest continuous-representation-based test problems in the literature. The properties of Data Sets SC30, SC35 are summarized in Table 4.7 (full details on these new data sets are provided in Appendix A.3.).

We use the common aspect ratio of 5 for SC30 and 4 for SC35 to control the department shape. For MULTIPLE and SABLE, we do not apply any department shape restrictions. We also compare the best objective value of SEQUENCE solutions in 10 runs with the best objective value of MULTIPLE and SABLE solutions in 10 runs in Table 4.8. We can see that for problems SC30 and SC35, SEQUENCE improves the best solution from MULTIPLE and SABLE by 39% and 41%, respectively, while maintaining better department shapes.

Table 4.7: Properties of Two Larger Industrial-Based Data Sets.

Problem	Department Number	Flow Density	Area Utilization	Aspect Ratio
SC30	30	11.49%	90.00%	5
SC35	35	9.08%	80.00%	4

Table 4.8: Results of Comparison for Heuristic Comparison Test 3.

Problem	Best Layout Solutions				Maximum Shape Factor		
	MULTIPLE	SABLE	SEQUENCE	Imp.	MULTIPLE	SABLE	SEQUENCE
SC30	5605	6175	3707	34%	1.38	1.43	1.34
SC35	6086	6733	3604	41%	1.43	1.53	1.25

Heuristic Comparison Test Summary

Through the heuristic comparison tests we conclude that SEQUENCE performs better than all heuristics we studied with respect to the test data sets in terms of the best objective function value. SEQUENCE also provides better department shapes for test data sets if compared with discrete-representation-based heuristics.

Table 4.9 shows the solution time of SEQUENCE for finding the best solutions in 10 runs (as the way used to report the computational effort in [65]) and the total run time of 10 runs of SEQUENCE for all test data sets used in the heuristic comparison tests.

Table 4.9: Solution Time for All Data Sets Used in the Heuristic Comparison Tests.

Problem	Solution Time (Hrs.)	Total Time of 10 Runs (Hrs.)
BM9	0.29	1.30
v10	1.85	2.16
M11*	0.19	2.00
BM12	0.28	2.53
Ba12	0.83	1.64
Ba13	0.46	2.69
Ba14	0.80	3.37
M15*	3.11	3.11
AB20	3.46	6.51
M25*	6.70	9.05
SC30	4.07	20.23
SC35	16.04	26.64

This improved performance in obtaining objective function values does come at a cost in terms of run time. Since GA solutions are based on the evolution of many generations of chromosomes and SEQUENCE solves one simplified MIP-FLP model for each chromosome in each generation, the solution time for SEQUENCE is relatively long. In general, the larger the test data set, the longer the run time. For the largest problem, SC35, it takes SEQUENCE approximately 26 hours to run SEQUENCE 10 times. Given that in most FLP applications layout planning is not a real-time decision process, and that a lower number of runs may be used (e.g., 4 runs instead of 10 runs), we believe that such a solution time can still be justified for large facility layout problems.

4.4 Summary

In this chapter we proposed a GA-based heuristic, SEQUENCE, to solve the sequence-pair representation based MIP-FLP with all rectangular-shaped departments. Different issues in the heuristic design are discussed in detail. We compare SEQUENCE with both optimal solutions and other heuristics based on the data sets from the literature and industrial applications. The results of the numerical experiments illustrate the effectiveness of SEQUENCE.

However, when there is at least one fixed department in the FLP, we found through research that it becomes difficult for SEQUENCE to generate feasible sequence-pairs with respect to the fixed department constraints. We address this difficulty by presenting an operator to "repair" an infeasible sequence-pair in SEQUENCE. The repair operator is shown to improve the efficiency of SEQUENCE to solve the FLP with fixed departments in the next chapter.

Chapter 5

A Heuristic for the FLP with Fixed Departments

In Chapter 4 we presented our algorithm, SEQUENCE, to solve the FLP. SEQUENCE solves the MIP-FLP by using the sequence-pair representation to eliminate all binary-infeasible overlapping department solutions. However, in the MIP-FLP there are other constraints in addition to the overlapping constraints. So, as we discussed in Section 3.3.3, a sequence-pair may not be feasible to the MIP-FLP with respect to the other constraints. Through our research, we have found one type of constraint that greatly impacts the performance of SEQUENCE: whether or not there are fixed departments in the MIP-FLP. That is, it is difficult to generate feasible sequence-pairs when the constraints associated with fixed departments are added and the algorithm may spend much of its time generating sequence-pairs that are infeasible with respect to the fixed department constraint(s) of the MIP-FLP. Since this is time that would be better spent on evaluating feasible sequence-pairs, we develop a "repair" operator for SEQUENCE that will be utilized when sequence-pairs are generated.

First, consider a simple case: Department i in Figure 5.1(a). We consider this a simple case since Department i is to the left of all other departments in the layout. According to Theorem 1 in Section 3.2.2, it is easy to conclude that a feasible sequence-pair should

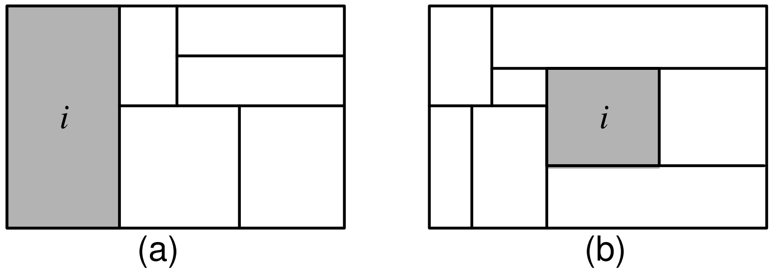


Figure 5.1: Illustration of FLP with a Fixed Department.

have i as the first component in both sequences. However, for the general case where a fixed department is located in the middle of a facility, as shown in Figure 5.1(b), it becomes very difficult to find the "feasible" positions for the fixed department in the sequence-pair. In order to improve the efficiency of SEQUENCE to generate feasible sequence-pairs when there are fixed departments, a repair operator is proposed to be utilized in SEQUENCE to filter the infeasible sequence-pairs without solving the MIP-FLP model.

In this chapter we first present a repair operator for the FLP with a single fixed department in Section 5.1, where the basic concepts and the procedures of the repair operator are described. We then extend the repair operator to further consider the FLP with multiple fixed departments in Section 5.2. The procedures of SEQUENCE for solving the FLP with fixed departments using the proposed repair operator are given in Section 5.3. In order to further improve the efficiency of SEQUENCE with the repair operator, especially for solving the FLP with 100% area utilization, we propose a modified penalty function method for the MIP-FLP model based on an exponentially reduced relaxation on the facility size in Section 5.4. Numerical experiments based on different sized data sets from both the literature and an industrial application are provided to illustrate the effectiveness of SEQUENCE with the repair operator to solve the FLP with fixed departments in Section 5.5. Finally, a summary of this chapter is provided in Section 5.6.

5.1 A Repair Operator for the FLP with a Single Fixed Department

Since it is very difficult for an arbitrary sequence-pair to be feasible with respect to a fixed department constraint in the MIP-FLP, we present a repair operator to be used in SEQUENCE to improve the likelihood that a sequence-pair will be feasible after repair with respect to the FLP with a single fixed department in this section.

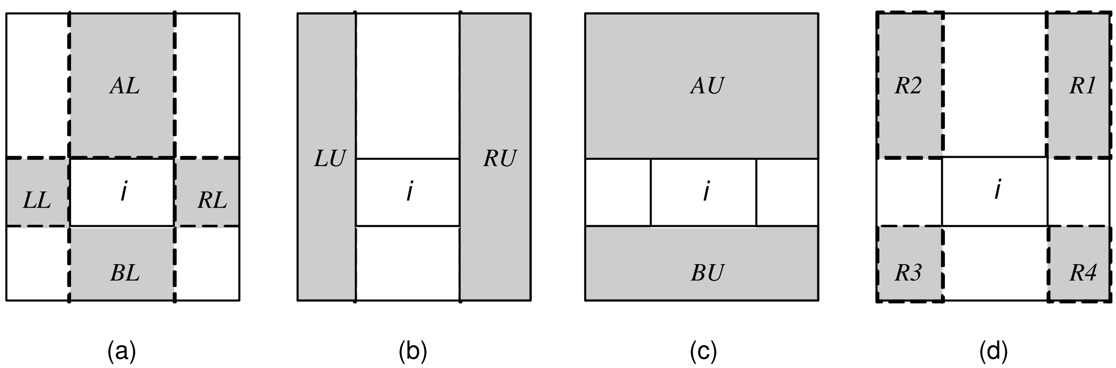


Figure 5.2: An Illustration of the FLP with a Fixed Department.

The following notation is used for the repair operator:

- T Set of relative location relationships between two different departments. $T = \{l, r, a, b\}$, where l represents the "left of" relationship, r represents the "right of" relationship, a represents the "above" relationship, and b represents the "below" relationship.
- t Relative location relationship index, where $t \in T$.
- A_i^t The total area of the departments that have relative location relationship t to the fixed department i.
- lb_i^t Lower bound of the total area of the departments that have relative location relationship t to the fixed department i. The values of lb_i^l, lb_i^r, lb_i^b and lb_i^a represent the area of the regions denoted by LL, RL, BL and AL in Figure 5.2(a), respectively.

ub_i^t Upper bound of the total area of the departments that have relative location relationship t to the fixed department i. The values of ub_i^l, ub_i^r, ub_i^b and ub_i^a represent the area of the regions denoted by LU, RU, BU and AU in Figures 5.2(b) and 5.2(c), respectively.

r_i^q Area of the corners formed by the fixed department i as shown in Figure 5.2(d), where $q = 1, 2, 3, 4$. The values of r_i^1, r_i^2, r_i^3 and r_i^4 represent the area of the regions denoted by $R1$, $R2$, $R3$ and $R4$ in Figure 5.2(d), respectively.

$a_{[j]}^+$ The area of the $[j]$th department in the first sequence, Γ_+, of a sequence-pair (Γ_+, Γ_-).

$a_{[j]}^-$ The area of the $[j]$th department in the second sequence, Γ_-, of a sequence-pair (Γ_+, Γ_-).

The manner in which to interpret the region denoted by LL in Figure 5.2 and its area lb_i^l is that if any part of department j ($j \neq i$) resides in some part of the region LL, j must be to the left of i in the layout solution. A department that is left of i may not overlap with the region LL, but all of the departments that overlap with the region LL must be left of i. So the area of LL, represented as lb_i^l, denotes a lower bound of the total area of the departments that are left of i in the layout. Similarly, the areas of the regions denoted by RL, BL and AL in Figure 5.2(a), represented as lb_i^r, lb_i^b and lb_i^a, denote the lower bounds of the total area of the departments that are right of, below and above i, respectively. Likewise, if any department j ($j \neq i$) is left of i, j must be entirely contained in the region denoted by LU in Figure 5.2(b). If j is not entirely contained in the region LU, j can not be left of i. So the area of LU, represented as ub_i^l, denotes an upper bound of the total area of the departments that are left of i in the layout. Similarly, the areas of the regions denoted by RU, BU and AU in Figures 5.2(b) and (c), represented as ub_i^r, ub_i^b and ub_i^a, denote the lower bounds on the total area of the departments that are right of, below and above i, respectively. The above analysis can be represented mathematically by the following constraint:

$$lb_i^t \leq A_i^t \leq ub_i^t \qquad \forall i, \forall t \in T \tag{5.1}$$

We can use (5.1) to find the potentially feasible positions for a fixed department in a sequence-pair. According to Theorem 1 presented in Chapter 3, we state the following corollary:

Corollary 1 *Given a sequence-pair,* (Γ_+, Γ_-)*, and* i *and* j *as two different departments in* (Γ_+, Γ_-)*, then the following relationships are satisfied:*

$$\begin{aligned}
j \textit{ is before } i \textit{ in } \Gamma_+ &\iff j \textit{ is either left of or above } i \textit{ in the layout;}\\
j \textit{ is after } i \textit{ in } \Gamma_+ &\iff j \textit{ is either right of or below } i \textit{ in the layout;}\\
j \textit{ is before } i \textit{ in } \Gamma_- &\iff j \textit{ is either left of or below } i \textit{ in the layout;}\\
j \textit{ is after } i \textit{ in } \Gamma_- &\iff j \textit{ is either right of or above } i \textit{ in the layout.}
\end{aligned}$$

Since we know that the lower bound of the total area of the departments that are left of or above i are lb_i^l and lb_i^a, respectively, we can use $lb_i^l + lb_i^a$ as a lower bound of the total area of the departments either left of or above i. We also notice that if any department j ($j \neq i$) overlaps with the region denoted by $R2$ (the area of $R2$ is represented by r_i^2) in Figure 5.2(d), it must either be left of or above i in the layout. So we further tighten the lower bound of the total area of the departments either left or above i by substituting $lb_i^l + lb_i^a + r_i^2$ for $lb_i^l + lb_i^a$. According to Corollary 1, this lower bound, $lb_i^l + lb_i^a + r_i^2$, is also the lower bound of the total area of the departments that are before i in Γ_+. In a similar way, we know the upper bound of the total area of the departments that are left or above i are ub_i^l and ub_i^a, respectively, so we can use $ub_i^l + ub_i^a$ as an upper bound of the total area of the departments before i in Γ_+. Since the regions LU and AU overlap the region denoted by $R2$ in Figure 5.2, we tighten the upper bound of the total area of the departments before i in Γ_+ by substituting $ub_i^l + ub_i^a - r_i^2$ for $ub_i^l + ub_i^a$. Therefore, the constraint on the total area of the departments that are before i in Γ_+ is given as follows:

$$lb_i^l + lb_i^a + r_i^2 \leq A_i^l + A_i^a \leq ub_i^l + ub_i^a - r_i^2 \qquad \forall i \tag{5.2}$$

Similarly, the constraints on the total area of the departments that are after i in Γ_+, before i in Γ_-, and after i in Γ_-, respectively, are represented in (5.3)–(5.5) as follows:

$$lb_i^r + lb_i^b + r_i^4 \leq A_i^r + A_i^b \leq ub_i^r + ub_i^b - r_i^4 \qquad \forall i \tag{5.3}$$

$$lb_i^l + lb_i^b + r_i^3 \leq A_i^l + A_i^b \leq ub_i^l + ub_i^b - r_i^3 \qquad \forall i \tag{5.4}$$

$$lb_i^r + lb_i^a + r_i^1 \leq A_i^r + A_i^a \leq ub_i^r + ub_i^a - r_i^1 \qquad \forall i \tag{5.5}$$

Thus, through (5.2)–(5.5), we know the lower and upper bound of the total area of the departments that are allowed to be placed before and after a fixed department i in a sequence-pair, which, combined with (5.1), can be used in searching for the potential feasible positions of the fixed department in the sequence-pair.

Based on (5.1)– (5.5), we present the procedures for a repair operator used in SEQUENCE to repair a sequence-pair for solving the FLP with a single fixed department. The goal of such an operator is to increase the likelihood that a sequence-pair that has been "repaired" is feasible (as compared to the original sequence-pair) for the FLP with a single fixed department.

The following notation is used in the description of the repair operator:

- l_i^+ The most-left potentially feasible position for i in Γ_+ that satisfies (5.1)–(5.5).
- r_i^+ The most-right potential feasible position for i in Γ_+ that satisfies (5.1)–(5.5).
- l_i^- The most-left potentially feasible position for i in Γ_- that satisfies (5.1)–(5.5).
- r_i^- The most-right potential feasible position for i in Γ_- that satisfies (5.1)–(5.5).

The detailed description of the repair operator is given as follows and an example is also provided to illustrate the usage of the repair operator.

1. Calculate the parameters lb_i^t, ub_i^t and r_i^q for the fixed department, Department i, with respect to its fixed location and dimensions in the layout ($\forall t$, $\forall q$).

2. Given a sequence-pair, (Γ_+, Γ_-), remove Department i from (Γ_+, Γ_-) and set the initial values of the potentially feasible positions of i in (Γ_+, Γ_-) as follows: $l_i^+ = 0$, $r_i^+ = N$, $l_i^- = 0$ and $r_i^- = N$.

3. If $l_i^+ > \min\{r_i^+, N\}$, stop (the sequence-pair cannot be repaired). Otherwise, if $A_i^l + A_i^a = \sum_{j=1}^{l_i^+} a_{[j]}^+$ satisfies (5.2), go to Step 4. Otherwise, $l_i^+ = l_i^+ + 1$ and go to Step 3.

4. If $r_i^+ < \max\{1, l_i^+\}$, stop (the sequence-pair cannot be repaired). Otherwise, if $A_i^r + A_i^b = \sum_{j=r_i^+}^{N-1} a_{[j]}^+$ satisfies (5.3), go to Step 5. Otherwise, $r_i^+ = r_i^+ - 1$ and go to Step 4.

5. If $l_i^- > \min\{r_i^-, N\}$, stop (the sequence-pair cannot be repaired). Otherwise, if $A_i^l + A_i^b = \sum_{j=1}^{l_i^-} a_{[j]}^-$ satisfies (5.4), go to Step 6. Otherwise, $l_i^- = l_i^- + 1$ and go to Step 5.

6. If $r_i^- < max\{1, l_i^-\}$, stop (the sequence-pair cannot be repaired). Otherwise, if $A_i^r + A_i^a = \sum_{j=r_i^-}^{N-1} a_{[j]}^-$ satisfies (5.5), go to Step 7. Otherwise, $r_i^- = r_i^- - 1$ and go to Step 6.

7. Randomly choose between l_i^+ and r_i^+ and between l_i^- and r_i^-. Insert i into the chosen positions in (Γ_+, Γ_-) and calculate the area of the departments that are left of, right of, above and below i. If (5.1) is satisfied, go to Step 9. Otherwise, remove i from (Γ_+, Γ_-) and go to Step 8.

8. Update the potentially feasible positions of i as follows: if l_i^+ or l_i^- is used as the insert position in Step 7, update it by $l_i^+ = l_i^+ + 1$ or $l_i^- = l_i^- + 1$; if r_i^+ or r_i^- is used as the insert position in Step 7, update it by $r_i^+ = l_i^+ - 1$ or $r_i^- = l_i^- - 1$. If $l_i^+ > r_i^+$ or $l_i^- > r_i^-$, stop (the sequence-pair cannot be repaired). Otherwise, go to Step 7.

9. Return (Γ_+, Γ_-) as the repaired sequence-pair and stop.

The following example illustrates how this repair operator works. Given a layout problem with 6 departments, the departments are located in a facility with dimensions 4×5. Table 5.1 summarizes the problem data, where Department 4 is a fixed department located at (3, 2) with department dimensions 2×2. The location of Department 4 in the layout is illustrated in Figure 5.3.

Table 5.1: A Sample Problem for the FLP with a Single Fixed Department.

Dept	**Area**	**Type**	**Aspect Ratio**
1	4	Soft	4
2	2	Soft	4
3	4	Soft	4
4	4	Fixed	1
5	2	Soft	4
6	4	Soft	4

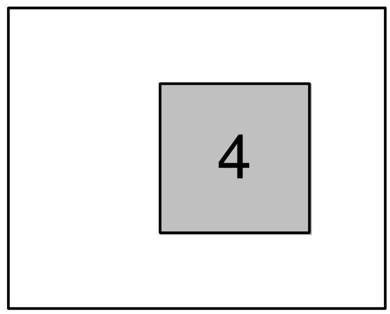


Figure 5.3: Illustration of a Sample Problem for the FLP with a Single Fixed Department.

We first calculate the parameters, lb_4^t, ub_4^t and r_4^q for Department 4 according to its fixed location and dimensions as follows:

t	$t = l$	$t = r$	$t = a$	$t = b$
lb_4^t	4	2	2	2
ub_4^t	8	4	5	5
q	$q = 1$	$q = 2$	$q = 3$	$q = 4$
r_4^q	1	2	2	1

Correspondingly, we express (5.2)–(5.5) as follows:

$$8 \leq A_4^l + A_4^a \leq 11 \tag{5.6}$$

$$5 \leq A_4^r + A_4^b \leq 8 \tag{5.7}$$

$$8 \leq A_4^l + A_4^b \leq 11 \tag{5.8}$$

$$5 \leq A_4^r + A_4^a \leq 8 \tag{5.9}$$

Given a sequence-pair, for example, $(\Gamma_+, \Gamma_-) = ((4,1,3,2,5,6),(4,3,1,5,2,6))$, it is obvious that this sequence-pair is infeasible since the fixed department, Department 4, is left of all other five departments based on this sequence-pair, which is in conflict with the fixed location of Department 4. Now we use the repair operator we proposed to "repair" this infeasible sequence-pair.

After removing Department 4, the resulting sequence-pair is $((1,3,2,5,6),(3,1,5,2,6))$. We then set the initial value of l_4^+, r_4^+, l_4^- and r_4^- as follows: $l_4^+ = 0$, $r_4^+ = 6$, $l_4^- = 0$ and $r_4^- = 6$. The next step is to look for the most-left potentially feasible position, l_4^+, that satisfies (5.6). Here the most-left position to satisfy (5.6) is the third position in $\Gamma_+ = (1,3,2,5,6)$, where the sum of the area of the departments left of the third position (Department 1 and 3) is equal to 8. So we assign $l_4^+ = 3$. Next, we find the most-right potentially feasible position, r_4^+, that satisfies (5.7). The result is $r_4^+ = 4$ since the sum of the area of the departments from position 4 to the last department (Department 5 and 6) in $\Gamma_+ = (1,3,2,5,6)$ satisfies (5.7). Similarly, we also update the values for l_4^- and r_4^-, where l_4^- is equal to 3 and r_4^- is equal to 4.

We then randomly pick, for example, l_4^+ between l_4^+ and r_4^+ and r_4^- between l_4^- and r_4^- to insert Department 4. After insertion, the sequence pair becomes $((1,3,4,2,5,6),(3,1,5,4,2,6))$. The actual area of the departments that are left of, right of, above and below Department 4 are 8, 6, 0, and 2, respectively. In doing so, (5.1) is not satisfied. So, we randomly pick l_4^+ from l_4^+ and r_4^- to update by letting $l_4^+ = l_4^+ + 1 = 4$. We then continue to randomly pick r_4^+ between l_4^+ and r_4^+ and r_4^- between l_4^- and r_4^- to insert Department 4. After insertion, the sequence pair becomes $((1,3,2,4,5,6),(3,1,5,4,2,6))$, which satisfies (5.1). So the repair operator stops and the resulting sequence-pair, ((1,3,2,4,5,6), (3,1,5,4,2,6)), is returned. Although the feasibility of the resulting sequence-pair from the repair operator is not guaranteed, the resulting sequence-pair $((1,3,2,4,5,6),(3,1,5,4,2,6))$ is actually feasible and the corresponding layout is shown in Figure 5.4.

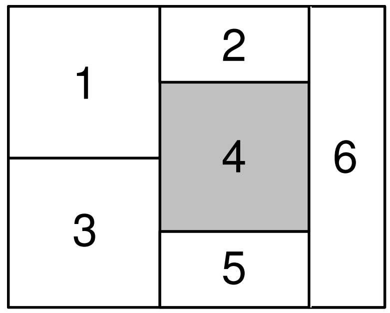


Figure 5.4: Illustration of a Layout for the Sample Problem After Repair.

Table 5.2: Efficiency Test of the Repair Operator for the FLP with a Single Fixed Department.

Problem	Feasible Sequence-Pairs (SPs)	Without Repair Operator		With Repair Operator		% Reduction in Inefficiency Factor
		No. of SPs Required	Inefficiency Factor	No. of SPs Required	Inefficiency Factor	
5	50	1857	37.04	93	1.87	94.95%
12	50	26937	538.74	950	19.00	96.47%
31	50	1,000,000[a]	–	925	18.50	–

[a]The maximum number of sequence-pairs has been reached before 50 feasible sequence-pairs are generated.

Table 5.2 shows the efficiency of our proposed repair operator for the FLP with a single fixed department. For each test problem, the objective is to generate 50 feasible sequence-pairs. The inefficiency factor is defined by dividing the total number of generated sequence-pairs by the number of feasible sequence-pairs and represents the number of feasible sequence-pairs that is needed on average to generate one feasible sequence-pair. The inefficiency factor is compared for the situations without and with the repair operator.

From Table 5.2 it is obvious that the repair operator greatly improves the efficiency of SEQUENCE to generate feasible sequence-pairs for the FLP with a single fixed department. However, the repair operator proposed in this section does not consider the FLP with multiple fixed departments. In the next section we will extend the repair operator to further consider the FLP with multiple fixed departments.

5.2 A Repair Operator for the FLP with Multiple Fixed Departments

For the FLP with a single fixed department, the proposed repair operator works effectively since once the single fixed department is inserted into the determined positions in the sequence-pair, the sequence-pair becomes complete and we can calculate the actual area of the departments before and after the fixed department in the sequence-pair. We then use the area bound of the departments before and after the fixed department in the sequence-pair to test the feasibility of the complete sequence-pair. However, when considering applying such a repair operator to the FLP with multiple fixed departments, this property no longer holds.

For a repair operator to the FLP with multiple fixed departments, we need to insert the fixed departments into the sequence-pair with incomplete information. As a result, the fixed departments inserted later will change the area of the departments before or after the previously-inserted fixed departments in the sequence-pair. That is, the area of the departments that are left of, right of, above and below a just inserted fixed department, which is calculated based on the current "incomplete" sequence-pair, will change after the insertion of another fixed department. Thus, a feasible position for a previously-inserted fixed department according to (5.1)–(5.5) may not be a "feasible" position after inserting another fixed department into the sequence-pair.

We propose an enhanced repair operator to repair a sequence-pair for the FLP with multiple fixed departments. The following notation is added to our previous repair operator notation to present our repair operator for the FLP with multiple fixed departments.

- F Set of the fixed departments.
- F' Set of the fixed departments that have not been inserted into the sequence pair, $F' \subseteq F$.
- m_F Number of fixed departments.

$m_{F'}$ Number of fixed departments in F'.

a_i Area of department i.

o^t_{ji} The overlapping area of fixed department j ($j \neq i$) with the regions that are used to represent the lower bound of the area of the departments that have a relative location relationship t with i. Specifically, o^l_{ji}, o^r_{ji}, o^b_{ji}, and o^a_{ji} are the overlapping areas of j with the regions denoted by LL, RL, BL and AL in Figure 5.2(a), respectively.

o^q_{ji} The overlapping area of fixed department j ($j \neq i$) with the regions that are used to represent the corner area formed by i as shown in Figure 5.2(d). Specifically, o^1_{ji}, o^2_{ji}, o^3_{ji}, and o^4_{ji} are the overlapping areas of j with the regions denoted by $R1$, $R2$, $R3$ and $R4$ in Figure 5.2(d), respectively. It should be noted that $\sum\limits_t o^t_{ji} + \sum\limits_q o^q_{ji} = a_j, \forall i, j \in F, i \neq j$.

$$a^t_{ji} = \begin{cases} a_j & \text{if } j \text{ has a relative location relationship } t \text{ to } i \\ 0 & \text{otherwise} \end{cases}.$$

It should be noted that $\sum\limits_t a^t_{ji} = a_j$.

Given a FLP with multiple fixed departments, we know exactly the relative location relationship between any two fixed departments because the locations and dimensions of these fixed departments are given *a priori*. Thus, parameters o^t_{ji}, o^q_{ji} and a^t_{ji} are also known *a priori*.

We modify (5.1)–(5.5) to consider the impact of the fixed departments inserted after other fixed departments to the area bounds of the departments before and after the previously-inserted fixed departments in the sequence-pair. The basic methodology is given as follows:

1. For fixed department i to be inserted, we appropriately subtract the area of all fixed departments that are not inserted from the area bound of Department i calculated through (5.1)–(5.5). Therefore, the resulting area bounds are actually the area bounds of the departments that currently exist in the sequence-pair instead of the area bounds

of all other departments in the FLP.

2. When inserting fixed department i into the sequence-pair, besides the adjusted area bound, we also consider the relative location relationship of i with those previously-inserted fixed departments in the sequence-pair to make sure that the correct relative location relationships between i and these previously-inserted fixed departments are satisfied.

The combination of the above two procedures guarantees that the fixed departments inserted later do not impact the potentially feasible positions of the previously-inserted fixed departments. To appropriately subtract the area of the other fixed departments that are not inserted yet from the area bound of a fixed department to be inserted into the sequence-pair, we propose the following revised area bound constraints:

$$lb_i^t - \sum_{j \in F'} o_{ji}^t \leq A_i^t \leq ub_i^t - \sum_{j \in F'} a_{ji}^t \qquad \forall i \in F, \forall t \in T \tag{5.10}$$

$$lb_i^l + lb_i^a + r_i^2 - \sum_{j \in F'} (o_{ji}^l + o_{ji}^a + o_{ji}^2) \leq A_i^l + A_i^a \leq ub_i^l + ub_i^a - r_i^2 - \sum_{j \in F'} (a_{ji}^l + a_{ji}^a) \quad \forall i \in F \tag{5.11}$$

$$lb_i^r + lb_i^b + r_i^4 - \sum_{j \in F'} (o_{ji}^r + o_{ji}^b + o_{ji}^4) \leq A_i^r + A_i^b \leq ub_i^r + ub_i^b - r_i^4 - \sum_{j \in F'} (a_{ji}^r + a_{ji}^b) \quad \forall i \in F \tag{5.12}$$

$$lb_i^l + lb_i^b + r_i^3 - \sum_{j \in F'} (o_{ji}^l + o_{ji}^b + o_{ji}^3) \leq A_i^l + A_i^b \leq ub_i^l + ub_i^b - r_i^3 - \sum_{j \in F'} (a_{ji}^l + a_{ji}^b) \quad \forall i \in F \tag{5.13}$$

$$lb_i^r + lb_i^a + r_i^1 - \sum_{j \in F'} (o_{ji}^r + o_{ji}^a + o_{ji}^1) \leq A_i^r + A_i^a \leq ub_i^r + ub_i^a - r_i^1 - \sum_{j \in F'} (a_{ji}^r + a_{ji}^a) \quad \forall i \in F \tag{5.14}$$

The lower and upper bounds of the area of the departments that exist in the current "incomplete" sequence-pair and have a relative location relationship t to i is represented in (5.10), which is equal to the lower and upper bounds of the area of all departments with relative location relationship t to i minus the overlapping area of the fixed departments that have not yet been inserted with the corresponding regions that represent these lower and upper bounds. For example, the lower bound of the area of the departments that exist in the current "incomplete" sequence-pair and are left of i is equal to the lower bound area, lb_i^t, minus the overlapping area of j with the region denoted by LL in Figure 5.2(a), o_{ji}^l. The upper bound of the area of the departments that exist in the current "incomplete" sequence-pair and are left of i is equal to the upper bound area, ub_i^l, minus the overlapping area of j with the region denoted by LU in Figure 5.2(b), a_{ji}^t.

The area bounds of the departments that currently exist in the sequence-pair that should be placed before and after i are given in (5.11)–(5.14). For example, on the left-hand side of (5.11), the lower bound of the area of the departments that are currently placed in the sequence-pair and should be placed before i in Γ_+ is calculated by subtracting the areas o_{ji}^l, o_{ji}^a and o_{ji}^2, which represents the overlapping area of the fixed departments that have not been inserted with the regions denoted by LL, AL and $R2$ in Figure 5.2, respectively, from the lower bound of the area of all departments that should be placed before i in the first sequence of the complete sequence-pair. On the right-hand side of (5.11), the upper bound of the area of the departments that currently exist in the sequence-pair and should be placed before i in Γ_+ is calculated by subtracting the areas a_{ji}^l and a_{ji}^a, which represents the overlapping area of the fixed departments that have not been inserted with the regions denoted by LU and AU in Figure 5.2, respectively, from the upper bound of the area of all departments that should be placed before i in the first sequence of the complete sequence-pair. In a similar way, the area bound constraints of the departments that currently exist in the sequence-pair that should be placed after i in Γ_+, before i in Γ_-, and after i in Γ_- are given in (5.11)–(5.14), respectively.

Besides the area bound constraints, the insertion of a fixed department also needs to satisfy the relative location relationship of that fixed department with the previously-inserted fixed departments based on Theorem 1.

The following additional notation is used in the description of the enhanced repair operator for the FLP with multiple fixed departments.

p_{ji}^{+} The position of previously-inserted fixed department, j $(j \in F - F')$, that should be placed before i $(i \in F')$ in Γ_+; i.e., j is either left of or above i.

q_{ji}^{+} The position of previously-inserted fixed department, j $(j \in F - F')$, that should be placed after i $(i \in F')$ in Γ_+; i.e., j is either right of or below i.

p_{ji}^{-} The position of previously-inserted fixed department, j $(j \in F - F')$, that should be placed before i $(i \in F')$ in Γ_+; i.e., j is either left of or below i.

q_{ji}^{-} The position of previously-inserted fixed department, j $(j \in F - F')$, that should be placed after i $(i \in F')$ in Γ_+; i.e., j is either right of or above i.

We next present the following procedure for an enhanced repair operator for the FLP with multiple fixed departments:

1. For each fixed department, j $(j \in F)$, calculate the corresponding parameters lb_j^t, ub_j^t and r_j^q with respect to the fixed location and dimensions of Department j in the layout.

2. Given a sequence-pair, (Γ_+, Γ_-), remove all fixed departments from (Γ_+, Γ_-), add them to F', and set $m_{F'} = m_F$. The resulting sequence-pair includes only non-fixed departments.

3. If $F' = \emptyset$, go to Step 12. Otherwise, pick a fixed department i from F' and for each j $(j \in F')$, calculate o_{ji}^t, o_{ji}^q and a_{ji}^t $(\forall t, q)$.

4. Set the initial values of the potentially feasible positions as follows: $l_i^+ = 0$, $r_i^+ = N - m_{F'} + 1$, $l_i^- = 0$ and $r_i^- = N - m_{F'} + 1$.

5. Update the values of l_i^+, r_i^+, l_i^- and r_i^- according to the positions of the previously-inserted fixed departments as follows:

   - If there is any previously-inserted fixed department that should be placed before i in Γ_+, set l_i^+ by assigning $l_i^+ = \max_{j \in F - F'} \{p_{ji}^+\} + 1$.
   - If there is any previously-inserted fixed department that should be placed after i in Γ_+, set r_i^+ by assigning $r_i^+ = \min_{j \in F - F'} \{q_{ji}^+\}$.

- If there is any previously-inserted fixed department that should be placed before i in Γ_-, set l_i^- by assigning $l_i^- = \max_{j \in F-F'}\{p_{ji}^-\} + 1$.
- If there is any previously-inserted fixed department that should be placed after i in Γ_-, set r_i^- by assigning $r_i^+ = \min_{j \in F-F'}\{q_{ji}^+\}$.

6. If $l_i^+ > min\{r_i^+, N - m_{F'} + 1\}$, stop (sequence-pair cannot be repaired). Otherwise, if $A_i^l + A_i^a = \sum_{j=1}^{l_i^+-1} a_{[j]}^+$ satisfies (5.11), go to Step 7. Otherwise, $l_i^+ = l_i^+ + 1$ and go to Step 6.

7. If $r_i^+ < max\{1, l_i^+\}$, stop (sequence-pair cannot be repaired). Otherwise, if $A_i^r + A_i^b = \sum_{j=r_i^+-1}^{N-m_{F'}-1} a_{[j]}^+$ satisfies (5.12), go to Step 8. Otherwise, $r_i^+ = r_i^+ - 1$ and go to Step 7.

8. If $l_i^- > min\{r_i^-, N - m_{F'} + 1\}$, stop (sequence-pair cannot be repaired). Otherwise, if $A_i^l + A_i^b = \sum_{j=1}^{l_i^--1} a_{[j]}^-$ satisfies (5.13), go to Step 9. Otherwise, $l_i^- = l_i^- + 1$ and go to Step 8.

9. If $r_i^- < max\{1, l_i^-\}$, stop (sequence-pair cannot be repaired). Otherwise, if $A_i^r + A_i^a = \sum_{j=r_i^--1}^{N-m_{F'}-1} a_{[j]}^-$ satisfies (5.14), go to Step 10. Otherwise, $r_i^- = r_i^- - 1$ and go to Step 9.

10. Randomly choose between l_i^+ and r_i^+ and between l_i^- and r_i^-. Insert i into the sequence-pair based on the chosen positions and calculate the area of the departments that are left of, right of, above and below i. If (5.10) is satisfied, remove i from F', set $m_{F'} = m_{F'} - 1$ and go to Step 3. Otherwise, remove i from the sequence-pair and go to Step 11.

11. Randomly update one insert position from the two insert positions used in Step 10. If l_i^+ or l_i^- is used for insertion in Step 10, update it by $l_i^+ = l_i^+ + 1$ or $l_i^- = l_i^- + 1$. If r_i^+ or r_i^- is used for insertion in Step 10, update it by $r_i^+ = r_i^+ - 1$ or $r_i^- = r_i^- - 1$. If $l_i^+ > r_i^+$ or $l_i^- > r_i^-$, stop (sequence-pair cannot be repaired). Otherwise, go to Step 10.

12. Return (Γ_+, Γ_-) as the repaired sequence-pair and stop.

We now provide a simple example to illustrate the use of the enhanced repair operator in SEQUENCE for the FLP with multiple fixed departments. The example problem used for the enhanced repair operator is similar to the example that we used in Section 5.1 except that we now further fix Department 3 in addition to (fixed) Department 4. Department 3 is now fixed at (2, 3.5) with department dimensions 4×1. The illustration for this problem is shown in Figure 5.5.

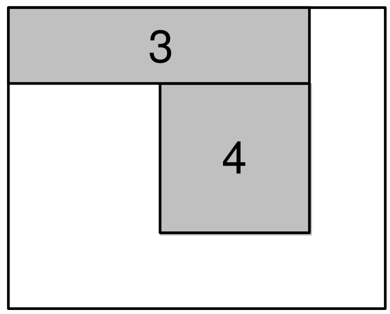


Figure 5.5: Illustration of the Sample Problem with Two Fixed Departments.

Given the locations and dimensions of the fixed departments, we first calculate the parameters, lb_i^t, ub_i^t and r_i^q for Department 3 and 4 as follows:

Department 3				
t	$t=l$	$t=r$	$t=a$	$t=b$
lb_3^t	0	1	0	12
ub_3^t	0	4	0	15
q	$q=1$	$q=2$	$q=3$	$q=4$
r_3^q	0	0	0	3
Department 4				
t	$t=l$	$t=r$	$t=a$	$t=b$
lb_4^t	4	2	2	2
ub_4^t	8	4	6	6
q	$q=1$	$q=2$	$q=3$	$q=4$
r_4^q	1	2	2	1

Assume that we have the initial sequence-pair, $(\Gamma_+, \Gamma_-) = ((4, 2, 5, 6, 3, 1), (4, 6, 5, 2, 1, 3))$. It is obvious that this sequence-pair is infeasible since Department 4 is left of all other five departments based on this sequence-pair, which is in conflict with the fixed location of Department 4. In addition, Departments 2, 5, and 6 are left of Department 3, which is in conflict with the fixed location of Department 3. In the following example, we use the repair operator we proposed to "repair" this infeasible sequence-pair.

After moving the fixed departments, Departments 3 and 4, to F', the resulting sequence-pair becomes $((2,5,6,1),(6,5,2,1))$ and $F' = \{3,4\}$ ($m_{F'} = 2$). Assume that we first insert Department 3 into the sequence-pair. The parameters, o^t_{43}, o^q_{43} and a^t_{43}, are calculated as follows:

Department 3				
t	$t=l$	$t=r$	$t=a$	$t=b$
a^t_{43}	0	0	0	4
o^t_{43}	0	0	0	4
q	$q=1$	$q=2$	$q=3$	$q=4$
o^q_{43}	0	0	0	0

The corresponding area constraints, (5.11)–(5.14), for Department 3 are given as follows:

$$0 \leq A^l_3 + A^a_3 \leq 0 \tag{5.15}$$

$$12 \leq A^r_3 + A^b_3 \leq 12 \tag{5.16}$$

$$8 \leq A^l_3 + A^b_3 \leq 11 \tag{5.17}$$

$$1 \leq A^r_3 + A^a_3 \leq 4 \tag{5.18}$$

We then set the initial values of l^+_3, r^+_3, l^-_3 and r^-_3 as follows: $l^+_3 = 0$, $r^+_3 = 5$, $l^-_3 = 0$ and $r^-_3 = 5$. Because there is no previously-inserted fixed department to consider, the next step is to look for the most-left potentially feasible position for l^+_3 so that (5.15) is satisfied, which is the first position in $\Gamma_+ = (2,5,6,1)$. Next, we find the most-right position for r^+_3, where $r^+_3 = 1$ since the sum of the area of the departments from position 1 to the last department in Γ_+ satisfies (5.16). Similarly, we also find the values for l^-_3 and r^-_3, where $l^-_3 = 4$ and $r^-_3 = 4$, respectively. We then randomly choose, for example, r^+_3 from l^+_3 and r^+_3 and l^-_3 from l^-_3 and r^-_3 as the positions to insert Department 3. After insertion, the sequence pair becomes $(\Gamma_+, \Gamma_-) = ((3,2,5,6,1),(6,5,2,3,1))$, which satisfies (5.10). So we remove

Department 3 from F' and now $F' = \{4\}$ $(m_{F'} = 1)$.

Next, we insert Department 4 into the sequence-pair. First, we assign the initial values for l_4^+, r_4^+, l_4^- and r_4^- as follows: $l_4^+ = 0$, $r_3^+ = 6$, $l_3^- = 0$ and $r_3^- = 6$. For Department 4, there is only one previously-inserted fixed department, Department 3, which is above Department 4 as shown in Figure 5.5. That is, Department 3 should be placed before Department 4 in Γ_+ and after Department 4 in Γ_-. Based on this relative location relationship, we update l_4^+ and l_4^- by letting $l_4^+ = p_{34}^+ + 1 = 2$ and $l_4^- = p_{34}^- = 4$, respectively. Such an update guarantees that Department 4 will be inserted into a position after Department 3 in Γ_+ and before Department 3 in Γ_-, which represents that Department 4 is below Department 3 in the layout. The corresponding area constraints for Department 4 are given as follows:

$$8 \leq A_4^l + A_4^a \leq 11 \tag{5.19}$$

$$5 \leq A_4^r + A_4^b \leq 8 \tag{5.20}$$

$$8 \leq A_4^l + A_4^b \leq 11 \tag{5.21}$$

$$5 \leq A_4^r + A_4^a \leq 8 \tag{5.22}$$

Next, we look for the most-left potentially feasible position, l_4^+, so that (5.19) is satisfied, where $l_4^+ = 4$, and the most-right potentially feasible position, r_4^+, so that (5.20) is satisfied, where $r_4^+ = 4$. In a similar manner, we update the value of l_4^- and r_4^-, where $l_4^- = 4$ and $r_4^- = 4$. We then randomly choose, for example, r_4^+ from l_4^+ and r_4^+ and r_4^- from l_4^- and r_4^- to insert Department 4. After insertion, the sequence pair becomes $(\Gamma_+, \Gamma_-) = ((3, 2, 5, 4, 6, 1), (6, 5, 2, 4, 3, 1))$. The actual area of the departments that are left of, right of, above and below Department 4 satisfies (5.10), so the repair operator stops and the resulting sequence-pair, $((3, 2, 5, 4, 6, 1), (6, 5, 2, 4, 3, 1))$, is returned. Although the feasibility of the returning sequence-pair from the repair operator is not guaranteed, the resulting sequence-pair $((3, 2, 5, 4, 6, 1), (6, 5, 2, 4, 3, 1))$ is actually feasible and the corresponding layout is shown in Figure 5.6.

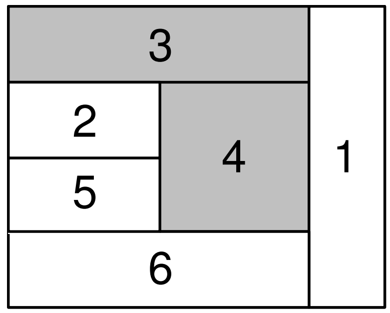


Figure 5.6: Illustration of a Layout of the Sample Problem After Repair.

Table 5.3 shows the effectiveness of our proposed repair operator for the FLP with multiple fixed departments. For each test problem, the objective is to generate 50 feasible sequence-pairs. The inefficiency factor is defined by dividing the total number of generated sequence-pairs by the number of feasible sequence-pairs and represents the number of feasible sequence-pairs that is needed on average to generate one feasible sequence-pair. The inefficiency factor is compared for the situations without and with the repair operator.

Table 5.3: Test on the Efficiency of the Repair Operator for the FLP with Multiple Fixed Departments.

Problem	No. of Fixed Depts.	Feasible Sequence-Pairs (SPs)	Without Repair Operator		With Repair Operator	
			No. of SPs Required	Inefficiency Factor	No. of SPs Required	Inefficiency Factor
5	2	50	4581	91.62	104	2.08
12	2	50	1,000,000[a]	–	953	19.05
25	2	50	1,000,000[a]	–	925	18.50

[a]The maximum number of sequence-pairs has been reached before 50 feasible sequence-pairs are generated.

5.3 The Combination of SEQUENCE with the Repair Operator

In this section we describe the procedure of SEQUENCE with the repair operator for the FLP with fixed departments. The following notation is used to describe the algorithm

SEQUENCE with the repair operator:

G	Maximum number of generations.
M	Population size of each generation.
m	Counter of the number of the chromosomes in the new population.
i	Generation index.
j, k	Chromosome indices.
$F(i, j)$	Fitness function value of Chromosome j in Generation i.
p_{ij}	Selection probability of chromosome j in Generation i based on the roulette selection rule.
$\bar{F}_i$	The average fitness function value of Generation i.
g_i^*	The fittest chromosome in Generation i.
f_i^*	The objective function value of the sequence-pair optimal solution corresponding to g_i^*.
g^*	The overall best chromosome.
f^*	The objective function value of the sequence-pair optimal solution corresponding to g^*.
K	The number of the best chromosomes to be copied to the next generation in the elitism operator.
PC	The probability of applying the crossover operator to the selected chromosomes.
PM	The probability of applying the mutation operator to the selected chromosomes.
S	The maximum number of successive generations without producing a new g^*.
ϵ	The tolerance value for the percentage difference between $\bar{F}_i$ and $\bar{F}_{i+1}$.

The genetic procedures of SEQUENCE with the repair operator to solve the FLP with fixed departments are given as follows:

1. Generate the initial generation, Generation 0, of size M as follows:

    (a) If $m < M$, randomly generate a sequence-pair and translate the sequence-pair into a position-pair based chromosome, Chromosome j. Otherwise, go to Step 1(c).

    (b) Repair Chromosome j with the repair operator. If Chromosome j is feasible after repair, add Chromosome j into Generation 0. Go to Step 1(a).

    (c) Calculate $F(0, j)$ by using (4.1) and p_{0j} by using (4.2). Record the fittest chromosome, g_0^*, and its corresponding objective function value, f_0^*. Set $i = 0$, $g^* = g_0^*$ and $f^* = f_0^*$.

2. Apply the revised elitism operator to Generation i as follows:

    (a) Select the fittest K chromosomes from Generation i, which include the best chromosome of Generation i, g_i^*.

    (b) If g_i^* is not a chromosome that represents a two-way optimal sequence-pair, apply the best two-way exchange operator to g_i^*. The result, g_i^*, represents a two-way optimal sequence-pair.

    (c) Copy the K chromosomes to Generation $i + 1$ and set $m = K$.

3. To fill the remaining $M - m$ chromosomes in the new generation, randomly select two different parent chromosomes, j_1 and j_2, from Generation i based on the roulette wheel selection rule.

4. With the probability of PC and PM, where $PC + PM = 1$, apply crossover and mutation operators as shown below to Chromosomes j_1 and j_2 to generate two offspring chromosomes, k_1 and k_2, for Generation $i + 1$.

    (a) Generate a random number, r, from a standard uniform distribution $U(0, 1)$.

    (b) If $r \leq PC$, apply crossover operator to Chromosomes j_1 and j_2 to generate Chromosomes k_1 and k_2.

(c) If $r > PC$, apply the random 2-way exchange mutation operator to j_1 and j_2 to generate Chromosomes k_1 and k_2.

5. Translate Chromosomes k_1 and k_2 into sequence-pairs, set the corresponding binary variables in the MIP-FLP model, and then solve the simplified MIP-FLP model to optimality. If Chromosome k_i $(i = 1, 2)$ corresponds to a feasible sequence-pair, add Chromosome k_i into the new population. Update the value of m as appropriate. If both k_1 and k_2 correspond to feasible sequence-pairs, go to Step 7. Otherwise, go to Step 6.

6. Repair Chromosome k_i, which represents an infeasible sequence-pair, by using the repair operator. Then translate Chromosomes k_i into sequence-pairs, set the corresponding binary variables in the MIP-FLP model, and then solve the simplified MIP-FLP model to optimality. If Chromosome k_i becomes feasible after repair, add Chromosome k_i into the new population and update the value of m as appropriate.

7. If $m < M$, go to Step 3. Otherwise, set the new generation as the current generation by $i = i + 1$ and $m = 0$..

8. In Generation i, calculate $F(i, j)$ using (4.1) and p_{ij} using (4.2) for each chromosome. Record the fittest chromosome, g_i^*, and its corresponding objective function value, f_i^*. If $f_i^* < f^*$, set $g^* = g_i^*$ and $f^* = f_i^*$.

9. If at least one of the following two stopping criteria is satisfied: (1) $i \geq G$; (2) $\dfrac{\|\bar{F}(i) - \bar{F}(i-1)\|}{\bar{F}(i-1)} \leq \epsilon$ and g^* has not been updated for S generations, go to Step 10. Otherwise, go to Step 2.

10. Apply the best two-way exchange operator to the best K chromosomes of the last generation. If the best chromosome of the K chromosomes after applying the best two-way exchange operator is better than g^*, update g^* and f^*. Stop SEQUENCE and output g^* and f^*.

5.4 Usage of a Penalty Function in the MIP Model

Because of the difficulty added when fixed departments are considered in the MIP-FLP (a lot of feasible layout solutions for the FLP without fixed departments or with just a single fixed department become infeasible for the FLP with multiple fixed departments), it is not easy to generate feasible sequence-pairs — even with the repair operator — especially when the area utilization is 100%. Through our research, we found that a relaxation to the facility size to decrease the area utilization can effectively improve the efficiency of generating "feasible" sequence-pairs under the constraints of the relaxed facility size.

So we utilize a penalty function method similar to the one we used for the FLP without fixed departments, which was given in (4.4)–(4.6). Because there is a much higher degree of infeasibility for the FLP with fixed departments as compared to the FLP without fixed departments, we consider using a larger initial relaxation (50%) of the facility dimensions in the MIP-FLP with fixed departments to improve the efficiency of SEQUENCE to generate the initial "feasible" sequence-pairs. Table 5.4 illustrates the effectiveness of a 50% ($r = 1.50$) relaxation as compared with a 5% ($r = 1.05$) relaxation of the facility dimensions on the efficiency of the generating "feasible" sequence-pairs (SPs) in SEQUENCE. We compared the total number of sequence-pairs and CPU time required to generate 50 initial "feasible" sequence-pairs with the different relaxations of the facility dimensions. Three data sets with a different number of departments and fixed departments are used in the test.

Table 5.4: Impact of Different Relaxation of the Facility Dimensions on SEQUENCE Performance for the FLP with Fixed Departments.

Problem	Number of Fixed Depts.	5% Relaxation		50% Relaxation	
		Number of SPs	CPU Time (sec.)	Number of SPs	CPU Time (sec.)
B12F1	1	191	20	76	8
B12F2	2	355	32	72	8
M25	1	5487	540	53	9

It is obvious that the application of a larger relaxation of the facility dimensions to SEQUENCE greatly improves the ability of SEQUENCE to generate "feasible" sequence-pairs. To guarantee the actual feasibility of the sequence-pairs in the final solution, the relaxation parameter, r ($r \geq 1$) is reduced exponentially as shown in (4.7) as the generations evolve.

The large initial relaxation of the facility dimensions leads to a large penalty value for some of the chromosomes in the first several generations. So, according to the roulette wheel selection rule, such chromosomes would have a very low probability to be chosen as the parent chromosomes for the next generation, which greatly restricts the diversity of the chromosomes in the first several generations. Therefore, instead of using an upper bound of the objective function value, $(\sum_i \sum_j f_{ij})(L^x + L^y)$, as the penalty multiplier, we use a substitute penalty multiplier, $\sum_i \sum_j f_{ij}$, in the MIP-FLP with fixed departments.

Table 5.5 illustrates the effectiveness of the different penalty function scenarios with different penalty multipliers for solving the FLP with fixed departments. Penalty Function Scenario 1 utilizes an upper bound of the objective function value, $(\sum_i \sum_j f_{ij})(L^x + L^y)$, as the penalty multiplier while Penalty Function Scenario 2 utilizes the flow sum, $\sum_i \sum_j f_{ij}$, as the penalty multiplier. A 50% relaxation of the facility dimensions is applied to both scenarios as the initial relaxation and the relaxation is reduced exponentially as the GA generation evolves according to (4.7). We run SEQUENCE with the repair operator 10 times for each test data set under different penalty function scenarios and compare the best solutions and total runtime in Table 5.5. The comparison results show that Penalty Function Scenario 2 overperformes Penalty Function Scenario 1 in terms of both the best solutions and the total runtime. Thus, Penalty Function Scenario 2 will be used for the following numerical tests.

Table 5.5: Impact of Different Penalty Functions on SEQUENCE with the Repair Operator.

Dept. #	Fixed Dept. #	Scenario 1		Scenario 2		Imp. on Best Sol.	Imp. on Runtime
		Best Sol.	Runtime (hrs.)	Best Sol.	Runtime (hrs.)		
12	1	11149	1.42	10650	1.41	4.47%	1.26%
12	2	10905	1.37	10884	1.23	0.20%	10.22%
25	1	1754	10.58	1657	9.10	5.53%	13.99%

5.5 Numerical Tests

To illustrate the effectiveness and efficiency of SEQUENCE to solve the sequence-pair based MIP-FLP with fixed departments using the proposed repair operator and penalty function method, a series of numerical tests based on the different sized test problems from both the literature and industrial practice were conducted. Because there are very few test data sets in the literature that include fixed departments, we revised some of the data sets from the literature to add fixed departments to the original problems.

The numerical experiments are conducted on two types of data sets: data sets with a single fixed department and data sets with multiple fixed departments. The heuristics we use for comparison are two discrete-representation-based heuristics, MULTIPLE and SABLE. We run MULTIPLE, SABLE (as implemented in LayoutSFC 1.1 [44]) and SEQUENCE 10 times for all test data sets and compare the best solutions in terms of both the objective function value and the department shapes as measured by (4.8).

5.5.1 Numerical Test for the FLP with a Single Fixed Department

We first conducted a numerical test on data sets where there is a single fixed department. Table 5.6 summarizes the properties of the test data sets we use in the numerical tests.

Table 5.6: Properties of the Test Data Sets for the FLP with a Single Fixed Department.

Data Set	Num. of Depts	Num. of Fixed Depts	Flow Density	Area Utilization	References
M11	11	1	32.73%	100.00%	[11, 43, 47]
Ba12F1	12	1	89.39%	88.33%	[8]
M15	15	1	20.00%	100.00%	[11, 43, 47]
M25R	25	1	11.33%	100.00%	[11, 43, 47]
SC30F1	30	1	11.49%	90.00%	New Data Set

Data Sets M11 and M15 are two data sets considered in [11, 43, 47], where a fixed department is located in the corner for each problem. Data Set Ba12F1 is originally presented by Bazaraa [8], where there are 12 non-fixed departments. We revised the original data set by fixing one of the departments in the middle of the facility. Data Set M25R is considered [11, 43, 47], where there is a non-rectangular fixed department in the top-right corner. We revised the original data set by reforming the shape of the non-rectangular fixed department to be rectangular and locating the fixed department in the top-right corner. Data Set SC30F1 is revised from the Data Set SC30 used in the numerical test in Section 4.3, where we fixed one of the largest departments in the middle of the facility. This data set comes from a recent industrial project concerned with facility re-layout design, where the fixed department represents an assembly line, which is very expensive, if not practically impossible, to move. The detailed data for all data sets are provided in Appendix B.1.

The results for the numerical tests and comparison are given in Table 5.7. From Table 5.7 it is obvious that SEQUENCE with the single-fixed-department repair operator provides better solutions than MULTIPLE and SABLE for all test data sets in terms of both the objective function value and the department shapes. The average improvement of the best objective function value for all five data sets is 12.37%.

Table 5.7: Numerical Test Results on the Data Sets with a Single Fixed Department.

Problem	Best Layout Solutions				Maximum Shape Factor		
	MULTIPLE	SABLE	SEQUENCE	Imp.	MULTIPLE	SABLE	SEQUENCE
M11	1373	1373	1251	8.90%	1.34	1.34	1.15
Ba12F1	12372	12319	10650	13.55%	1.42	1.43	1.25
M15	34558	32319	31851	1.45%	1.30	1.42	1.29
M25R	1838	1877	1657	9.86%	1.34	1.34	1.34
SC30F1	5685	5616	4038	28.10%	1.81	1.59	1.34

5.5.2 Numerical Test for the FLP with Multiple Fixed Departments

We next conducted a numerical test on data sets where there are multiple fixed departments, where the properties of the test data sets are summarized in Table 5.8.

Table 5.8: Properties of the Test Data Sets for the FLP with Multiple Fixed Departments.

data Set	Num. of Depts	Num. of Fixed Depts	Flow Density	Area Utilization	References
Ba12F2	12	2	89.39%	88.33%	[8]
M25F2	25	2	11.33%	100.00%	[11, 43, 47]
SC30F2	30	2	11.49%	90.00%	New Data Set
SC30F3	30	3	11.49%	90.00%	New Data Set

Data Set Ba12F2 is a data set with two fixed departments in the middle of the facility, which is revised from Data Set Ba12 presented by Bazaraa [8]. Data Set M25F2 is a data set with two fixed departments, which is revised from Data Set M25 presented by Bozer, Meller and Erlebacher [11]. Data Sets SC30F2 and SC30F3 are two data sets revised from Data Set SC30, where in SC30F2 we use two fixed large departments to represent two different lines that are difficult to move and in SC30F3 we add a third fixed department to represent the same assembly line used as a fixed department for Data Set SC30F1. The detailed data of all data sets are provided in Appendix B.2. The results for this numerical test are provided in Table 5.9.

Table 5.9: Numerical Test Results on the Data Sets with Multiple Fixed Department.

Problem	Best Layout Solutions				Maximum Shape Factor		
	MULTIPLE	SABLE	SEQUENCE	Imp.	MULTIPLE	SABLE	SEQUENCE
Ba12F2	11709	11709	10884	7.04%	1.33	1.33	1.25
M25F2	1990	1928	1838	4.65%	1.34	1.50	1.30
SC30F2	6297	6665	4545	27.83%	1.50	1.53	1.34
SC30F3	6929	6815	6274	7.94%	1.50	1.43	1.34

From Table 5.9 it is clear that SEQUENCE with the multiple-fixed-department repair operator provides better solutions for all test data sets in terms of both the objective function value and the department shapes. The average improvement on all data sets in terms of the best objective function value is 11.87%. We also notice that as the number of the fixed departments increases, the best objective function value (the minimum material handling distances) increases as well. This is easy to understand since as more fixed departments are added, more layout solutions are eliminated from the feasible solution space.

5.5.3 Computational Effort

As a cost of achieving the improved solutions in terms of both the objective function values and the department shapes, the solution time for SEQUENCE with the repair operator to solve the MIP-FLP with fixed departments is considerable. Table 5.10 presents the solution time for the data sets we used for the numerical tests when no fixed department constraints are imposed and when they are imposed.

Table 5.10: Solution Time for All Data Sets with Fixed Departments.

Problem	Area Util.	No Fixed Departments (Hrs.)		Fixed Departments (Hrs.)		Reductio on Total Run Time
		Sol. Time	Total Run Time	Sol. Time	Total Run Time	
M11	100%	0.19	2.00	1.50	2.43	-21%
Ba12F1	89%	0.83	1.64	1.03	1.41	14%
M15	100%	3.11	3.11	0.78	3.43	-10%
M25R	100%	6.70	9.05	7.34	9.10	-1%
SC30F1	90%	4.07	20.23	6.24	17.21	15%
Ba12F2	89%	0.83	1.64	0.56	1.23	25%
M25F2	100%	6.70	9.05	13.05	14.93	-65%
SC30F2	90%	4.07	20.23	13.83	15.04	26%
SC30F3	90%	4.07	20.23	12.17	13.68	32%

As we can see from Table 5.10, the impact of adding fixed department(s) on the total runtime is not consistent for different data sets. We notice that for the data sets where the area utilization is 100% (M11, M15, M25R, and M25F2), adding fixed department(s) increases the total runtime, while for the data sets where the area utilization is less than 100% (Ba12F1, SC30F1, Ba12F2, SC30F2, and SC30F3), the total runtime is reduced after adding fixed department(s). A similar observation can be made for the impact of the number of fixed departments on the total runtime. For example, as one of the data sets with 100% area utilization, Data Set M25F2 (2 fixed departments) has a longer run time than M25R (1 fixed department). For the data sets with less than 100% area utilization (Ba12F1, Ba12F2, SC30F1, SC30F2 and SC30F3), increasing the number of fixed departments actually reduces the solution time. On the one hand, increasing the number of fixed departments reduces the number of departments with unknown dimensions and locations, thus reduces the problem size. On the other hand, the fixed dimensions and locations of fixed departments "shrink" the feasible sequence-pair space and increase the difficulty for SEQUENCE, even with the repair operator, to find feasible sequence-pairs. The above observation can be explained by noting that as the area utilization increases (to 100%), the difficulty for SEQUENCE to find feasible sequence-pairs gradually tends to dominate the benefits of reducing the problem size brought on by increasing the number of fixed departments. It also should be noted that even with a relatively high area utilization (88% for Ba12F1 and Ba12F2 and 90% for SC30F1, SC30F2 and SC30F3), increasing the number of fixed departments can still significantly reduce the solution time. Given that in most FLP applications, the area utilization is not as high as 100%, when using SEQUENCE to solve the problem, one strategy that might be considered to reduce the total runtime would be to fix some departments at their preferred locations.

Furthermore, the longest total runtime for 10 runs corresponds to Data Set SC30F1, which is about 17 hours. Given that in most FLP applications layout planning is not a real-time decision process, and that a lower number of runs may be used (i.e., 4 runs instead of 10 runs), we believe that such a solution time can still be justified for large facility layout problems with fixed departments.

5.6 Summary

In this chapter we addressed the difficulty of SEQUENCE to generate feasible sequence-pairs when there are fixed departments by presenting a repair operator. The repair operator alters the sequence-pair by re-arranging the positions of the fixed departments in the sequence-pair according to the lower and upper bounds of the area of the departments that are left of, right of, above and below the fixed department. We combine SEQUENCE with the repair operator to solve the FLP with fixed departments. Numerical tests based on different sized problems with a different number of fixed departments were conducted to test SEQUENCE with the repair operator to solve the FLP with fixed departments. The comparison with two heuristics, MULTIPLE and SABLE, illustrates the effectiveness of SEQUENCE with the repair operator for the FLP with fixed departments.

Chapter 6

MIP Model and a Heuristic for the FLP with an Existing Aisle Structure

6.1 FLP with an Existing Aisle Structure

Most FLP algorithms do not consider the facility's main-aisle structure. In some cases the aisle structure may be determined before the block layout design due to practical material handling considerations. For example, consider a plant that is expected to modify its current layout and the plant uses automatic guided vehicles (AGVs) as the primary material handling equipment. Many existing AGV systems use AGVs that navigate through an inductive guide-path; i.e., a wire embedded in the floor that carries an alternating current to induce a magnetic field that is detected by antennae mounted on the bottom of the vehicles. Thus, these guide-paths serve as the main aisles within the facility. Modifications to such an aisle structure can be extremely expensive and/or destructive. An illustration of a facility with an existing aisle structure is shown in Figure 6.1.

In this chapter we further extend our research on combining the sequence-pair representation and the MIP-FLP model to consider the FLP with an existing aisle structure (FLPAL).

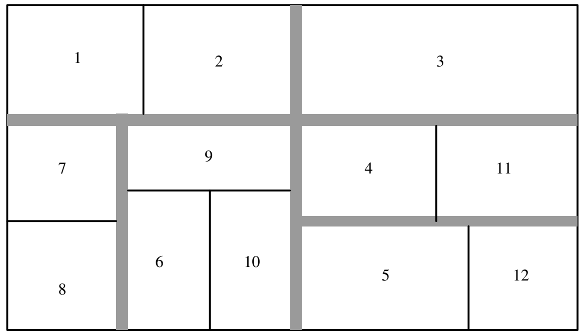


Figure 6.1: A Facility Layout with an Existing Aisle Structure.

We first formulate the FLPAL by presenting an MIP model that we name MIP-FLPAL. We then present a genetic algorithm based heuristic, SEQUENCE-AL, that combines the sequence-pair and MIP-FLPAL to solve the FLPAL problem. To illustrate the effectiveness of SEQUENCE-AL, we first compare the SEQUENCE-AL solutions with the optimal solutions of the MIP-FLPAL for some small-sized data sets. We then compare the SEQUENCE-AL solutions with the solutions of two other heuristics: MULTIPLE-AL and SABLE-AL, which are revised versions of two existing heuristics, MULTIPLE [11] and SABLE [43].

6.2 An MIP Model for the FLP with Aisle Structure

Given a facility with a fixed aisle structure, the following assumptions are used to formulate the problem.

1. The aisle structure divides the facility into several rectangular-shaped zones.
2. The location and dimensions of each zone are know *a priori*.
3. Each department must be contained completely in only one zone. Departments are not allowed to cross the boundaries of the zones.

Using the same notation as in FLP2, we now add the following additional notation for new parameters and decision variables.

New Parameters:

- Z Number of zones in the given facility partitioned by the aisle structure.
- z Zone indices ($z = \{1, \ldots, Z\}$).
- C_z^s The location of the centroid of Zone z in the s-direction.
- L_z^s Half side length of Zone z in the s-direction.

New Decision Variables:

- r_{iz} Binary decision variables, which denote whether department i is located in Zone z or not. The definition of r_{iz} is as follows:

$$r_{iz} = \begin{cases} 1 & \text{if department } i \text{ is located in Zone } z, \\ 0 & \text{otherwise} \end{cases}.$$

Our MIP-FLPAL model is formulated as follows:

$$\min \quad \sum_i \sum_{j>i} f_{ij}(d_{ij}^x + d_{ij}^y) \tag{6.1}$$

$$\text{s.t.} \quad d_{ij}^s = |c_i^s - c_j^s|, \qquad \forall i < j; \forall s \tag{6.2}$$

$$l_i^s + \sum_z [r_{iz}(C_z^s - L_z^s)] \leq c_i^s \leq \sum_z [r_{iz}(C_z^s + L_z^s)] - l_i^s, \qquad \forall i; \forall s \tag{6.3}$$

$$lb_i \leq 2l_i^s \leq ub_i, \qquad \forall i \tag{6.4}$$

$$z_{ij}^x + z_{ji}^x + z_{ij}^y + z_{ji}^y = 1, \qquad \forall i < j \tag{6.5}$$

$$\sum_z r_{iz} = 1, \qquad \forall i \tag{6.6}$$

$$c_i^s + l_i^s \leq c_j^s - l_j^s + L^s z_{ij}^s, \qquad \forall i \neq j; \forall s \tag{6.7}$$

$$a_i l_i^x + 4\bar{x}^2 l_i^y \geq 2a_i\bar{x}, \qquad \forall lb_i^x \leq \bar{x} \leq ub_i^x, \tag{6.8}$$

$$z_{ij}^s \in [0, 1], r_{iz} \in [0, 1] \qquad \forall i, j; \forall s \tag{6.9}$$

where

$$\bar{x} = lb_i^x + \frac{\lambda}{\Delta - 1}(ub_i^x - lb_i^x), \forall \lambda = 0, 1, \ldots, \Delta - 1, \text{for any selected integer } \Delta \geq 2. \quad (6.10)$$

The MIP-FLPAL is very similar to the MIP-FLP in terms of the objective function and the constraints. The only difference is that in the MIP-FLPAL each department is constrained within the zone that the department is assigned to as shown in (6.3), while in the MIP-FLP each department is only constrained within the facility. In (6.6) each department must be assigned to only one zone.

We conduct a series of numerical tests to test the performance of the MIP-FLPAL model for solving the FLPAL. The data sets we use in this test are revised from the data sets used in the research conducted by Sherali, Fraticelli and Meller regarding the FLP2 model [61]. The properties of these data sets are summarized in Table 6.1. All numerical tests are conducted on a computer with a Pentium IV 3.2M Hz CPU and 2.0 GB of physical memory. The optimal solutions and the run time are summarized in Table 6.1. The detailed description of the data sets and the optimal solutions are given in Appendix C.1.

Table 6.1: Summary of the Optimal Solutions for Test Data Sets.

Data Set	Zone Num.	Dept. Num.	Area Utilization	Optimal Solution	Run Time (sec.)
FO7a-1	3	7	87%	20.10	34.34
FO7a-2	3	7	87%	20.10	26.77
O7a-1	3	7	87%	133.91	359.59
O7a-2	3	7	87%	133.39	260.11
O8a	4	8	88%	293.47	2761.76
O9a	4	9	80%	232.71	10595.11

Data Set O9a is the largest problem we can solve due to the limitation of physical memory on the test computer. Obviously, similar to the MIP-FLP, MIP-FLPAL can only solve limited-sized FLPAL problems. It is interesting to note that MIP-FLPAL appears to be similar in difficulty as compared to MIP-FLP.

Therefore, we need a heuristic for solving the larger-sized problems that are typical of industrial applications. In the remainder of this chapter we present our genetic algorithm based heuristic, SEQUENCE-AL, to combine the sequence-pair representation and the MIP-FLPAL to solve larger-sized FLPAL problems.

6.3 Encoding Scheme of SEQUENCE-AL

Due to the existence of the aisle structure, the facility is divided into several zones with fixed location and dimensions. A department must be assigned to only one zone. The original sequence-pair representation is not suitable for representing the FLPAL due to such a restriction. We propose a modified sequence-pair structure, which we name *zone-based sequence-pair*. A zone-based sequence-pair consists of a two-level hierarchical structure. The higher level is a parent sequence-pair, which is determined *a priori* and is used to represent the relative location relationship between zones according to the aisle structure in the facility. For example, for the facility with aisle structure shown in Figure 6.2(a), the parent sequence-pair is given as follows:

$$(\Gamma_+, \Gamma_-) = ((I, III, IV, II, V, VI), \ (III, IV, VI, V, I, II)).$$

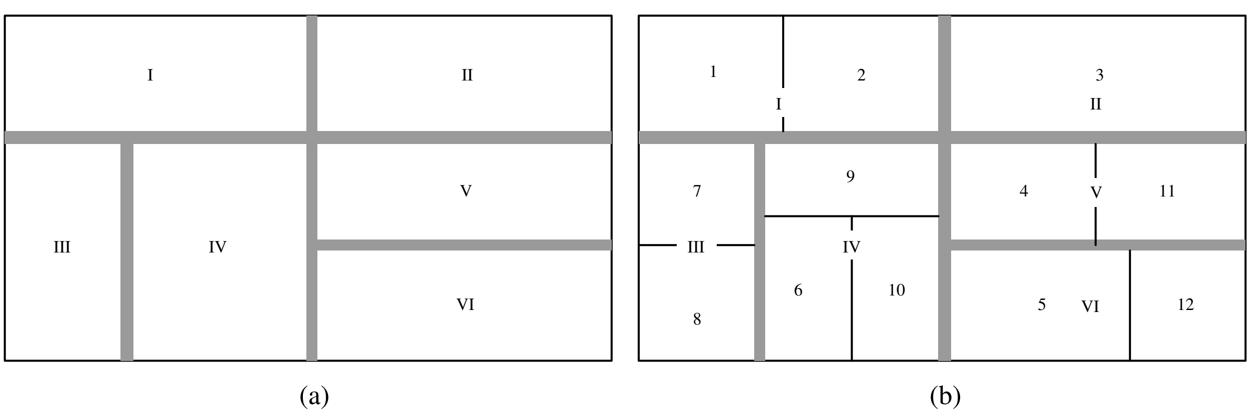


Figure 6.2: A Facility Layout with (a) Aisle Only and (b) Aisle and Departments.

The lower level of a zone-based sequence-pair is made up of several child sequence-pairs. Each child sequence-pair corresponds to one of the zones and is used to represent the relative location relationship of the departments assigned to that zone. For example, for sub-area IV, the corresponding child sequence-pair is $(\Gamma_+, \Gamma_-) = ((9, 6, 10), (6, 10, 9))$. The complete sequence-pair is obtained by replacing the zones in the parent sequence-pair with their corresponding child sequence-pairs. The resulting sequence-pair for the layout shown in Figure 6.2(b) is as follows:

$$\{[(1, 2), (7, 8), (9, 6, 10), (3), (4, 11), (5, 12)], [(8, 7), (6, 10, 9), (5, 12), (4, 11), (1, 2), (3)]\}$$

Therefore, given a zone-based sequence-pair, we not only know the relative location relationship between departments, but also the assignment of the departments to the zones. Therefore, for any given zone-based sequence-pair, we can simplify the MIP-FLPAL model by setting the values for all of the binary variables in the model. We use the position-pair based string as our encoding scheme for SEQUENCE-AL.

6.4 Department Assignment Operator

We present an assignment operator to generate the zone-based sequence-pair from a regular sequence-pair in this section.

Given a regular sequence-pair, (Γ_+, Γ_-), we first randomly choose (with equal probability) one sequence from Γ_+ and Γ_- as the primary sequence. The other sequence is used as the secondary sequence. In general, we use the primary sequence to determine the assignment of the departments to the zones and then alter the positions of the departments in the secondary sequence according to the assignment of the departments to the zones and the relative positions of the departments in the original secondary sequence.

To represent the process of transforming a regular sequence-pair into a zone-based sequence-pair, the following notation is used:

(Γ_+, Γ_-)	The given sequence-pair.
(Γ_+^Z, Γ_-^Z)	The sequence-pair corresponding to the zone layout, which is known *a priori* due the fixed location and dimensions of the zones.
Γ_d	The primary sequence for (Γ_+, Γ_-).
Γ_c	The initial secondary sequence for (Γ_+, Γ_-).
Γ_c'	The resulting secondary sequence for (Γ_+, Γ_-).
Γ_d^Z	The zone sequence that corresponds to the primary sequence. That is, if Γ_+ is used as the primary sequence, then $\Gamma_d^Z = \Gamma_+^Z$. Otherwise, $\Gamma_d^Z = \Gamma_-^Z$.
Γ_c^Z	The zone sequence that corresponds to the secondary sequence.
a_i	The area of the ith department in Γ_d $(i = 1, \ldots, N)$.
A_k	The unassigned area of the kth zone in Γ_z.
$\bar{A}_k$	The area of the kth zone in Γ_z $(k = 1, \ldots, Z)$.
r_{ik}	The binary variable that is used to denote whether Department i is assigned to Zone k. If Department i is assigned to Zone k, $r_{ik} = 1$. Otherwise, $r_{ik} = 0$.

The following procedure is used to determine the assignment of the departments to the zones and to transform the regular sequence-pair into a zone-based sequence-pair:

1. Set $r_{ik} = 0$ $(\forall i, k)$ and $A_k = \bar{A}_k$ $(\forall k)$. Then set $i = 1$ and $k = 1$.

2. If $a_i < A_k$, set $r_{ik} = 1$, $A_k = A_k - a_i$, and then set $i = i + 1$ and go to Step 3. Otherwise, let $k = k + 1$ and go to Step 4.

3. If $i \leq N$, go to Step 2. Otherwise, go to Step 5.

4. If $k \leq Z$, go to Step 2. Otherwise, stop and the departments cannot be assigned to the zones for the given sequence-pair and the chosen primary sequence.

5. For each zone in Γ_c^Z, generate the child sequence composed of the departments that are assigned to the zone. The relative positions of the departments within each zone are determined by the relative positions of these departments in Γ_c. Combine these child

sequences based on the sequence of zones in Γ_c^Z to generate a new secondary sequence, Γ_c'. Stop and return the resulting sequence-pair by replacing Γ_c with Γ_c'.

The following example illustrates how to transform a regular sequence-pair into a zone-based sequence-pair.

In this example we are given a FLPAL where there are nine departments to be allocated within a facility of dimensions 13×15. The existing aisle structure divides the facility into four zones as shown in Figure 6.3.

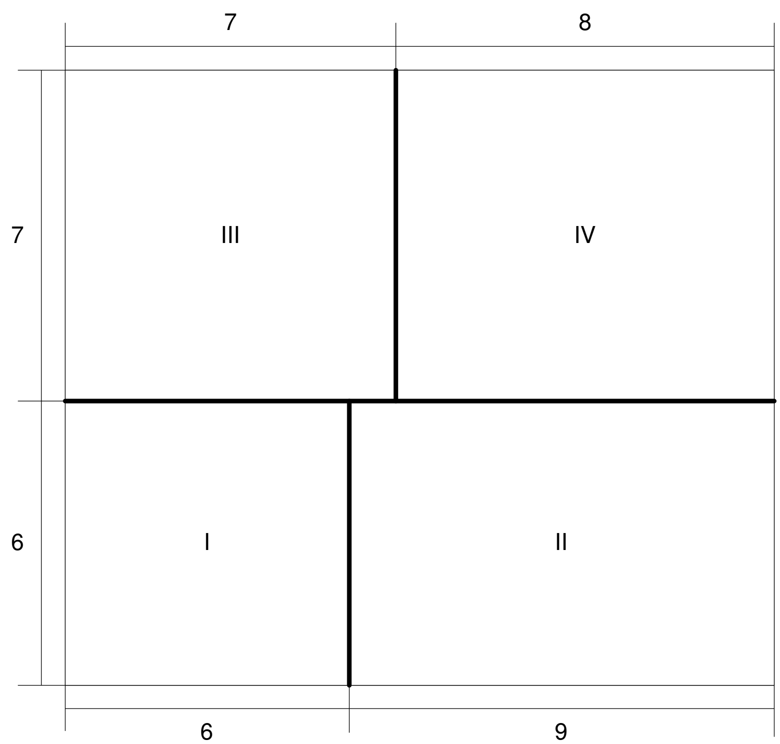


Figure 6.3: Illustration of the Aisle Structure for the Example Problem.

According to the procedure we presented in Section 3.2.1, the zone sequence-pair is given as $(III, IV, I, II), (I, II, III, IV)$. The department area information is given as follows:

Dept.	1	2	3	4	5	6	7	8	9
Area	16	16	16	36	36	9	9	9	9

Given a sequence-pair, $(\Gamma_+, \Gamma_-) = (2,7,9,4,6,1,3,5,8), (4,1,3,9,8,2,7,5,6)$, we randomly choose Γ_+ as the primary sequence. The zone sequence corresponding to the primary sequence is (III, IV, I, II). The first zone in Γ_d^Z is Zone III. So, we first assign as many as possible departments, which are counted from the left hand side of the Γ_+, to Zone III. The maximum number of departments that can be assigned to Zone III without violating the area restriction of Zone III is equal to 3 (Departments 2, 7 and 9). We then continue assigning the remaining departments to Zone IV, Zone I and Zone II, respectively. The resulting assignment is shown in Figure 6.4

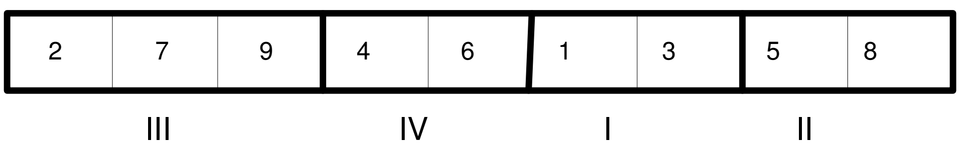


Figure 6.4: Assignments of the Departments to the Zones for the Example Problem.

We then alter the secondary sequence, which is Γ_- in this case, to comply with the assignment of departments to zones determined by the primary sequence. The zone sequence corresponding to Γ_- is (I, II, III, IV), where the first zone is Zone I. We first generate the child sequence for Zone I. From the department assignment shown in Figure 6.4, the departments assigned to Zone I are Departments 1 and 3. Noting that the relative position between Departments 1 and 3 in Γ_- is that Department 1 is placed before Department 3, so the child sequence for Zone I is $(1, 3)$; i.e., the first two positions in the new secondary sequence, Γ'_-, are occupied by Departments 1 and 3, respectively. We continue the process to decide the other positions in Γ'_- according to the department assignment and the relative position relationship provided in Γ_-. The resulting Γ'_- is $(1,3,8,5,9,2,7,4,6)$. So the sequence-pair after the department assignment operator is given as follows: $((2,7,9),(4,6),(1,3),(5,8)),((1,3),(8,5),(9,2,7),(4,6))$. This sequence-pair is feasible with respect to department-to-zone assignments, as are all sequence-pairs after the department assignment operator.

6.5 Fitness Function, Selection Rule and Elitism Operator in SEQUENCE-AL

In SEQUENCE-AL we use the same fitness function as we used for SEQUENCE in Chapter 4, which is calculated based on the objective function value of the sequence-pair optimal solution of the chromosomes. That is,

$$F(g,m) = f_g^0 - f_{gm}, \qquad \forall g \in \{1,\dots,G\}, \forall m \in \{1,\dots,M\}, \tag{6.11}$$

where $F(g,m)$ is the fitness score function for Chromosome m in Generation g, f_{gm} is the objective function value of the sequence-pair optimal solution corresponding to Chromosome m in Generation g and $f_g^0 = \max_m \{f_{gm}\}$. Parameter G is the total number of generations and M is the size of population in each generation.

Given the above fitness score function, one of the most widely applied selection rules, the "roulette wheel," is used in SEQUENCE-AL. Roulette wheel selection is a fitness-proportionate selection, where each chromosome is assigned a slice of a circular "roulette wheel," the size of the slice being proportional to the individual's fitness score in comparison with the fitness scores of the other chromosomes in the population. The probability that a chromosome is selected on a particular spin is given as follows:

$$p_{gm} = \frac{F(g,m)}{\sum\limits_{k=1}^{M} F(g,k)}, \qquad \forall g \in \{1,\dots,G\}, m \in \{1,\dots,M\}. \tag{6.12}$$

We use a very similar elitism operator as we used in Chapter 4, where the traditional elitism operator is combined with a best two-way exchange operator. The only difference is that for the best two-way exchange operator used in SEQUENCE-AL, we need to check the area feasibility of the current department assignment when considering whether the positions of two departments in the sequence-pair can be exchanged or not. That is, we filter the two-way exchanges that lead to a department assignment violating the zone area constraints.

6.6 GA Operator Design in SEQUENCE-AL

For the GA operators, we directly apply the crossover and the mutation operators we designed for SEQUENCE to SEQUENCE-AL.

Due to the restriction caused by the zones, the offspring chromosomes after the crossover and mutation operators may not be a feasible zone-based sequence-pair. Therefore, we apply the department assignment operator to the sequence-pairs corresponding to the offspring chromosomes after the crossover and mutation operators to guarantee that the offspring chromosomes are feasible zone-based sequence-pairs.

6.7 Algorithm Scheme of SEQUENCE-AL

The following notation is used to describe the algorithm SEQUENCE-AL:

G	Maximum number of generations.
M	Population size of each generation.
m	Counter for the number of the chromosomes in the new population.
i	Generation index.
j, k	Chromosome indices.
$F(i, j)$	Fitness function value of Chromosome j in Generation i.
p_{ij}	Selection probability of Chromosome j in Generation i based on the roulette selection rule.
$\bar{F}_i$	The average fitness function value of Generation i.

g_i^*	The fittest chromosome in Generation i.
f_i^*	The objective function value of the sequence-pair optimal solution corresponding to g_i^*.
g^*	The overall best chromosome.
f^*	The objective function value of the sequence-pair optimal solution corresponding to g^*.
K	The number of the best chromosomes to be copied to the next generation with the elitism operator.
PC	The probability of applying the crossover operator to the selected chromosomes.
PM	The probability of applying the mutation operator to the selected chromosomes.
S	The maximum number of successive generations without producing a new g^*.
ϵ	The tolerance value for the percentage difference between $\bar{F}_i$ and $\bar{F}_{i+1}$.

The genetic algorithm procedures of SEQUENCE-AL to solve the sequence-pair based MIP-FLPAL are given as follows:

1. Generate the initial generation, Generation 0, of size M, where we first transform each generated sequence-pair into a zone-based sequence-pair by using the department assignment operator and then transform each zone-based sequence-pair into a position-pair based chromosome.

2. Each resulting chromosome in Generation 0 corresponds to a zone-based feasible sequence-pair and has an objective function value of f_{0j}. Calculate $F(0, j)$ by using (6.11) and p_{0j} by using (6.12). Record the fittest chromosome, g_0^*, and its corresponding objective function value, f_0^*. Set $i = 0$, $g^* = g_0^*$ and $f^* = f_0^*$.

3. Apply the revised elitism operator to Generation i as follows:

   (a) Select the fittest K chromosomes from Generation i, which include the best chromosome of Generation i, g_i^*.

   (b) If g_i^* is not a chromosome that represents a two-way optimal sequence-pair, apply the best two-way exchange operator to g_i^*. The resulting, g_i^*, represents a chromosome corresponding to a two-way optimal sequence-pair.

(c) Copy these K chromosomes to Generation $i+1$ and set $m = K$.

4. To fill the remaining $M - m$ chromosomes in the new generation, randomly select two different parent chromosomes, j_1 and j_2, from Generation i based on the roulette wheel selection rule.

5. With the probability of PC and PM, where $PC + PM = 1$, apply crossover and mutation operators as shown below to Chromosomes j_1 and j_2 to generate two offspring chromosomes, k_1 and k_2, for Generation $i+1$.

   (a) Generate a random number, r, from a standard uniform distribution $U(0,1)$.

   (b) If $r \leq PC$, apply the crossover operator to Chromosomes j_1 and j_2 to generate Chromosomes k_1 and k_2.

   (c) If $r > PC$, apply the random 2-way exchange mutation operator to j_1 and j_2 to generate Chromosomes k_1 and k_2.

6. Apply the department assignment operator to Chromosomes k_1 and k_2 to transform them into feasible zone-based sequence-pairs.

7. After translating Chromosomes k_1 and k_2 into sequence-pairs, set the corresponding binary variables in the MIP-FLP model, and then solve the simplified MIP-FLP model to optimality. If Chromosome k_i $(i = 1, 2)$ corresponds to a feasible sequence-pair, add Chromosome k_i to the new population. Update the value of m as appropriate.

8. If $m < M$, go to Step 3. Otherwise, set the new generation as the current generation by $i = i + 1$ and $m = 0$.

9. In Generation i, calculate $F(i,j)$ using (6.11) and p_{ij} using (6.12) for each chromosome. Record the fittest chromosome, g_i^*, and its corresponding objective function value, f_i^*. If $f_i^* < f^*$, set $g^* = g_i^*$ and $f^* = f_i^*$.

10. If at least one of the following two stopping criteria is satisfied: (1) $i \geq G$; (2) $\frac{\|\bar{F}(i) - \bar{F}(i-1)\|}{\bar{F}(i-1)} \leq \epsilon$ and g^* has not been updated for S generations, go to Step 11. Otherwise, go to Step 2.

11. Apply the best two-way exchange operator to the best T chromosomes of the last generation. If the best chromosome of the T chromosomes after applying the best two-way exchange operator is better than g^*, update g^* and f^*. Stop SEQUENCE-AL and output g^* and f^*.

6.8 Parameter Settings of SEQUENCE-AL

Parameter setting is another important aspect in GA design since it has a great impact on the performance of the GA. However, these parameters typically interact with each other and their effects cannot be isolated, so it is extremely difficult to optimize them one at a time.

Although parameter settings have been discussed extensively in the GA literature, no conclusive results have been presented. So, in most cases, researchers either conduct experimental tests to find "good" parameter settings or they set the parameters according to experience or knowledge about the specific problems where GAs are applied. Through an experimental design, we set the parameters for SEQUENCE-AL as follows: $G = 200$, $M = 50$, $K = 10$, $PC = 0.90$, $PM = 0.10$, $S = 10$, $\epsilon = 0.1\%$ and $T = 5$.

6.9 Numerical Experiments

To illustrate the effectiveness of SEQUENCE-AL for solving the FLPAL, a series of numerical experiments based on different sized test problems are conducted in two phases: (1) optimality comparison test; and (2) heuristic comparison test. In the optimality comparison test, the SEQUENCE-AL solutions are compared with the optimal solutions for the data sets we used in Section 6.2 to show the quality of the SEQUENCE-AL solutions for these test data sets. We then consider larger-sized test problems and compare SEQUENCE-AL with two other heuristics: MULTIPLE-AL and SABLE-AL, which are revised versions of two well-know FLP heuristics, MULTIPLE [11] and SABLE [43]. All numerical tests are conducted on a computer with a Pentium IV 3.2M Hz CPU and 2.0 GB of physical memory.

6.9.1 Optimal Comparison Test

In the optimality comparison test, for each test data set, we run SEQUENCE-AL until the optimal solution reported in 6.2 is found. The maximum number of runs of SEQUENCE-AL for the test problems is 5; i.e., if SEQUENCE-AL cannot achieve the optimal solution in 5 runs, we stop SEQUENCE-AL and report the optimality gap between the best SEQUENCE-AL solution and the optimal solution. Correspondingly, the reported SEQUENCE solution time is the total run time for SEQUENCE to find the optimal solution or the total run time of 5 runs if SEQUENCE fails to find the optimal solution in 5 runs.

The results of the optimality comparison test are summarized in Table 6.2. Here the optimality gap represents the percentage of the difference between the objective function value of the best SEQUENCE-AL solution and the objective function value of the optimal solution for each test data set.

Table 6.2: Comparison Between SEQUENCE-AL Solutions and the Optimal Solutions.

Problem Name	Optimal Solution		SEQUENCE Solution			Optimality Gap
	Objective	Time (sec.)	Objective	Num. of Runs	Time (sec.)	
FO7a-1	20.10	34.34	20.10	1	555	0%
FO7a-2	20.10	26.77	20.10	1	187	0%
O7a-1	133.91	359.59	133.91	1	276	0%
O7a-2	133.39	260.11	133.39	1	161	0%
O8a	293.47	2761.76	293.47	2	394	0%
O9a	232.71	10595.11	237.76	5	1426	2.17%

From Table 6.2 we can see that SEQUENCE-AL achieves the optimal solutions for 5 of 6 test data sets in 5 runs and the optimality gap for the one problem that SEQUENCE-AL did not solve to optimality in 5 runs is only about 2%. Therefore, according to the results for the optimality comparison test, the best solution from 5 runs of SEQUENCE-AL is equal to or at least very close to the global optimal layout solution and the solution time for the larger test problems is greatly reduced. The detailed SEQUENCE-AL solutions for all data sets used in the optimality comparison test are summarized in Appendix C.1.

6.9.2 Heuristic Comparison Test

In the heuristic comparison test we use SEQUENCE-AL to solve 5 larger-sized data sets revised from the data sets we used in Chapter 4. We compare SEQUENCE-AL solutions with two other heuristics: MULTIPLE-AL and SABLE-Al, which are revised versions of two well-know FLP heuristics, MULTIPLE [11] and SABLE [43], respectively.

We first describe briefly how we revise MULTIPLE and SABLE to extend these two heuristics to solve the FLPAL.

MULTIPLE [11] and SABLE [43] are two discrete representation based heuristics to solve the multiple-floor FLP. Both heuristics improve the layout based on a spacefilling curve representation. The spacefilling curve is a continuous curve going through all of the available facility area on the same floor. All non-fixed departments are placed along the spacefilling curve. Such a representation makes it difficult to apply the zone restrictions to the FLP where the departments may cross the boundary of the zones along the continuous spacefilling curve. Our methodology is to first transform a single-floor FLPAL into a multiple-"floor" FLP, where each floor represents a zone, and then we solve the multiple-floor FLP by MULTIPLE and SABLE to obtain heuristic comparison solutions.

Given an FLPAL with 3 zones partitioned by the aisle structure, we transform the FLPAL into a multiple-floor FLP as illustrated in Figure 6.5.

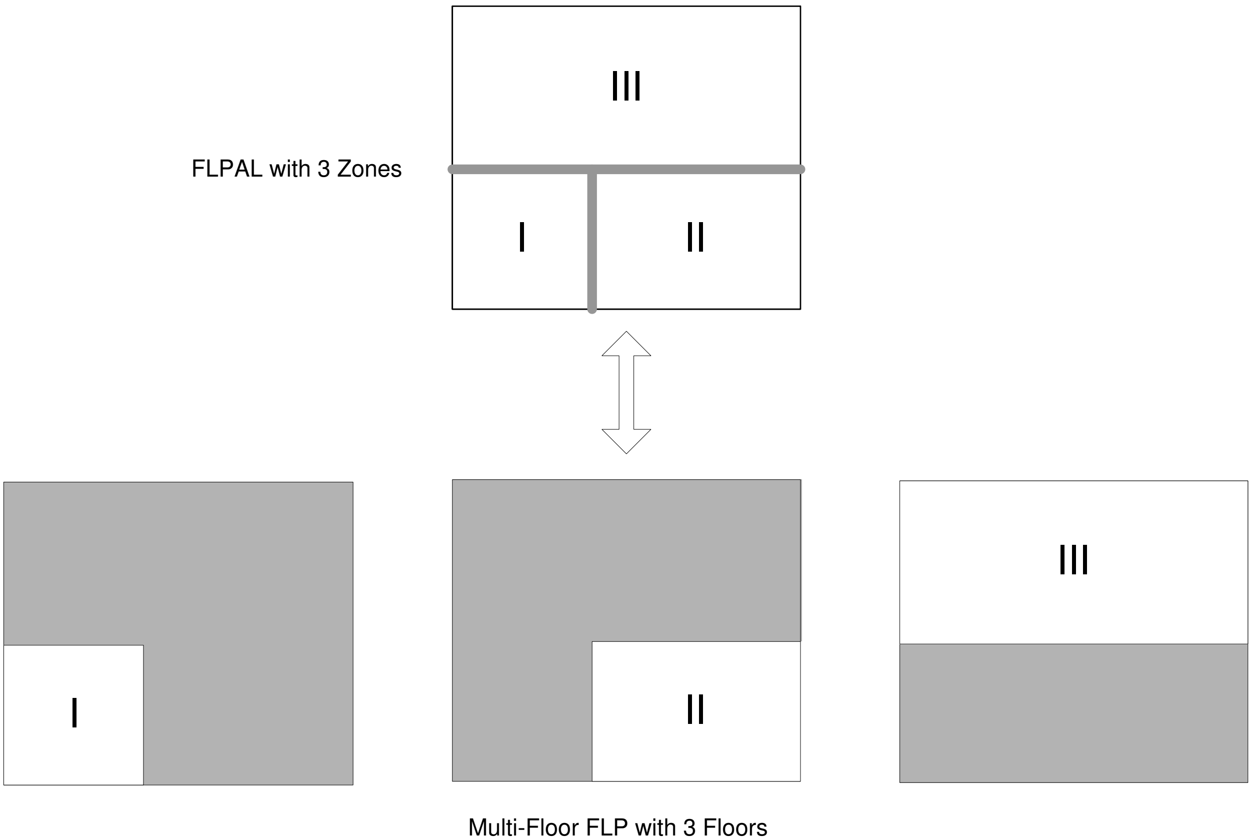


Figure 6.5: Illustration of Transforming a FLPAL into a Multi-Floor FLP.

We then substitute the original multiple-floor FLP objective function, which includes both a horizontal distance term and a vertical distance term with the following objective function:

$$\min \quad \sum_{i} \sum_{j>i} f_{ij}(|c_i^x - c_j^x| + |c_i^y - c_j^y|) \tag{6.13}$$

where c_i^x and c_i^y are the x- and y-coordinates of Department i in the horizontal plane. With such a modification, departments cannot cross the boundaries of the zones since they can only be placed on a single floor in MULTIPLE and SABLE. The revised objective function value removes the impact of the vertical distance between departments and calculates the material handling cost in exactly the same way as if all departments were on the same floor.

The test data sets we used for the heuristic comparison test for SEQUENCE-AL are revised from the data sets we used to test SEQUENCE in Chapter 4. The properties of the test data sets are summarized in Table 6.3. We run MULTIPLE-AL, SABLE-AL and SEQUENCE-AL 10 times for the test data sets and compare both the best solutions and the maximum shape factor (the same parameter we used as a measurement of department shape in the heuristic comparison tests of Chapters 4 and 5, which is defined in (4.8)) in the best solutions to illustrate that SEQUENCE-AL can provide overall better solutions in terms of both the material handling distances and the resulting department shapes.

Table 6.3: Properties of the Test Problems for the Heuristic Comparison Test.

Problem	Dept. Num.	Zone Num.	Flow Density	Area Utilization
M11a	11	3	32.73%	83.33%
BM12a	12	3	25.76%	100.00%
M15a	15	5	20.00%	87.56%
M25a	25	3	11.33%	80.00%
SC30a	30	4	11.49%	82.78%

The test results are summarized in Table 6.4. Through the heuristic comparison test we conclude that SEQUENCE-AL performs better than MULTIPLE-AL and SABLE-AL with respect to the test data sets in terms of the best objective function value and department shapes. The average improvement of the objective function value for the test data sets is 33.06%. The detailed solutions for these test data sets are given in Appendix C.2.

Table 6.4: Results of Heuristic Comparison Test.

Problem	Best Layout Solutions				Maximum Shape Factor		
	MULTIPLE	SABLE	SEQUENCE	Imp.	MULTIPLE	SABLE	SEQUENCE
M11a	1498.13	1458.67	1052.73	27.83%	1.34	1.34	1.25
BM12a	224.25	219.13	173.56	20.79%	1.13	1.38	1.25
M15a	41569.04	41747.39	29206.90	29.74%	1.45	1.38	1.34
M25a	2111.33	2065.50	1040.81	49.61%	1.34	1.34	1.34
SC30a	6052.89	5860.27	3671.54	37.35%	1.51	1.38	1.34

The solution time of SEQUENCE-AL for finding the best solutions in 10 runs and the total run time of 10 runs of SEQUENCE-AL for all test data sets used in the heuristic comparison test are given in Table 4.9. For the largest problem SC30, where we have 30 departments and 4 zones, the total runtime of 10 runs is less than 21 hours, which, in our opinion, is justifiable for such a large problem given that FLP design is not a real-time decision.

Table 6.5: Solution Times for the Data Sets Used in the Heuristic Comparison Test.

Problem	Solution Time (Hrs.)	Total Time of 10 Runs (Hrs.)
M11a	2.03	2.20
BM12a	2.61	4.28
M15a	0.54	2.13
M25a	1.82	7.69
SC30a	3.95	20.34

6.10 Summary

In this chapter we conducted research on the continuous-representation based facility layout problem with an existing aisle structure. Such an aisle structure partitions the facility into different zones while the departments are typically not allowed to cross the aisle (i.e., each department must be contained completely in one zone). We first formulated the problem with an MIP model and tested the capability of the model for solving the FLPAL. The test showed that the MIP model can only solve limited-sized problems (no more than 9 departments), and a heuristic is needed for solving larger-sized industrial problems.

We presented a genetic algorithm based heuristic, named SEQUENCE-AL, which combines the sequence-pair representation with the MIP-FLPAL model, to solve the FLPAL. In order to consider the aisle structure, in SEQUENCE-AL we revised the original sequence-pair representation to a zone-based sequence-pair representation. We also developed a department assignment operator to assign the departments to the zones, which is used to translate an original sequence-pair to a zone-based sequence-pair. The effectiveness of SEQUENCE-AL was illustrated through a series of tests, where we compared the SEQUENCE-AL solutions with both the optimal solutions and two other heuristics' solutions.

Chapter 7

MIP Model and a Heuristic for the FLP with Non-Rectangular-Shaped Departments

7.1 Facility Layout Problem with Non-Rectangular Departments

In many industrial applications there are examples where departments within the facility are intended to be non-rectangular in shape (e.g., L-shaped, U-shaped, T-shaped departments in an assembly-line facility). However, there is little research with respect to the FLP to address non-rectangular-shaped departments under the continuous representation. In this chapter we propose a MIP model to solve the FLP with non-rectangular departments (FLPNR) and a heuristic, which we name SEQUENCE-NR, based on the sequence-pair representation.

Some non-rectangular departments can be addressed as rectangular-shaped departments because the "void" area in their bounding rectangular is not allowed to be occupied by other departments due to the production requirements, such as Departments 4 and 7 in Figure 7.1. Since the area and dimension of this type of non-rectangular departments are actually the area and dimension of their bounding rectangular, this type of non-rectangular department can be treated as a rectangular department with fixed dimensions. The non-rectangular departments we address in this chapter are the "true" non-rectangular departments, such as Departments 3 and 5 in Figure 7.1. To our knowledge, there is very little research conducted to solve the FLP with arbitrarily non-rectangular departments based on the continuous representation, both in the area of exact algorithms and heuristic approaches, although non-rectangular departments are very common in industrial applications.

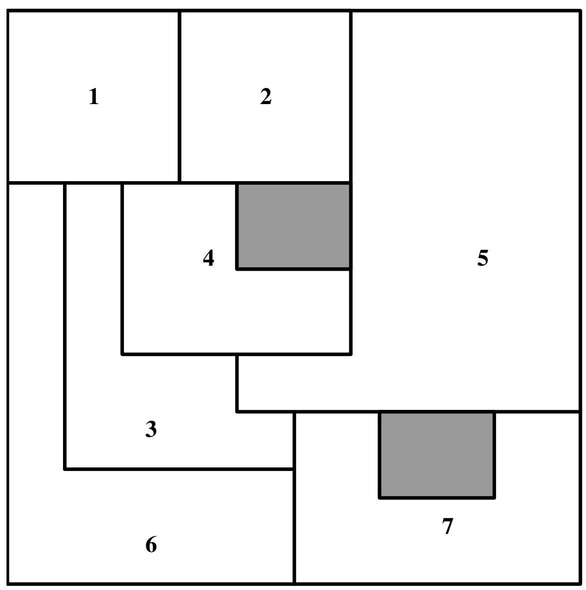


Figure 7.1: A Layout Including Compact and Bounded Non-Rectangular Departments.

In this chapter we first propose an MIP model to formulate a specific type of the FLPNR, where all non-rectangular departments are L-shaped. Since department shapes and I/O point locations are known, we use a distance measure based on output point to input point distances instead of centroid-to-centroid distances. We then extend the MIP model to formulate the generic FLPNR (MIP-FLPNR) with arbitrarily non-rectangular-shaped departments using this distance metric. A sensitivity analysis is conducted to test the impact of different factors on the performance of the proposed MIP-FLPNR model. A numerical test on the computational efforts of the MIP-FLPNR model is also conducted to explore the computational capability of the MIP-FLPNR to solve the different types of the FLPNR. Based on that, we propose a genetic algorithm, SEQUENCE-NR, that combines the sequence-pair representation and the MIP-FLPNR to solve larger-sized FLPNR problems. Different design issues for SEQUENCE-NR are discussed in detail. In addition to SEQUENCE-NR, we also provide two repair operators to address different constraints in the MIP-FLPNR that determine the feasibility of a sequence-pair with respect to the MIP-FLPNR. To illustrate the effectiveness of SEQUENCE-NR, we compare the SEQUENCE-NR solutions with both optimal solutions and another heuristic's solutions, as shown in a set of numerical tests.

7.2 An MIP Model for the FLP with Non-Rectangular Departments

7.2.1 An MIP Model for the FLP with L-Shaped Departments

Since L-shaped departments are one of the simplest non-rectangular department types, we first formulate the FLP with only L-shaped departments. Given an L-shaped department, we assume that the dimension of the L-shaped department and the relative location of the input/output points are known *a priori*. For any L-shaped department, we can always partition it into two adjacent rectangular sub-departments vertically as shown in Figure 7.2(a). After indexing the sub-departments, we can have four possible orientations for the L-shaped department as shown in Figure 7.2. For the convenience of defining department dimensions, location parameters and decision variables, we also denote the orientation in Figure 7.2(a) as the standard orientation of an L-shaped department (in particular, sub-department 1 must be to the left of sub-department 2). The following MIP model is proposed to solve the FLP with L-shaped departments.

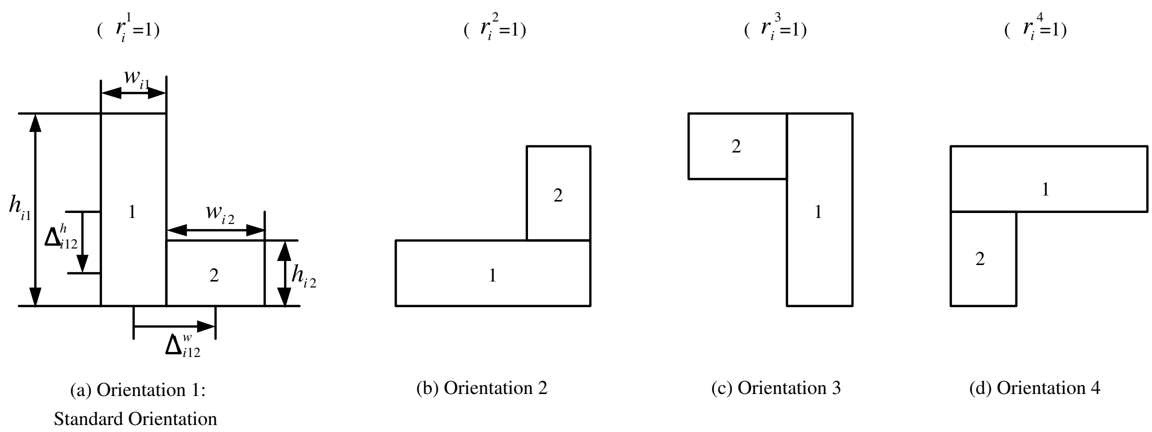


Figure 7.2: Four Different Orientations of an L-Shaped Department.

Parameters:

N	Set of L-shaped departments.
i	Department indices ($i \in N$).
$i(i')$	Sub-department indices of L-shaped department i ($i \in N, i' = 1, 2$).
$h_{i(i')}$	Height of sub-department i' for L-shaped department i in standard orientation.
$w_{i(i')}$	Width of sub-department i' for L-shaped department i in standard orientation.
$\Delta^h_{i(1)(2)}$	The height difference of subdepartments 1 and 2 centroids for L-shaped department i in standard orientation ($\Delta^h_{i(1)(2)} = 1/2(h_{i(1)} - h_{i(2)})$).
$\Delta^w_{i(1)(2)}$	The width difference of subdepartments 1 and 2 centroids for L-shaped department i in standard orientation ($\Delta^w_{i(1)(2)} = 1/2(w_{i(1)} + w_{i(2)})$).
FI^s_k	The location of input point k of the facility.
FO^s_k	The location of output point k of the facility.
$a^s_{i(i')}$	The relative location from the output point of department i located in sub-department i' to the centroid of i' in the s-direction as shown in Figure 7.6.
$b^s_{i(i')}$	The relative location from the input point of department i located in sub-department i' to the centroid of i' in the s-direction as shown in Figure 7.6.

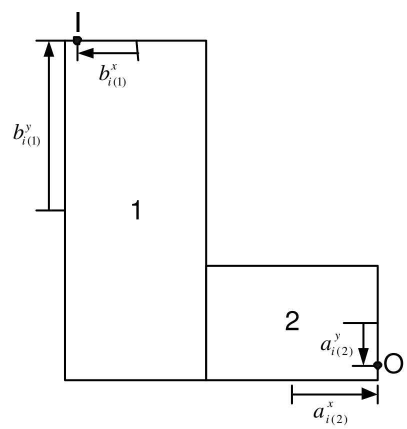


Figure 7.3: Illustration of the Input/Output Points of Department i.

$f_{i(i')j(j')}$ The material flow from the output point of department i located in sub-department i' to the input point of department j located in sub-department j'.

$f^I_{i(i')k}$ The material flow from input point k of the facility to the input point of department i located in sub-department i'.

$f^O_{i(i')k}$ The material flow from the output point of department i located in sub-department i' to output point k of the facility.

Decision Variables:

$c^s_{i(i')}$ Centroid of sub-department i' of L-shaped department i in the s-direction.

$l^s_{i(i')}$ Side length of sub-department i' of L-shaped department i in the s-direction.

$I^s_{i(i')}$ Location of input point of L-shaped department i located in sub-department i' in the s-direction.

$O^s_{i(i')}$ Location of output point of L-shaped department i located in sub-department i' in the s-direction.

$z^s_{i(i')j(j')}$ Binary decision variables, which denote relative locations of sub-department i' of i and j' of j ($i \neq j$) with respect to x- and y-coordinates and are used to prevent the overlapping of the sub-departments from different L-shaped departments.

r_i^q Binary decision variables ($q = 1, 2, 3, 4$), which denote the orientation of the L-shaped department i and are used to ensure the correct connection of sub-departments in the same L-shaped department, the correct dimension of sub-departments, and the correct locations of the I/O points of the L-shaped departments.

Given L-shaped departments i, j and $i \neq j$,

$$z^s_{i(i')j(j')} = \begin{cases} 1 & \text{if sub-department } i' \text{ of } i \text{ proceeds sub-department } j' \text{ of } j \text{ in the } s\text{-direction}, \\ 0 & \text{otherwise.} \end{cases}.$$

Given L-shaped department i and $q = 1, 2, 3, 4$,

$$r_i^q = \begin{cases} 1 & \text{if department } i \text{ takes Orientation } q \text{ as illustrated in Figure 7.2}, \\ 0 & \text{otherwise.} \end{cases}.$$

The MIP-FLP formulation for the FLP with all L-shaped departments is presented as follows:

$$\begin{aligned}
\min \quad & \sum_i \sum_{j>i} \sum_{i'} \sum_{j'} f_{i(i')j(j')}(|O^x_{i(i')} - I^x_{j(j')}| + |O^y_{i(i')} - I^y_{j(j')}|) + \\
& \sum_i \sum_{i'} \sum_k f^I_{i(i')k}(|FI^x_k - I^x_{i(i')}| + |FI^y_k - I^y_{i(i')}|) + \\
& \sum_i \sum_{i'} \sum_l f^O_{i(i')l}(|O^x_{i(i')} - FO^x_l| + |O^y_{i(i')} - FO^y_l|) && (7.1)\\
\text{s.t.} \quad & l^s_{i(i')} \le c^s_{i(i')} \le L^s - l^s_{i(i')}, && \forall i, i' \in \{1,2\}, s \quad (7.2)\\
& \sum_{q=1}^{4} r_i^q = 1, && \forall i \quad (7.3)\\
& c^x_{i(1)} = c^x_{i(2)} + (r_i^3 - r_i^1)\Delta^w_{i(1)(2)} + (r_i^4 - r_i^2)\Delta^h_{i(1)(2)}, && \forall i \quad (7.4)\\
& c^y_{i(1)} = c^y_{i(2)} + (r_i^1 - r_i^3)\Delta^h_{i(1)(2)} + (r_i^4 - r_i^2)\Delta^w_{i(1)(2)}, && \forall i \quad (7.5)\\
& l^x_{i(i')} = (r_i^1 + r_i^3)w_{i(i)} + (r_i^2 + r_i^4)h_{i(i')}, && \forall i, i' \in \{1,2\} \quad (7.6)\\
& l^x_{i(i')} + l^y_{i(i')} = w_{i(i')} + h_{i(i')}, && \forall i, i' \in \{1,2\} \quad (7.7)\\
& O^x_{i(i')} = c^x_{i(i')} + (r_i^1 - r_i^3)a^x_{i(i')} + (r_i^4 - r_i^2)a^y_{i(i')}, && \forall i, i' \in \{1,2\} \quad (7.8)
\end{aligned}$$

$$O^y_{i(i')} = c^y_{i(i')} + (r^1_i - r^3_i)a^y_{i(i')} + (r^2_i - r^4_i)a^x_{i(i')}, \qquad \forall i, i' \in \{1,2\} \tag{7.9}$$

$$I^x_{i(i')} = c^x_{i(i')} + (r^1_i - r^3_i)b^x_{i(i')} + (r^4_i - r^2_i)b^y_{i(i')}, \qquad \forall i, i' \in \{1,2\} \tag{7.10}$$

$$I^y_{i(i')} = c^y_{i(i')} + (r^1_i - r^3_i)b^y_{i(i')} + (r^2_i - r^4_i)b^x_{i(i')}, \qquad \forall i, i' \in \{1,2\} \tag{7.11}$$

$$\sum_s (z^s_{i(i')j(j')} + z^s_{j(j')i(i')}) = 1, \qquad \forall i \neq j; i', j' \in \{1,2\} \tag{7.12}$$

$$c^s_{i(i')} + l^s_{i(i')} \leq c^s_{j(j')} - l^s_{j(j')} + L^s(1 - z^s_{i(i')j(j')}), \quad \forall i \neq j; i', j' \in \{1,2\}, s \tag{7.13}$$

where objective function (7.1) minimizes the total material flow travel distances, including the internal material flow travel distances (material flow travel between L-shaped departments) and the external material flow travel distances (material flow travel between L-shaped department and the I/O points of the facility). The boundary of all L-shaped departments are constrained within the facility in (7.2). Only one orientation can be chosen according to (7.3). The sub-departments of the same L-shaped department are connected through (7.4)–(7.7) according to the orientation of the L-shaped department, where (7.4)–(7.5) ensure that the centroids of the two sub-departments of the L-shaped department are positioned correctly with respect to one another in different orientations and (7.6)–(7.7) guarantee that the dimensions of the sub-departments are set correctly in different orientations. The location of the I/O points of the sub-departments are determined with respect to different orientations in (7.8)–(7.11). The sub-departments of different L-shaped departments are prevented from overlapping in (7.12)–(7.13).

7.2.2 An MIP-FLP Model with General Non-Rectangular Departments

We now extend our model for the FLP with L-shaped departments to further consider the general FLPNR and present a generic mixed integer programming model for the FLPNR (MIP-FLPNR) in this section.

For a general non-rectangular-shaped rectilinear department, we can always partition it into a group of adjacent rectangular-shaped sub-departments by adding some dummy

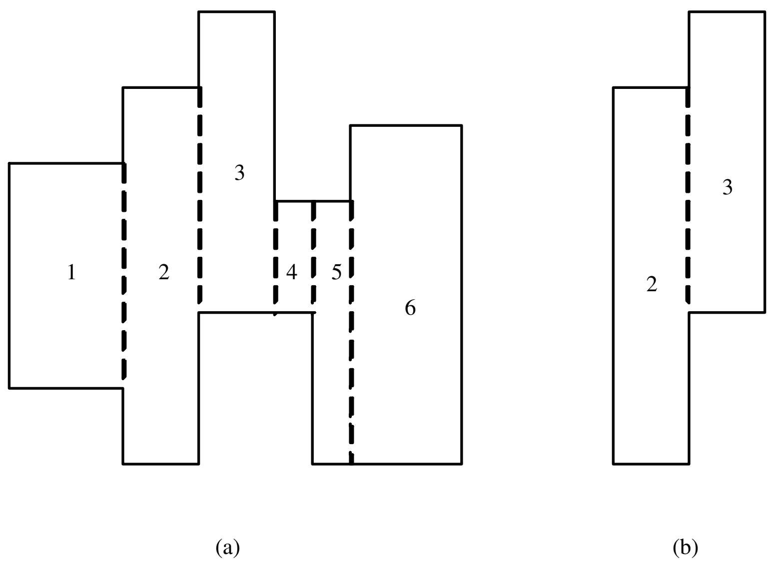


Figure 7.4: An Illustration of (a) a Partitioned Non-Rectangular Department and (b) a Pair of Adjacent Sub-Departments.

vertical borders. An illustration of such a partition is given in Figure 7.4(a), where a non-rectangular-shaped department is partitioned into six sub-departments. In such a case, we can take a pair of adjacent sub-departments as the basic "block" to form the non-rectangular department constraints. Therefore, if we can formulate the appropriate constraints to ensure that adjacent sub-departments are positioned correctly in different orientations, we will, by extension, tie together the entire non-rectangular department. For example, for the non-rectangular department shown in Figure 7.4(a), we can first formulate the MIP model to maintain the shape of the combined area consisting of sub-departments 1 and 2. Then, in the same way, we can maintain the shape of the combined area of sub-departments 2 and 3, and so on. The fundamental blocks of any non-rectangular department (i.e., the two adjacent rectangular sub-departments as shown in Figure 7.4(b)) can take one of the four possible orientations in the layout, which are summarized in Figure 7.5.

For the convenience of defining department dimensions, location parameters and decision variables, we give the following rules for department partitioning:

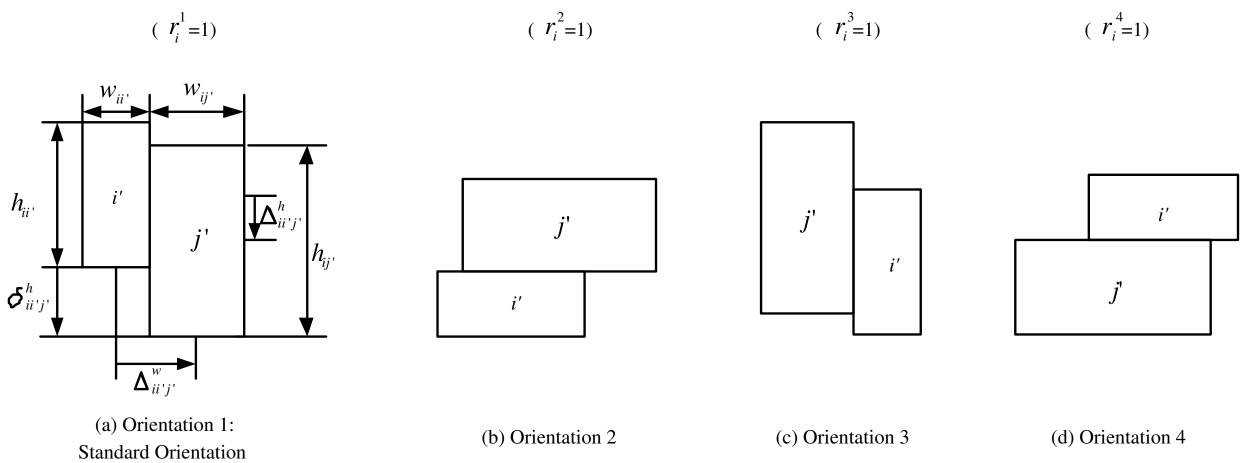


Figure 7.5: Four Orientations of an Adjacent Sub-Line Pair for a Non-Rectangular Department.

1. Each non-rectangular department can be placed in one of the four possible different orientations and one of them is taken as the standard orientation.

2. In the standard orientation, the non-rectangular departments are partitioned into all-rectangular sub-departments by vertical dummy borders only.

3. The sub-departments are ordered from left to right in the same way as shown in Figure 7.4 in the standard orientation; that is, for each adjacent sub-department pair, the sub-department with the lower index is to the left of the sub-department with the higher index in the standard orientation.

We now present the general MIP formulation for the FLP with arbitrarily non-rectangular departments, which is composed of a group of adjacent rectangular-shaped sub-departments.

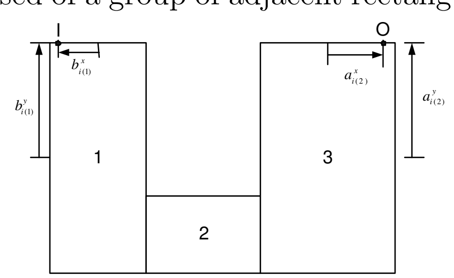


Figure 7.6: Illustration of the Input/Output Points of Generic Non-Rectangular Department.

New Parameters:

n	Number of departments.
N	Department set ($N = \{1, \ldots, n\}$).
i	Department indices ($i \in N$).
m_i	Number of sub-departments for department i.
M_i	Sub-department set for department i ($M_i = \{1, \ldots, m_i\}$).
$i(i')$	Sub-department indices of department i ($i' \in M_i$).
$h_{i(i')}$	Height of sub-department i' for department i in the standard orientation.
$w_{i(i')}$	Width of sub-department i' for department i in the standard orientation.
$\Delta^h_{i(i')(j')}$	The height difference of sub-department i' and j' ($j' = i' + 1$) centroids for department i in the standard orientation.
$\Delta^w_{i(i')(j')}$	The width difference of sub-department i' and j' ($j' = i' + 1$) centroids for department i in the standard orientation.
$a^s_{i(i')}$	The relative location in direction s from the output point of department i located in sub-department i' to the centroid of i' of i in the standard orientation.
$b^s_{i(i')}$	The relative location in direction s from the input point of department i located in sub-department i' to the centroid of i' of i in the standard orientation.
$f_{i(i')j(j')}$	The material flow from the output point of department i located in sub-department i' to the input point of department j located in sub-department j'.
$f^I_{i(i')k}$	The material flow from input point k of the facility to the input point of department i located in sub-department i'.
$f^O_{i(i')k}$	The material flow from the output point of department i located in sub-department i' to output point k of the facility.
FI^s_k	The location of input point k of the facility.
FO^s_k	The location of output point k of the facility.

New Decision Variables:

$c^s_{i(i')}$	Centroid of sub-department i' of department i in s-direction.
$l^s_{i(i')}$	Side length of sub-department i' of department i in s-direction.

$I^s_{i(i')}$ Location of input point of department i located in sub-department i' in s-direction.

$O^s_{i(i')}$ Location of output point of department i located in sub-department i' in s-direction.

$z^s_{i(i')j(j')}$ Binary decision variables, which denote relative locations of sub-line i' of i and j' of j with respect to x- and y-coordinates and are used to prevent the overlapping of the sub-departments from different departments.

r^q_i Binary decision variables ($q = 1, 2, 3, 4$) that denote the orientation that department i takes and are used to ensure the correct connection, dimensions and I/O point locations of the sub-departments of the same department.

The definition of $z^s_{i(i')j(j')}$ and r^q_i are given as follows:

Given arbitrarily shaped departments i, j and $i \neq j$,

$$z^s_{i(i')j(j')} = \begin{cases} 1 & \text{if sub-department } i' \text{ of } i \text{ proceeds sub-department } j' \text{ of } j \text{ in the } s\text{-direction}, \\ 0 & \text{otherwise.} \end{cases}.$$

Given arbitrarily shaped department i and $q = 1, 2, 3, 4$,

$$r^q_i = \begin{cases} 1 & \text{if department } i \text{ takes Orientation } q \text{ as illustrated in Figure 7.5}, \\ 0 & \text{otherwise.} \end{cases}.$$

The MIP formulation for the FLPNR with arbitrarily shaped departments is presented as follows:

$$\begin{aligned} \min \quad & \sum_i \sum_{j>i} \sum_{i'} \sum_{j'} f_{i(i')j(j')}(|O^x_{i(i')} - I^x_{j(j')}| + |O^y_{i(i')} - I^y_{j(j')}|) + \\ & \sum_i \sum_{i'} \sum_k f^I_{i(i')k}(|FI^x_k - I^x_{i(i')}| + |FI^y_k - I^y_{i(i')}|) + \\ & \sum_i \sum_{i'} \sum_l f^O_{i(i')l}(|O^x_{i(i')} - FO^x_l| + |O^y_{i(i')} - FO^y_l|) \end{aligned} \tag{7.14}$$

$$\text{s.t.} \quad l^s_{i(i')} \leq c^s_{i(i')} \leq L^s - l^s_{i(i')}, \qquad \forall i, i' \in M_i, s \tag{7.15}$$

$$\sum_q r^q_i = 1, \qquad \forall i, q = 1, 2, 3, 4 \tag{7.16}$$

$$c^x_{i(i')} = c^x_{i(i'+1)} + (r^3_i - r^1_i)\Delta^w_{i(i')i(i'+1)} + (r^4_i - r^2_i)\Delta^h_{i(i')i(i'+1)}, \quad \forall i, 1 \leq i' \leq m_i - 1 \tag{7.17}$$

$$c^y_{i(i')} = c^y_{i(i'+1)} + (r^1_i - r^3_i)\Delta^h_{i(i')i(i'+1)} + (r^4_i - r^2_i)\Delta^w_{i(i')i(i'+1)}, \quad \forall i, 1 \le i' \le m_i - 1 \tag{7.18}$$

$$l^x_{i(i')} = (r^1_i + r^3_i)w_{i(i')} + (r^2_i + r^4_i)h_{i(i')}, \quad \forall i, i' \in M_i \tag{7.19}$$

$$l^x_{i(i')} + l^y_{i(i')} = w_{i(i')} + h_{i(i')}, \quad \forall i, i' \in M_i \tag{7.20}$$

$$O^x_{i(i')} = c^x_{i(i')} + (r^1_i - r^3_i)a^x_{i(i')} + (r^4_i - r^2_i)a^y_{i(i')}, \quad \forall i, i' \in M_i \tag{7.21}$$

$$O^y_{i(i')} = c^y_{i(i')} + (r^1_i - r^3_i)a^y_{i(i')} + (r^2_i - r^4_i)a^x_{i(i')}, \quad \forall i, i' \in M_i \tag{7.22}$$

$$I^x_{i(i')} = c^x_{i(i')} + (r^1_i - r^3_i)b^x_{i(i')} + (r^4_i - r^2_i)b^y_{i(i')}, \quad \forall i, i' \in M_i \tag{7.23}$$

$$I^y_{i(i')} = c^y_{i(i')} + (r^1_i - r^3_i)b^y_{i(i')} + (r^2_i - r^4_i)b^x_{i(i')}, \quad \forall i, i' \in M_i \tag{7.24}$$

$$\sum_s (z^s_{i(i')j(j')} + z^s_{j(j')i(i')}) = 1, \quad \forall i \ne j \tag{7.25}$$

$$c^s_{i(i')} + l^s_{i(i')} \le c^s_{j(j')} - l^s_{j(j')} + L^s(1 - z^s_{i(i')j(j')}), \quad \forall i \ne j; i', j' \in M_i, s \tag{7.26}$$

where objective function (7.14) minimizes the total material flow travel distances, including the internal material flow travel distances (material flow travel between departments) and the external material flow travel distances (material flow travel between departments and the I/O points of the facility). The *facility size constraint* is given in (7.15), where the boundaries of all departments are constrained within the facility. Each department can only take one orientation according to (7.16). The *sub-department connection constraints* are given in (7.17)–(7.20), where the sub-departments of the same department are connected according to the orientation of the department. For these sub-department connection constraints, (7.17)–(7.18) ensure that the centroids of the all sub-departments of each department are positioned correctly with respect to one another in different orientations and (7.19)–(7.20) guarantee that the dimensions of all sub-departments of each department are set correctly in different orientations. The location of the I/O points of all sub-departments of each department are determined according to the different orientations in (7.21)–(7.24). The sub-departments of different departments are prevented from overlapping in (7.25)–(7.26).

In (7.14)–(7.26), we extend our MIP-FLPNR model for the FLP with L-shaped departments to the FLP with arbitrarily non-rectangular-shaped departments. By partitioning the non-rectangular departments into rectangular sub-departments and connecting the sub-departments of each non-rectangular department correctly according to department orientation, we transform the general FLPNR into the FLP with all-rectangular departments. The optimal layout for the FLP with arbitrarily non-rectangular departments can be obtained by solving the MIP model for all-rectangular departments, using sub-departments as departments.

Generally, the more non-rectangular a department is, the more sub-departments result from partitioning that non-rectangular department, and then the more solution effort will be required. Some other factors, like the facility size and the facility I/O points, also have an impact on the computational efforts to solve the FLPNR. In the next section, numerical experiments will be conducted to test the computational efforts needed to solve the MIP-based FLPNR to optimality with respect to these different factors.

7.2.3 Numerical Experiments for the MIP-FLPNR

We conducted a series of numerical tests to test the performance of the MIP-FLPNR model for solving the FLPNR. The purposes for these tests are: (1) to study the impact of different factors on the computational effort; and (2) to explore the capability of the MIP-FLPNR model to solve the FLPNR. All numerical tests are conducted on a computer with a Pentium IV 3.2M Hz CPU and 2.0 GB of physical memory.

To study the impact of the different factors on the computational efforts of the MIP-FLPNR model, four main types of problems are solved: (1) the FLPNR with all I-shaped departments; (2) the FLPNR with all L-shaped departments; (3) the FLPNR with all U-shaped departments; (4) the FLPNR with mixed types of non-rectangular departments. For each type of test problem, a series of data sets with different characteristics (e.g., the number of departments, the size of the rectangular facility, and the number and location of the facility I/O points) are used. The main characteristics and the run time for each test data set are summarized in Table 7.1.

Table 7.1: Solution Times of the MIP-FLPNR Model.

Data Set	Dept. Num.	Dept. Type	Sub-Dept. Num.	Fac. X	Fac. Y	Area Util. (%)	FI Num.	FO Num.	Run Time (sec.)
1-1	12	I	12	50	40	7.2	1	1	0.41
1-2	12	I	12	40	30	12.0	1	1	0.64
1-2	12	I	12	30	25	19.2	1	1	22.77
1-4	12	I	12	30	25	19.2	1	1	1.47
1-5	12	I	12	30	25	19.2	2	1	20.27
2-1	15	I	15	50	16	30.0	2	1	1.05
2-2	15	I	15	43	16	34.9	2	1	10.66
3-1	20	I	20	50	30	21.2	2	2	18.50
3-2	20	I	20	43	20	37.0	2	2	207.80
4-1	25	I	25	50	50	15.1	2	2	2197.52
4-2	25	I	25	43	40	22.0	2	2	17085.00
5-1	5	L	10	50	40	6.6	1	1	0.06
5-2	5	L	10	40	30	11.0	1	1	0.64
5-3	5	L	10	30	25	17.6	1	1	0.25
5-4	5	L	10	25	20	26.4	1	1	1.08
5-5	5	L	10	20	15	44.0	1	1	2.63
5-6	5	L	10	20	10	66.0	1	1	6.39
6-1	8	L	16	50	40	10.4	2	1	6.78
6-2	8	L	16	40	30	17.3	2	1	78.09
6-3	8	L	16	30	30	23.1	2	1	12.36
6-4	8	L	16	20	20	52.0	2	1	10194.62
6-5	8	L	16	15	30	46.2	2	1	21804.66
7-1	10	L	20	50	50	10.2	2	2	3.80
7-2	10	L	20	40	40	15.9	2	2	6.44
7-3	10	L	20	35	35	20.7	2	2	33.34
7-4	10	L	20	35	31	23.4	2	2	40.36
7-5	10	L	20	30	30	28.2	2	2	12924.31
8-1	12	L	24	45	45	15.8	2	2	42857.95
8-2	12	L	24	40	30	26.7	2	2	15788.31
9-1	15	L	30	60	60	11.0	2	2	11717.23
10-1	5	U	15	50	50	8.7	1	1	0.48
10-2	5	U	15	35	35	17.8	1	1	0.59
10-3	5	U	15	25	25	34.9	1	1	13.06
11-1	7	U	21	50	50	13.1	1	1	1.77
11-2	7	U	21	35	35	26.8	1	1	2.44

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Data Set	Dept. Num.	Dept. Type	Sub-Dept. Num.	Fac. X	Fac. Y	Area Util. (%)	FI Num.	FO Num.	Run Time (sec.)
12-1	8	U	24	50	50	15.8	2	1	315.09
12-2	8	U	24	40	40	24.6	2	1	840.58
13-1	10	U	30	50	50	18.6	2	1	496.20
13-2	10	U	30	40	40	29.0	2	1	13264.16
14-1	11	U	33	50	50	20.0	2	1	844.77
15-1	12	U	36	50	50	22.6	2	2	9124.63
17-1	9	Mixed	18	50	50	8.2	2	1	13.00
17-2	9	Mixed	18	50	30	13.6	2	1	20.09
17-3	9	Mixed	18	35	30	19.4	2	1	17.25
18-1	12	Mixed	24	50	50	10.9	2	1	2.59
18-2	12	Mixed	24	35	30	25.9	2	1	12111.50
19-1	15	Mixed	30	40	40	0.0	2	2	9196.17

In order to examine how the problem parameters affect the run time, a multiple regression analysis was conducted with four independent variables: (1) the total number of departments, (2) the total number of sub-departments, (3) the facility area utilization, and (4) the total number of facility I/O points. The model with $\log_{10} runtime$ as the dependent variable shows that the run time increases significantly with the number of sub-departments, the area utilization, and the number of I/O points. The impact of the number of the sub-departments on the run time is due to the fact that the number of sub-lines is directly associated with problem size. The effect of the area utilization can be explained in that it is more difficult to find the optimal layout solution when there is a tight facility size constraint as compared to when there is a loose, or even no, facility size constraint. Furthermore, as the number of the I/O points increases, there are more options for the departments with respect to I/O placement to be evaluated and balanced, and thus, the more difficult to solve the problem to optimality.

Although we know that the number of sub-departments, the facility area utilization and the number of facility I/O points have a significant impact on the solution time of the MIP-FLPNR model, we still want to explore how large of a problem can be solved by the MIP-FLPNR model. To perform this test, we remove the impact of the area utilization and the number of facility I/O points from consideration by fixing the area utilization to 50% (a relatively high value) and eliminating all facility I/O points. We then run a series of numerical tests to test the capability of our MIP-FLPNR model to solve different sized data sets. Four main types of data sets are tested: (1) the FLPNR with all I-shaped departments; (2) the FLPNR with all L-shaped departments; (3) the FLPNR with all U-shaped departments; and (4) the FLPNR with mixed types of non-rectangular departments. Table 7.2 summarizes the test results.

Table 7.2: Numerical Test for the Computational Capacity of the MIP-FLPNR.

Problem	Dept. #	Dept. Type	Sub-Dept. #	Area Util.	Opt. Sol.	CPU Time (sec.)
I7	7	I	7	50%	10.33	50
I8	8	I	8	50%	21.50	429
I9	9	I	9	50%	19.50	3047
I10	10	I	10	50%	25.50	9503
L4	4	L	8	50%	16.50	8
L5	5	L	10	50%	7.50	37
L6	6	L	12	50%	17.50	7082
U4	4	U	12	50%	14.50	434
M5	5	Mixed	11	50%	16.00	48
M6	6	Mixed	12	50%	22.00	2741

From Table 7.2 it is clear that the largest problem that can be solved by the MIP-FLPNR is the problem with about 12 sub-departments (the number of departments varies based on the department shapes). Figure 7.7 illustrates the optimal solution for such a problem (Data Set M6). It is also obvious that a heuristic is needed for the larger sized FLPNR problems. In the remainder of this chapter we propose a genetic algorithm based heuristic, named SEQUENCE-NR, for solving the sequence-pair representation and the MIP-based FLPNR.

7.3 Encoding Scheme of SEQUENCE-NR

In the FLPNR, because of the non-rectangularity of the departments, a department may not have a "clear" relative location relationship to another department. For example, for the layout shown in Figure 7.8, the first sub-department (Sub-Department 1-1) of Department

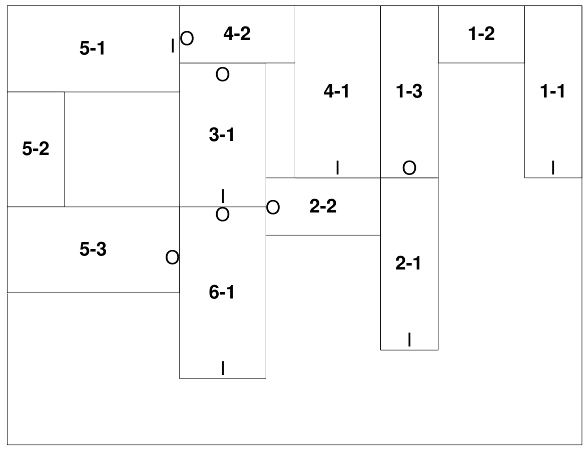

Figure 7.7: Illustration of the MIP-FLPNR Capability of Solving the FLPNR Problem.

1 is to the left of Department 2 while the second sub-department (Sub-Department 1-2) of Department 1 is above Department 2. So it is difficult to represent the FLPNR in a sequence-pair representation that is composed of a pair of department sequences.

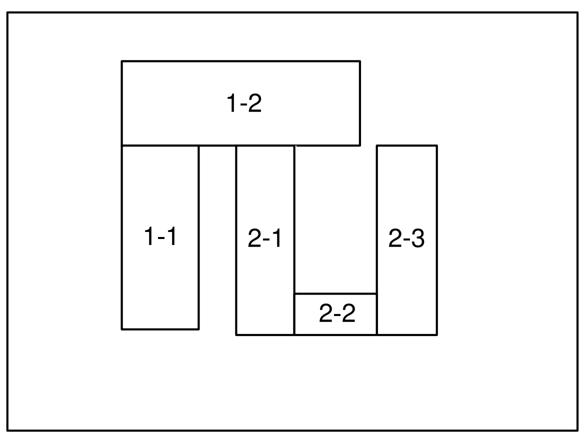

Figure 7.8: An Illustration of the Multiple Relative Location Relationships Between Departments in the FLPNR.

However, by partitioning the non-rectangular department into rectangular-shaped sub-departments, there is a single relative location relationship for each pair of sub-departments. Therefore, we can represent the FLPNR in a sequence-pair representation based on a pair of sub-department sequences; i.e., instead of using a sequence-pair to represent the relative location relationship of departments, we utilize a sequence-pair to represent the relative location relationship of sub-departments and encode that sequence-pair into a position-pair based string.

Nevertheless, unlike the continuous-representation-based FLP where each sequence-pair is feasible in terms of representing a feasible relative location relationship between departments, an arbitrary sequence-pair may not represent a feasible relative location relationship between sub-departments in the FLPNR due to the existence of the orientation restriction of departments. That is, the relative location relationship of the sub-departments partitioned from the same non-rectangular department has to be consistent with the orientation of the non-rectangular department. Corollary 2 presents the relationship between the relative location relationship of the sub-departments partitioned from the same non-rectangular department and the orientation of that non-rectangular department.

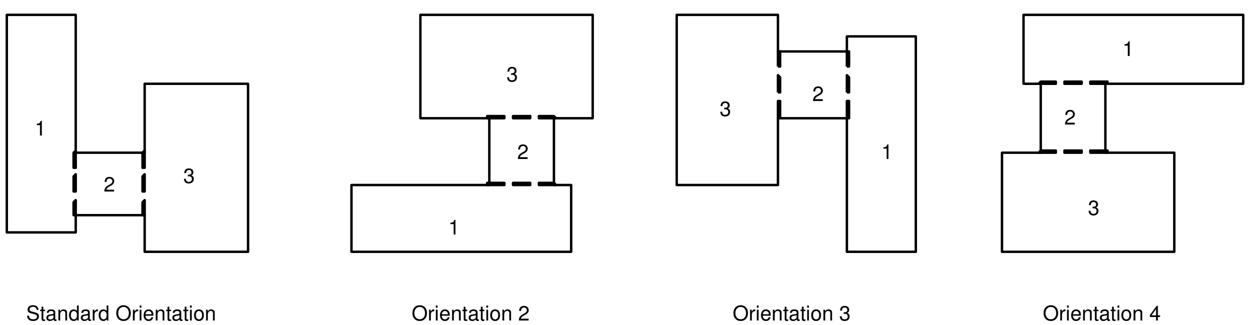

Figure 7.9: An Illustration of Four Orientations of a Non-Rectangular Department.

Corollary 2 *Given any non-rectangular department, i, there are four different orientations by rotating department i in a counterclockwise manner as shown in Figure 7.9. As discussed in Section 7.2.2, we can always define one of the four orientations of department i as a standard orientation and partition department i into a series of rectangularly-shaped sub-departments by vertical borders in the standard orientation. These rectangularly-shaped sub-departments are indexed from left to right in the standard orientation. Given any two sub-departments, i' and j' ($i' < j'$), from the same non-rectangular shaped department, the relative location relationship between i' and j' are determined by the orientation of the department in the following way:*

Department i assumes Orientation 1 (standard orientation) $\Longleftrightarrow$ *i' is left of j';*

Department i takes Orientation 2 $\Longleftrightarrow$ *i' is below j';*

Department i takes Orientation 3 $\Longleftrightarrow$ *i' is right of j';*

Department i takes Orientation 4 $\Longleftrightarrow$ *i' is above j';*

Therefore, we also need to represent the orientation information in our encoding scheme to completely describe the relative location relationship between the sub-departments from the same department and between different departments. We add an extra string for each position-pair based chromosome in order to represent the orientation of the departments in our encoding scheme. The string length is equal to the number of departments and each gene of the string represents the orientation of the corresponding department. The new encoding scheme is named, *position-pair-orientation encoding scheme*. An example of a chromosome based on the position-pair-orientation encoding scheme is given in Figure 7.10. For example, Department 1 takes Orientation 3, which means that the first sub-department (Sub-Department 1-1) is right of the second sub-department (Sub-Department 1-2); i.e., Sub-Department 1-1 must be after Sub-Department 1-2 in both sequences.

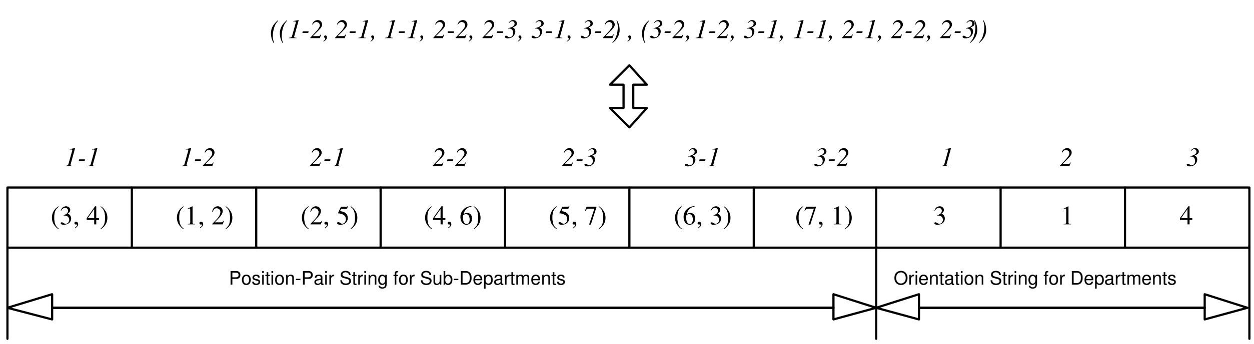

Figure 7.10: An Illustration of the Encoding Scheme in SEQUENCE-NR.

Given a chromosome encoded as a position-pair-orientation string, we can fix the value of all binary variables in the MIP-FLPNR, which includes the relative location variables $z^s_{i(i')j(j')}$ and the orientation variables r^q_i. The MIP-FLPNR is therefore simplified into a linear programming model. We then solve the simplified model to find the sequence-pair optimal solution that satisfies the relative location relationships and orientation requirements determined by the corresponding sequence-pair.

7.4 Fitness Function, Selection Rule and Elitism Operator in SEQUENCE-NR

In SEQUENCE-NR we use the same fitness function as we used for SEQUENCE in Chapter 4, which is calculated based on the objective function value of the sequence-pair optimal solution of the chromosomes. That is,

$$F(g,m) = f_g^0 - f_{gm}, \qquad \forall g \in \{1,\dots,G\}, \forall m \in \{1,\dots,M\}, \tag{7.27}$$

where $F(g,m)$ is the fitness score function for Chromosome m in Generation g, f_{gm} is the objective function value of the sequence-pair optimal solution corresponding to Chromosome m in Generation g and $f_g^0 = \max\limits_m \{f_{gm}\}$. Parameter G is the total number of generations and M is the size of population in each generation.

Given the above fitness score function, one of the most widely applied selection rules, the "roulette wheel," is used in SEQUENCE-NR. Roulette wheel selection is a fitness-proportionate selection, where each chromosome is assigned a slice of a circular "roulette wheel," the size of the slice being proportional to the individual's fitness score in comparison with the fitness scores of the other chromosomes in the population. The probability that a chromosome is selected on a particular spin is given as follows:

$$p_{gm} = \frac{F(g,m)}{\sum\limits_{k=1}^{M} F(g,k)}, \qquad \forall g \in \{1,\dots,G\}, m \in \{1,\dots,M\}. \tag{7.28}$$

We also consider applying the elitism operator to SEQUENCE-NR. As we have discussed in Chapter 4, an elitism operator is an addition to the roulette wheel selection, where the elitism operator forces the GA to retain some number of the best individuals at each generation. To further strengthen the effect of the elitism operator, we combine the original elitism operator, which simply copied a certain number of the best chromosomes from the last generation to the new generation, with some local greedy search operator. Our methodology for the revised elitism operator is to first copy a certain number of the best chromosomes from the last generation, apply the local greedy search operator to the best chromosome of the selected chromosomes (also the best chromosome in the last generation) to further improve that chromosome, and then copy the resulting chromosomes to the new generation.

The local greedy search operator considers the neighborhood of a sequence-pair as the search region, which includes all the sequence-pairs generated by applying two types of changes to the given sequence-pair: two-way department exchange and department rotation change. The two-way department exchange swaps the positions of two departments in the sequence-pair. The department rotation change simply changes the department orientation. As a result of trading off the benefits obtained by applying the local greedy search operator and the computational effort it adds, we combine the two type of changes in the local greedy search operator in the following way: for the given chromosome, test all possible two-way exchanges of the department positions and all possible one-department-at-a-time department rotations, then make the actual change to the chromosome that results in the largest decrease in terms of the objective function value. This process continues until there are no such two-way exchanges of the department positions or changes of the department orientation that result in a reduced objective function value.

7.5 GA Operator Design in SEQUENCE-NR

Because the encoding scheme for SEQUENCE-NR includes not only the position-pair sub-string, but also the orientation sub-string, the GA operators used in SEQUENCE cannot be applied to SEQUENCE-NR. We propose to use the following GA operators that we specifically designed for SEQUENCE-NR. The GA operators we use in SEQUENCE-NR include: crossover operator, mutation operator and orientation adjustment operator.

7.5.1 Crossover Operator

As the major instrument of variation and innovation in GA, a crossover operator exchanges sub-chromosomes between two parent chromosomes, which results in two new offspring chromosomes. To address the difference between the position-pair sub-string and the orientation sub-string in SEQUENCE-NR encoding scheme, we present the following two crossover operators.

For the position-pair sub-string, where each gene corresponds to a pair of positions of a rectangular-shaped sub-department in the sequence-pair, we apply the revised order-based crossover operator proposed for SEQUENCE in Chapter 4.

For the orientation sub-string, where each gene corresponds to the orientation of a department, we use the uniform crossover operator. To implement a uniform crossover operator, a binary bit string is generated to denote the selection of positions. Offspring 1 copies the genes from Parent 1 in those positions in the bit string that are marked by a “1” bit and from Parent 2 in those positions in the bit string that are marked by a “0” bit. Similarly, offspring 2 copies the genes from Parent 2 in those positions that are marked by a “1” bit and from Parent 1 in those positions that are marked by a “0” bit.

We randomly choose (with equal probability) one of the two sub-string crossover operators given above to apply to the selected parent chromosomes. For the parent chromosomes selected for crossover, either the position-pair sub-strings are crossed over or the orientation sub-strings are crossed over to generate two new offspring chromosomes. If the revised order-based crossover operator is chosen, the offspring chromosomes cross over the position-pair sub-strings of the parent chromosomes and copy the orientation sub-strings from the corresponding parent chromosomes (Offspring 1 copies the orientation sub-string from Parent 1 and Offspring 2 copies the orientation sub-string from Parent 2). If the uniform crossover is chosen, the offspring chromosomes cross over the orientation sub-strings of the parent chromosomes and copy the position-pair sub-strings from the corresponding parent chromosomes. The reason why we cross over only one of the two sub-strings (position-pair or orientation) in a SEQUENCE-NR chromosome instead of both is because we believe that it is easier to keep certain "good patterns" by changing either the relative location relationships between the departments or the orientation of the departments rather than by changing both simultaneously.

7.5.2 Mutation Operator

Similar to the crossover operator, we design different mutation operators for the position-pair sub-string and orientation sub-string in SEQUENCE-NR.

For the position-pair sub-string, we utilize a two-position inverse operator, which randomly chooses two positions in the position-pair sub-string and reverses the genes between the two positions. For the orientation sub-string, we utilize a two-position replacement operator, which randomly chooses two positions in the orientation sub-string and replaces the genes between the two positions with randomly generated new orientation values.

We randomly choose (with equal probability) one of the two mutation operators given above to apply to the selected parent chromosomes. For the parent chromosomes, either the position-pair sub-strings or the orientation sub-strings are mutated. Similar to the crossover operators, if the position-pair sub-strings are mutated, the offspring chromosomes copy the orientation sub-strings from the corresponding parent chromosomes (Offspring 1 copies the orientation sub-string from Parent 1 and Offspring 2 copies the orientation sub-string from Parent 2). If the orientation sub-strings are mutated, the offspring chromosomes copy the position-pair sub-strings from the corresponding parent chromosomes.

7.5.3 Orientation Adjustment Operator

A chromosome after crossover and mutation may become infeasible because of the inconsistency between the orientation of departments in the orientation sub-string and the relative positions of sub-departments from the same department in the position-pair sub-string. For example, consider a case where there are three departments for a given FLPNR and the number of rectangular sub-departments for these three departments are 1, 2, and 2, respectively. An example chromosome is given in Figure 7.11.

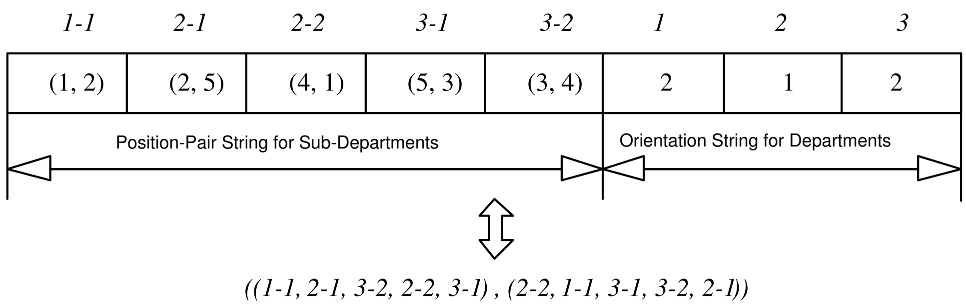

Figure 7.11: Illustration of the Inconsistency Between Position-Pair Sub-String and Orientation Sub-String.

The orientation value of Department 2 is 1, which means that Sub-Department 2-1 should be placed before Sub-Department 2-2 in both sequences. Such a relative location relationship between Sub-Departments 2-1 and 2-2 have conflicts with the actual relative positions of Sub-Departments 2-1 and 2-2 in the position-pair sub-string.

To eliminate the infeasibility caused by such an inconsistency, we propose an *orientation adjustment operator* to adjust the relative positions of the sub-departments from the same department according to the department's orientation. For example, given a chromosome (((1,2),(2,5),(4,1),(5,3),(3,4)),(2,1,2)), we know that the relative positions of the two sub-departments of Department 2 are inconsistent with the orientation of Department 2. Now we use the orientation adjustment operator to adjust the relative positions of the two sub-departments in the position-pair sub-string. Given the chromosome, we know Sub-Department 2-1 corresponds to the position-pair (2,5) and Sub-Department 2-2 corresponds to the position-pair (4,1), so the two sub-departments of Departments 2 correspond to the second and fourth genes in the first sequence and the fifth and first genes in the second sequence. According to the orientation value of Department 2, which is equal to 1, we know that Sub-Department 2-1 should be placed before Sub-Department 2-2 in both sequences, so we adjust the positions of Sub-Department 2-1 to (2,1) and the positions of Sub-Department 2-2 to (4,5). Such an adjustment does not affect the positions of the sub-departments of other departments in the sequence-pair or the orientations of other departments. The resulting chromosome is (((1,2),(2,1),(4,5),(5,3),(3,4)),(2,1,2)), which is now feasible with respect to the orientation of Department 2.

7.5.4 Diversification Operator

In order to further increase the population diversity and prevent SEQUENCE-NR from premature termination, we utilize a diversification operator, which simply prevents the reoccurrence of the current best chromosome. This means that multiple copies of the same chromosome corresponding to the best sequence-pairs (in terms of the objective function value of the sequence-pair optimal solution) in each population are eliminated, although it is still possible that there are multiple different chromosomes that corresponds to the best sequence-pairs in each generation.

7.6 Repair Operators for the SEQUENCE-NR

Given a sequence-pair, all binary variables in the MIP-FLPNR ($z^s_{i(i')j(j')}$ and r^q_i) are set to certain values according to the relative location relationship between sub-departments and the orientation of the departments determined by the sequence-pair. The MIP-FLPNR model is thus simplified to a linear programming model with only two sets of constraints: the facility size constraints and the sub-department connection constraints. The feasibility of any sequence-pair is determined by whether the corresponding simplified MIP-FLPNR model with these two constraint sets is feasible. In this section we propose two repair operators to improve the efficiency of SEQUENCE-NR to generate feasible sequence-pairs and the performance of SEQUENCE-NR to solve the sequence-pair based MIP-FLPNR by addressing these two types of constraints. The following definition is useful in presenting the repair operator.

Definition 6 *Given a sequence-pair,* (Γ_+, Γ_-)*, if there is at least one corresponding layout solution that satisfies the constraint* Θ *defined in the MIP-FLPNR, we say that the sequence-pair* (Γ_+, Γ_-) *is* Θ*-feasible.*

For the repair operator to address the facility size constraints, we first present a sufficient and necessary condition for a sequence-pair to be *facility-size-constraint-feasible*. We test whether a sequence-pair is facility-size-constraint-feasible based on this sufficient and necessary condition without actually solving the simplified MIP-FLPNR model. For a sequence-pair that is not facility-size-constraint-feasible, we present a "rotating" repair operator to improve the likelihood that the sequence-pair becomes facility-size-constraint-feasible after repair.

For the repair operator to address the sub-department connection constraints, we present a necessary condition for a sequence-pair to be *sub-department-connection-constraint-feasible*. We filter sequence-pairs that do not satisfy this necessary condition for being sub-department-connection-constraint-feasible without actually solving the simplified MIP-FLPNR. We then repair each sequence-pair that is filtered by applying a "connection" repair operator to improve the probability that the sequence-pair becomes sub-department-connection-constraint-feasible after repair.

7.6.1 A Repair Operator for the Facility Size Constraints

As we discussed in Chapter 3, for a given sequence-pair, there are a series of corresponding packings that satisfy the relative location relationship between the rectangular sub-departments. Based on the orientation information provided by the sequence-pair, the sub-department dimensions are also known. Murata *et al.* [54] defined the optimal packing of a sequence-pair as the packing with the minimum size of the chip (facility) that can include all the modules within it. It is also shown in [54] that given the relative location relationship and dimension information of all rectangular-shaped modules, the optimal packing of a sequence-pair can be obtained by applying the longest path algorithm to two vertex weighted directed acyclic graphs: a horizontal graph $G_H(V, E)$ and a vertical graph $G_V(V, E)$. We transform Murata's formulation for these two graphs to the MIP-FLP as follows:

1. Horizontal Graph $G_H(V, E)$:
   V: source node s, sink node t, and m vertices labeled as sub-departments.
   E: (s, x) and (x, t) $(\forall x \in V, x \neq s, t)$, (x, x') $(\forall x, x' \in V$ and $x \in M_{bb}(x'))$.
   Vertex weight: $w_s = w_t = 0$ and $w_x =$ width of sub-department x.

2. Vertical Graph $G_V(V, E)$:
   V: source node s, sink node t, and m vertices labeled as sub-departments.
   E: (s, x) and (x, t) $(\forall x \in V, x \neq s, t)$, (x, x') $(\forall x, x' \in V$ and $x \in M_{ab}(x'))$.
   Vertex weight: $w_s = w_t = 0$ and $w_x =$ height of sub-department x.

It is shown in [54] that the coordinate of the top-right side of each department can be minimized by assigning the longest path length between the source node s and the node of the department in G_H and G_V, respectively. In addition, the width and the height of the facility that includes all departments are determined by assigning the longest path length between the source and the sink nodes in G_H and G_V, respectively, where the width and the height of the facility are minimized and the packing is the optimal packing of the given sequence-pair.

Therefore, for every sequence-pair, we can find an optimal packing of the rectangular sub-departments with the minimum horizontal and vertical length by applying the longest path algorithm to the graph formulated as above. Although the objective function value of the MIP-FLPNR is different from the objective function value of the packing problem of the sequence-pair, we present a sufficient and necessary condition for a sequence-pair to be facility-size-constraint-feasible in Theorem 5.

Theorem 5 *Given the MIP-FLPNR, a sequence-pair,* (Γ_+, Γ_-)*, is facility-size-constraint-feasible if and only if the optimal packing of* (Γ_+, Γ_-) *can be included in the given facility.*

Proof:

If the optimal packing of (Γ_+, Γ_-) can be included in the given facility, then for (Γ_+, Γ_-), there is at least one corresponding layout solution, the layout solution that corresponds to the optimal packing of (Γ_+, Γ_-), that satisfies the facility size constraint. Therefore, according to Definition 6, the sequence-pair (Γ_+, Γ_-) is facility-size-constraint feasible.

On the other hand, if (Γ_+, Γ_-) is facility-size-constraint-feasible, then according to Definition 6 there is at least one corresponding layout solution, the layout solution that satisfies the relative location and orientation information determined by (Γ_+, Γ_-), that satisfies the facility size constraint. That is, for (Γ_+, Γ_-), there is at least one corresponding layout solution that can be included in the given facility. Since the optimal packing of (Γ_+, Γ_-) has the minimum horizontal and vertical length in all possible packings that correspond to (Γ_+, Γ_-), the optimal packing of (Γ_+, Γ_-) must also be included in the given facility. ∎

Therefore, we can test whether a sequence-pair is facility-size-constraint-feasible by solving the optimal packing problem formulated as above without actually solving the whole simplified MIP-FLPNR model.

For the sequence-pairs that do not satisfy the facility size constraint, we present a rotating repair operator that tries to rotate the department on the longest path of the horizontal graph and vertical graph to reduce the horizontal and vertical dimensions of the optimal packing, thus repairing the sequence-pair in an effort towards satisfying the facility size constraint. The following notation is used in the rotating repair operator.

(Γ_+^0, Γ_-^0)	The given initial sequence-pair.
(Γ_+, Γ_-)	The current sequence-pair.
(Γ'_+, Γ'_-)	The new sequence-pair.
L^x	The width of the given facility.
L^y	The height of the given facility.
L^H	The width of the facility in the optimal packing of the current sequence-pair, which corresponds to the longest path length from the source node to the sink node of G_H formulated based on (Γ_+, Γ_-).
L^V	The height of the facility in the optimal packing of the current sequence-pair, which corresponds to the longest path length from the source node to the sink node of G_V formulated based on (Γ_+, Γ_-).
$L^{H'}$	The width of the facility in the optimal packing of the new sequence-pair, which corresponds to the longest path length from the source node to the sink node of G_H formulated based on (Γ'_+, Γ'_-).
$L^{V'}$	The height of the facility in the optimal packing of the new sequence-pair, which corresponds to the longest path length from the source node to the sink node of G_V formulated based on (Γ'_+, Γ'_-).
n^H	The number of the departments on the longest path from the source node to the sink node of G_H formulated based on (Γ_+, Γ_-).
n^V	The number of the departments on the longest path from the source node to the sink node of G_V formulated based on (Γ_+, Γ_-).
$k^H_{[i]}$	The index of the $[i]$th department on the longest path from the source node to the sink node of G_H formulated based on (Γ_+, Γ_-).
$k^V_{[i]}$	The index of the $[i]$th department on the longest path from the source node to the sink node of G_V formulated based on (Γ_+, Γ_-).

The procedure for the rotating repair operator for the facility size constraint is given as follows:

1. Let $(\Gamma_+, \Gamma_-) = (\Gamma_+^0, \Gamma_-^0)$ and $i1 = i2 = 0$.

2. Formulate G_H and G_V based on (Γ_+, Γ_-). Apply the longest path algorithm to G_H and G_V and the resulting longest path length are assigned to L^H and L^V, respectively.

3. If $L^H > L^x$, let $i1 = 1$ and go to Step 5. Otherwise, go to Step 4.

4. If $L^V > L^y$, let $i2 = 1$ and go to Step 6. Otherwise, go to Step 7.

5. If $i1 > n^H$, stop the repair operator (the sequence-pair cannot be repaired). Otherwise, randomly rotate Department $k^H_{[i1]}$ in a clockwise or counterclockwise manner. Adjust the sequence-pair by using the orientation adjustment operator presented in Section 7.5.3. The resulting sequence-pair is assigned to (Γ'_+, Γ'_-). Formulate G_H and G_V based on (Γ'_+, Γ'_-). Apply the longest path algorithm to G_H and G_V and the resulting longest path lengths are assigned to $L^{H'}$ and $L^{V'}$, respectively. If $L^{H'} \leq L^H$ and $L^{V'} \leq \max\{L^V, L^y\}$, accept the rotation by letting $(\Gamma_+, \Gamma_-) = (\Gamma'_+, \Gamma'_-)$ and go to Step 4. Otherwise, $i1 = i1 + 1$ and go to Step 5.

6. If $i2 > n^V$, stop the repair operator (the sequence-pair cannot be repaired). Otherwise, randomly rotate Department $k^V_{[i2]}$ in a clockwise or counterclockwise manner. Adjust the sequence-pair by using the orientation adjustment operator presented in Section 7.5.3. The resulting sequence-pair is assigned to (Γ'_+, Γ'_-). Formulate G_H and G_V based on (Γ'_+, Γ'_-). Apply the longest path algorithm to G_H and G_V and the resulting longest path lengths are assigned to $L^{H'}$ and $L^{V'}$, respectively. If $L^{V'} \leq L^V$ and $L^{H'} \leq \max\{L^H, L^x\}$, accept the rotation by letting $(\Gamma_+, \Gamma_-) = (\Gamma'_+, \Gamma'_-)$ and go to Step 3. Otherwise, $i2 = i2 + 1$ and go to Step 6.

7. If $L^H > L^x$ or $L^V > L^y$, go to Step 3. Otherwise, stop the repair operator and return the repaired sequence-pair, (Γ_+, Γ_-), which is guaranteed to be facility-size-constraint-feasible.

7.6.2 A Repair Operator for the Sub-Department Connection Constraints

For the sub-department connection constraints, we first present the following necessary condition for a sequence-pair to be sub-department-connection-constraint feasible.

Theorem 6 *Given the MIP-FLPNR with N departments, n_i ($i = 1, \ldots, N$) is the number of rectangular sub-departments for Department i. Given a sequence-pair, (Γ_+, Γ_-), if (Γ_+, Γ_-) is sub-department-connection-constraint-feasible, then the following condition must be satisfied:*

For any two adjacent sub-departments of Department i, Sub-Department $i(j)$ and Sub-Department $i(j+1)$ ($j = 1, \ldots, n_i - 1$), there are no other sub-departments that are placed between Sub-Department $i(j)$ and Sub-Department $i(j+1)$ in both Γ_+ and Γ_-.

Proof:

Assume there is another sub-department, $k(l)$, that is placed between Sub-Department $i(j)$ and Sub-Department $i(j+1)$ in both Γ_+ and Γ_-. More specifically,

- If Department i takes the standard orientation as shown in Figure 7.9, then $(\Gamma_+, \Gamma_-) = ((\ldots i(j) \ldots k(l) \ldots i(j{+}1) \ldots), (\ldots i(j) \ldots k(l) \ldots i(j{+}1) \ldots))$. So Sub-Department $i(j)$ must be left of Sub-Department $k(l)$ and Sub-Department $k(l)$ must be left of Sub-Department $i(j+1)$, which is in conflict with the adjacency relationship of $i(j)$ and $i(j+1)$ provided by the sub-department connection constraint.

- If Department i takes Orientation 2 as shown in Figure 7.9, then $(\Gamma_+, \Gamma_-) = ((\ldots i(j+1) \ldots k(l) \ldots i(j) \ldots), (\ldots i(j) \ldots k(l) \ldots i(j+1) \ldots))$. So Sub-Department $i(j)$ must be below of Sub-Department $k(l)$ and Sub-Department $k(l)$ must be below of Sub-Department $i(j+1)$, which is in conflict with the adjacency relationship of $i(j)$ and $i(j+1)$ provided by the sub-department connection constraint.

- If Department i takes Orientation 3 as shown in Figure 7.9, then $(\Gamma_+, \Gamma_-) = ((\ldots i(j+1)\ldots k(l)\ldots i(j)\ldots), (\ldots i(j+1)\ldots k(l)\ldots i(j)\ldots))$. So Sub-Department $i(j)$ must be right of Sub-Department $k(l)$ and Sub-Department $k(l)$ must be right of Sub-Department $i(j+1)$, which is in conflict with the adjacency relationship of $i(j)$ and $i(j+1)$ provided by the sub-department connection constraint.

- If Department i takes Orientation 4 as shown in Figure 7.9, then $(\Gamma_+, \Gamma_-) = ((\ldots i(j)\ldots k(l)\ldots i(j+1)\ldots), (\ldots i(j+1)\ldots k(l)\ldots i(j)\ldots))$. So Sub-Department $i(j)$ must be above Sub-Department $k(l)$ and Sub-Department $k(l)$ must be above Sub-Department $i(j+1)$, which is in conflict with the adjacency relationship of $i(j)$ and $i(j+1)$ provided by the sub-department connection constraint.

Therefore, we prove that the existence of another sub-department between $i(j)$ and $i(j+1)$ in both Γ_+ and Γ_- is in conflict with the adjacency relationship determined by the sub-department connection constraint. ∎

Given a sequence-pair that does not satisfy the necessary conditions given in Theorem 6, we provide a repair operator for each specific department that does not satisfy the necessary conditions, then "congregate" the sub-departments of that department in one of the two sequences, which means that the new sequence-pair satisfies the necessary condition. The detailed procedure is given as follows:

1. Set the department index $i = 1$.

2. For Department i, scan the sequence-pair to check whether the necessary condition given in Theorem 6 is satisfied. If the necessary condition is satisfied, go to Step 4. Otherwise, go to Step 3.

3. Randomly choose one of the sub-departments of Department i and congregate all other sub-departments of Department i based on the two positions of the chosen sub-department in the sequence-pair. More specifically, move all other sub-departments

of Department i adjacent to each other based on the positions of the chosen sub-department while keeping the original relative position that is consistent with the orientation of Department i.

4. Set $i = i + 1$. If $i > N$, stop and return the resulting sequence-pair. Otherwise, go to Step 2.

7.6.3 Combination of the Two Repair Operators

Since both repair operators make changes to the sequence-pair, we need to determine how to combine the two repair operators. On the one hand, the sub-department connection repair operator repairs a sequence-pair by congregating the sub-departments of the department that do not satisfy the necessary condition in Theorem 6. The process of "congregating" may change the longest path of the horizontal graph, G_H, and the vertical graph, G_V, formulated as shown in Section 7.6.1. So, a sequence-pair that satisfies the sufficient and necessary condition for the facility size constraint before being repaired by the sub-department connection repair operator may not satisfy the sufficient and necessary condition after the repair.

On the other hand, the facility size repair operator repairs a sequence-pair by only changing the orientation of some of the departments, whose dimensions are included in the longest path of the horizontal graph, G_H, and the vertical graph, G_V. Such a "rotation" process only changes the relative location of the sub-departments from the same department and does not affect the absolute positions occupied by the sub-departments of the same department. For example, if the two sub-departments of a department are in position (3, 5) in the first sequence and (6, 9) in the second sequence, then after rotation, they are still in the same positions in both sequences. The only change is the relative location of these two sub-departments (e.g., the first sub-department is left of the second sub-department before rotation, and it is above the second sub-department after rotation). Therefore, a department that is "congregated" in one of the sequences will still be "congregated" (but the relative positions of the sub-departments of that department may be changed due to the orientation change of that department) in that sequence, which means that the departments repaired by the sub-department connection repair operator will still satisfy the sub-department connection constraint.

Therefore, we combine the two repair operators by first applying the sub-department connection repair operator to the sequence-pair to generate a sequence-pair that satisfies the necessary condition for being sub-department-connection-constraint-feasible. We then apply the facility size repair operator to repair the sequence-pair for satisfying the sufficient and necessary condition for being facility-size-constraint-feasible. In doing so, we keep the "congregated" nature of the sequence-pair.

We test the efficiency of the proposed repair operators on a few test problems in this section. Since the two repair operators are combined to repair the sequence-pair regarding different constraints, we test the combination effects of the two repair operators instead of the individual effect. However, we implicitly test the individual effect of the repair operator for the facility size constraint in the first test problem, where all departments are I-shaped and thus there is no sub-department connection constraint. All problems are tested for two cases: the one without the repair operators and the one with the two repair operators. For each test problem, the objective is to generate 50 feasible sequence-pairs. The inefficiency factor is defined by dividing the total number of generated sequence-pairs by the number of feasible sequence-pairs and represents the number of sequence-pairs that are needed to be generated on average to yield one feasible sequence-pair. The inefficiency factor is compared for the situations without and with the repair operator. The test results are summarized in Table 7.3. It is obvious from Table 7.3 that the repair operators greatly improve the efficiency of generating feasible sequence-pairs.

Table 7.3: Test on the Efficiency of the Repair Operator for the FLPNR.

No. of Depts.	No. of Sub-Depts.	No. of Feasible SPs	Without Repair Operators		With Repair Operators		Reduction on Inefficiency Factor
			No. of SPs	Inefficiency Factor	No. of SPs	Inefficiency Factor	
10	10	50	537	10.74	50	1.00	90.69%
4	8	50	29552	591.04	462	9.24	98.44%
5	10	50 (16[a])	100000[a]	6250.00	2115	42.30	99.32%
6	12	50 (2[b])	100000[b]	50000.00	4920	98.40	99.80%

[a]SEQUENCE-NR only generates 16 feasible sequence-pairs before reaching the maximum number of sequence-pairs.

[b]SEQUENCE-NR only generates 2 feasible sequence-pairs before reaching the maximum number of sequence-pairs.

7.7 Algorithm Scheme of SEQUENCE-NR

In this section we describe the procedure of SEQUENCE-NR with the repair operators for the FLP with non-rectangular departments. The following notation is used to describe the algorithm SEQUENCE-NR with repair operators:

G	Maximum number of generations.
M	Population size of each generation.
m	Counter of the number of the chromosomes in the new population.
i	Generation index.
j, k	Chromosome indices.
$F(i, j)$	Fitness function value of Chromosome j in Generation i.
p_{ij}	Selection probability of chromosome j in Generation i based on the roulette selection rule.
$\bar{F}_i$	The average fitness function value of Generation i.
g_i^*	The fittest chromosome in Generation i.
f_i^*	The objective function value of the sequence-pair optimal solution corresponding to g_i^*.
g^*	The overall best chromosome.

f^*	The objective function value of the sequence-pair optimal solution corresponding to g^*.
K	The number of the best chromosomes to be copied to the next generation in the elitism operator.
PC	The probability of applying the crossover operator to the selected chromosomes.
PM	The probability of applying the mutation operator to the selected chromosomes.

The generic procedure of SEQUENCE-NR with the repair operators to solve the FLPNR is given as follows:

1. Generate the initial generation, Generation 0, of size M as follows:

   (a) Set the initial value of the number of chromosomes in the initial population by letting $m = 0$.

   (b) Randomly generate a sequence-pair and an orientation string. Adjust the sequence-pair by using the orientation adjustment operator. Translate the sequence-pair into a position-pair and attach the orientation sub-string to the end of the position-pair to generate the corresponding chromosome, Chromosome j.

   (c) First, repair Chromosome j with the sub-department connection repair operator. Then, repair Chromosome j with the facility size repair operator. Transform the resulting Chromosome j into a sequence-pair, set the binary variables in the MIP-FLPNR correspondingly, and solve the simplified MIP-FLPNR model. If Chromosome j is feasible after repair, add Chromosome j to Generation 0 and $m = m + 1$. Go to Step 1b.

   (d) Calculate $F(0, j)$ by using (7.27) and p_{0j} by using (7.28). Record the fittest chromosome, g_0^*, and its corresponding objective function value, f_0^*. Set $i = 0$, $g^* = g_0^*$ and $f^* = f_0^*$.

2. Apply the revised elitism operator (with the steepest change operator) to Generation i to generate K chromosomes for Generation $i + 1$ and set $m = K$.

3. To fill the remaining $M - m$ chromosomes in the new generation, randomly select two different parent chromosomes, j_1 and j_2, from Generation i based on the roulette wheel selection rule.

4. With the probability of PC and PM, where $PC + PM = 1$, apply crossover and mutation operators as shown below to Chromosomes j_1 and j_2 to generate two offspring chromosomes, k_1 and k_2, for Generation $i + 1$:

   (a) Generate a random number, r, from a standard uniform distribution $U(0, 1)$.

   (b) If $r \leq PC$, apply crossover operator to Chromosomes j_1 and j_2 to generate Chromosomes k_1 and k_2.

   (c) If $r > PC$, apply the mutation operator to j_1 and j_2 to generate Chromosomes k_1 and k_2.

5. Translate Chromosomes k_1 and k_2 into sequence-pairs, set the corresponding binary variables in the MIP-FLPNR model, and then solve the simplified MIP-FLPNR model to optimality. If Chromosome k_i $(i = 1, 2)$ corresponds to a feasible sequence-pair, add Chromosome k_i to the new population. Update the value of m as appropriate. If both k_1 and k_2 correspond to feasible sequence-pairs, go to Step 7. Otherwise, go to Step 6.

6. Repair Chromosome k_i, which represents an infeasible sequence-pair, by using the two repair operators (first applying the sub-department connection repair operator and then applying the facility size repair operator). Then translate Chromosomes k_i into a sequence-pair, set the corresponding binary variables in the MIP-FLP model, and then solve the simplified MIP-FLP model to optimality. If Chromosome k_i becomes feasible after repair, add Chromosome k_i to the new population and update the value of m as appropriate.

7. If $m < M$, go to Step 3. Otherwise, set the new generation as the current generation by $i = i + 1$ and $m = 0$..

8. In Generation i, calculate $F(i,j)$ using (7.27) and p_{ij} using (7.28) for each chromosome. Record the fittest chromosome, g_i^*, and its corresponding objective function value, f_i^*. If $f_i^* < f^*$, set $g^* = g_i^*$ and $f^* = f_i^*$.

9. If $i \geq G$, go to Step 10. Otherwise, go to Step 2.

10. Apply the steepest change operator to the best K chromosomes of the last generation. If the best chromosome of the K chromosomes after applying the best two-way exchange operator is better than g^*, update g^* and f^*. Stop SEQUENCE-NR and output g^* and f^*.

7.8 Parameter Settings of SEQUENCE-NR

Parameter setting is another important aspect in GA design since it has a great impact on the performance of the GA. However, these parameters typically interact with each other and their effects cannot be isolated, so it is extremely difficult to optimize them one at a time.

Although parameter settings have been discussed extensively in the GA literature, no conclusive results have been presented. So, in most cases, researchers either conduct experimental tests to find "good" parameter settings or they set the parameters according to experience or knowledge about the specific problems where GAs are applied. Through an experimental design, we set the parameters for SEQUENCE-NR as follows: $G = 100$, $n = 50$, $K = 10$, $PC = 0.90$, and $PM = 0.10$.

7.9 Utilization of the Penalty Function in the MIP-FLPNR Model

As we showed in Table 7.3, although the repair operators greatly improve the efficiency of generating feasible sequence-pairs in SEQUENCE-NR, there are still a lot of initial infeasible sequence-pairs generated. One of the reasons for such a difficulty is because the dimensions of departments in the FLPNR are fixed instead of flexible as in the continuous-representation-based FLP.

Through our initial testing, we found that a relaxation on the facility size can greatly improve the number of feasible sequences in the first several generations, thus greatly improving the efficiency of SEQUENCE-NR. We utilize the same penalty function method with the same initial relaxation on the facility size as we did in Chapter 5 for the FLP with fixed departments. The relaxation on the facility size is reduced exponentially as shown in (4.7) as the generations evolve.

To show the effectiveness of the penalty function method with a relaxation on the facility size, we compare the efficiency of SEQUENCE-NR without the penalty function and with the penalty function in generating "feasible" sequence-pairs in Table 7.4. For each test problem, the comparison objective is the number of the sequence-pairs generated in order to generate 50 feasible sequence-pairs. From Table 7.4 it is obvious that the adoption of the penalty function method improves the efficiency of SEQUENCE-NR in generating feasible sequence-pairs.

7.10 Numerical Experiments

To illustrate the effectiveness and efficiency of SEQUENCE-NR for solving the MIP-FLPNR, a series of numerical experiments based on different sized test problems are conducted. The

Table 7.4: Illustration of the Efficiency of the Penalty Function Method on Generating the Feasible Sequence-Pairs.

No. of Depts.	No. of Sub-Depts.	No. of Feasible SPs	Without Penalty Function		With Penalty Function		Reduction on Inefficiency Factor
			No. of SPs	Inefficiency Factor	No. of SPs	Inefficiency Factor	
4	8	50	462	9.24	50	1.00	89.18%
5	10	50	2115	42.30	51	1.02	97.64%
6	12	50	4920	98.40	50	1.00	98.98%
10	19	50 (32[a])	100000[a]	3125.00	51	1.02	99.97%

[a]SEQUENCE-NR fails to find 50 feasible sequence-pair before reaching the maximum number of sequence-pairs.

following numerical tests are conducted in two phases: (1) optimality comparison test; and (2) heuristic comparison test. All numerical tests are conducted on a computer with a Pentium IV 3.2M Hz CPU and 2.0 GB of physical memory.

7.10.1 Optimality Comparison Test

In the optimality comparison test, our purpose is to compare SEQUENCE-NR solutions with optimal solutions to show the quality of SEQUENCE-NR solutions. The data sets we use for the optimality comparison test are the 10 test problems we used for testing the computational capability of MIP-FLPNR in Section 7.2.3.

For each test problem, we run SEQUENCE-NR until the optimal solution given in Section 7.2.3 is found. The maximum number of runs of SEQUENCE-NR for the test problems is 10; i.e., if SEQUENCE-NR cannot achieve the optimal solution in 10 runs, we stop SEQUENCE-NR and report the optimality gap between the best SEQUENCE-NR solution and the optimal solution. Correspondingly, the reported SEQUENCE-NR solution time is the total run time for SEQUENCE-NR to find the optimal solution or the total run time of 10 runs if SEQUENCE-NR fails to find the optimal solution in 10 runs.

The results of the optimality comparison test are summarized in Table 7.5. Here the optimality gap represents the percentage of the difference between the objective function value of the best SEQUENCE-NR solution and the objective function value of the optimal solution for each test problem.

Table 7.5: Results of Optimality Comparison Test for SEQUENCE-NR.

Problem	Optimal Solution		SEQUENCE-NR Solution		Optimality Gap
	Objective	CPU Time (sec.)	Objective	CPU Time (sec.)	
I7	10.33	50	10.33	1042	0.00%
I8	21.50	429	21.50	1156	0.00%
I9	38.00	3047	41.00	6051	7.89%
I10	25.50	9503	26.50	6455	3.92%
L4	16.50	8	16.50	1160	0.00%
L5	7.50	37	7.50	3853	0.00%
L6	17.50	7082	19.50	7320	11.43%
U4	14.50	434	14.50	1176	0.00%
M5	16.00	48	16.00	2660	0.00%
M6	22.00	2741	22.00	6726	0.00%

From Table 7.5 we can see that SEQUENCE-NR achieves the optimal solution for 7 of the 10 test problems with no more than 10 runs. Therefore, according to the results for the optimality comparison test, the best solutions from 10 runs of SEQUENCE-NR are equal to or at least close to the globally-optimal layout solutions of the test problems. The detailed best SEQUENCE-NR solutions for all data sets used in the optimality comparison test are summarized in Appendix D.1.

7.10.2 Heuristic Comparison Test

In the heuristic comparison test, we use SEQUENCE-NR to solve larger test data sets. Because there is little research that has been conducted on this problem, and consequently no competing methods to compare with, we propose nine different sized test problems to act as the benchmark for our tests and for future research. These nine test data sets are divided into three groups, where in each group there are three problems with the same size, but different configurations. The size of the problems in three groups are 10, 15 and

Table 7.6: Properties of the Data Sets for the Heuristic Comparison Test.

Data Set	Dept. #	Sub-Dept #	Fac. Input #	Fac. Output #	Uniform Flow
M10-1	10	19	0	0	Yes
M10-2	10	19	1	1	Yes
M10-3	10	19	1	1	No
M15-1	15	27	0	0	Yes
M15-2	15	27	1	1	Yes
M15-3	15	27	1	1	No
M20-1	20	35	0	0	Yes
M20-2	20	35	1	1	Yes
M20-3	20	35	1	1	No

20 departments, respectively. Within each group, the first test problem does not consider the facility input/output points and the material flows between different department pairs are equal (i.e., the flows are uniform). The facility input/output points are included in the second problem with uniform flow between different department pairs. For the third problem in each group, we consider the facility input/output points and non-uniform flow between department pairs. The properties of the test problems are given in Table 7.6.

As mentioned above, since little research has been conducted in the area of FLPNR, especially in the area of FLPNR heuristics, it is difficult to compare SEQUENCE-NR results with some other FLPNR heuristics from the literature. Therefore, we compare the SEQUENCE-NR solutions with the solutions from a greedy search algorithm based on a steepest-descent-pairwise-interchange algorithm, which we name SDPI-NR. Given an initial feasible sequence-pair, in each iteration SDPI-NR takes the steepest move in its "neighborhood," which is defined as the move that leads to the largest reduction in terms of the objective function value. The neighborhood of a sequence-pair, (Γ_+, Γ_-), is defined as a set that includes all of the possible sequence-pairs that can be obtained by implementing one two-way exchange of the positions of a pair of departments in (Γ_+, Γ_-) or rotating the orientation of one department in the sequence-pair. That is, for each possible pair of departments, the positions of all sub-departments of these two departments in the sequence-pair are exchanged and then all possible combination of different orientation settings for these two departments are explored (there are eight different combinations of the orientation settings for a pair of departments). In each iteration, all possible sequence-pairs in the neighborhood of the given sequence-pair are examined, and the sequence-pair that leads to the largest reduction in the objective function value is accepted as the updated sequence-pair. The heuristic stops when there are no sequence-pairs in the neighborhood of the current sequence-pair that can reduce the objective function value. Obviously, the final result of SDPI-NR depends on the initial feasible sequence-pair. We run SDPI-NR and SEQUENCE-NR 10 times and compare the best solutions found over the 10 runs. The comparison results are summarized in Table 7.7, where we provide the best objective function values over the 10 runs of each algorithm.

Table 7.7: Objective Function Value Results for a Heuristic Comparison Test for SEQUENCE-NR.

Data Set	SDPI-NR	SEQUENCE-NR	Improvement
M10-1	40.00	18.00	57.50%
M10-2	81.80	56.20	31.30%
M10-3	747.40	519.60	30.48%
M15-1	64.00	40.00	37.50%
M15-2	152.00	121.00	20.39%
M15-3	1256.00	863.50	31.25%
M20-1	N/A	88.50	N/A
M20-2	N/A	193.50	N/A
M20-3	N/A	2095.00	N/A

We can see from Table 7.7 that SEQUENCE-NR provides better solutions than the greedy algorithm SDPI-NR for all 6 of the 9 test data sets SDPI-NR was able to solve with an average improvement of 34.74% in terms of the objective function value. For the largest three test data sets, SDPI-NR exceeds the time limitation of 24 hours for each run and fails to solve the problem (i.e., SDPI-NR fails to find one initial feasible sequence-pair within 24 hours).

The solution time of SEQUENCE-NR and SDPI-NR for the test problems are provided in Table 7.8. Similar to the manner in which we reported the run time for SEQUENCE, we report both the time when SEQUENCE-NR and SDPI-NR found their best solution, respectively, and the total time for 10 runs. According to Table 7.8, the total run time of SEQUENCE-NR is much less than the total run time of SDPI-NR for the large test problems.

Also, unlike with the MIP-FLPNR, adding the facility I/O points does not significantly affect the solution time, which shows a higher degree of robustness on the part of SEQUENCE-NR. For the largest test problem, the total run time for 10 runs is less than 12 hours, which to us is justifiable for the FLPNR since facility design is not a real-time decision process. The detailed best SEQUENCE-NR solutions for all data sets used in the heuristic comparison test are summarized in Appendix D.2.

Table 7.8: Solution Time for All Data Sets Used in the Heuristic Comparison Test.

Problem	SEQUENCE-NR		SDPI-NR	
	Solution Time (Hrs.)	Total Time of 10 Runs (Hrs.)	Solution Time (Hrs.)	Total Time of 10 Runs (Hrs.)
M10-1	0.80	2.61	0.51	0.74
M10-2	2.62	2.62	0.74	0.74
M10-3	1.81	2.54	0.76	0.76
M15-1	2.41	4.04	6.25	39.61
M15-2	0.89	4.14	29.68	39.68
M15-3	1.32	4.25	29.61	39.68
M20-1	2.85	6.87	N/A	N/A
M20-2	0.67	6.72	N/A	N/A
M20-3	1.44	7.15	N/A	N/A

7.11 Summary

In this chapter we first presented an MIP framework for the FLPNR problem. The MIP-FLPNR model is formulated based on a partition methodology, which partitions a non-rectangular department into a series of rectangular sub-departments and the sub-departments are then connected correctly according to the orientation of the department by appropriate constraints. We tested the MIP-FLPNR model to explore the impact of different factors on the solution time of the model. We also explored the capability of the MIP-FLPNR model to solve the FLPNR problem in different configurations. Through our tests, it is obvious that the MIP-FLPNR model can only solve moderately-sized FLPNR problems.

Therefore, following the MIP-FLPNR model, we presented a sequence-pair representation based heuristic, SEQUENCE-NR, for solving larger-sized MIP-FLPNR problems. Different design issues, such as the encoding scheme, fitness function, selection rule, GA operator design, and parameter settings in SEQUENCE-NR were discussed in detail. Given a sequence-pair, the binary variables in the MIP-FLPNR are fixed, so there are only two types of constraints to affect the feasibility of the sequence-pair: the facility size constraints and the sub-department connection constraints. We presented a repair operator to test whether or not a sequence-pair satisfies the facility size constraints without actually solving the simplified MIP-FLPNR model according to a sufficient and necessary condition for satisfying the facility size constraints. We also presented a repair operator for the sub-department connection constraints to filter some sequences that do not satisfy the sub-department connection constraints without actually solving the simplified MIP-FLPNR model based on a necessary condition for satisfying the sub-department constraints. A combination repair method was provided to combine the two repair operators. The detailed procedures for SEQUENCE-NR were also given in Section 7.7.

We ran two types of numerical tests to test the efficiency and the effectiveness of SEQUENCE-NR to solve the sequence-pair based MIP-FLPNR. The optimality comparison test compared SEQUENCE-NR solutions with the optimal solutions based on some small- and medium-sized problems that were solved to optimality. The heuristic comparison test compared SEQUENCE-NR solutions with another heuristic for larger problems. The results from the two tests illustrate that SEQUENCE-NR can effectively solve MIP-FLPNR problems.

Chapter 8

Conclusions and Future Research

As one of the most important and challenging problems in both the operations research and industrial engineering research domains, the facility layout problem (FLP) can have a great impact on the production efficiency of modern industry. The facility layout determines the efficiency of the material handling system within a facility, and its impact extends far beyond material handling expenses. A well-designed layout can effectively reduce the material handling batch size, decrease the WIP, shorten the manufacturing lead time, increase the product quality, and thus provide more opportunities for a company's product. Due to the importance of the FLP, a great deal of research has been conducted in this area.

There are two types of representations in FLP research: the discrete representation and the continuous representation. Only the continuous-representation-based FLP can consider all possible all-rectangular-department solutions and this property makes the continuous-representation the representation-of-choice in today's FLP research, where much of the research is based on a methodology of mixed integer programming (MIP) models. However, these MIP-FLP models can only solve problems with a limited number of departments to optimality due to the large number of binary variables used in the model to represent the relative location between departments that prevent departments from overlapping. More specifically, there are many infeasible binary variable settings that waste a great deal of computational effort. Therefore, the main motivation of our research was to look for an effective way to eliminate these binary-infeasible variable settings and to solve the continuous-representation-based FLP more efficiently.

Our research focused on the sequence-pair representation, a concept that originated from the Very Large Scale Integration (VLSI) design literature. A sequence-pair is used to represent the relative location relationships between departments in the layout. We showed that one of the most important features of the sequence-pair representation is that each sequence-pair represents a feasible binary variable setting with respect to the relative location relationships between departments. This result turns out to be very powerful since it eliminates all binary-feasible — yet layout infeasible — variable settings. This represents a reduction in the number of layout solutions that need to be considered by over 99% even for a layout problem with a small number of departments (i.e., 6 departments) and that this percentage nearly approaches 100% for problems with a larger number of departments. We also showed that an exhaustive search of the sequence-pair solution space will result in finding the optimal layout of the MIP-FLP. Based on this fact, we proposed a methodology to combine the sequence-pair and MIP-FLP model to efficiently solve the larger-sized continuous-representation-based FLPs.

In the remainder of this chapter we first provide conclusions on our research contributions beyond a general methodology for combining the sequence-pair representation and the MIP-FLP and the associated progress we have made with this dissertation research. We then discuss our perspectives about future research in the research domain of applying the sequence-pair representation to the FLP.

8.1 Conclusions

In Chapter 4 we first presented a genetic algorithm based heuristic, SEQUENCE, that combines the sequence-pair representation and the most recent MIP-FLP model to solve the all-rectangular-department continuous-representation-based FLP. We designed a specific encoding scheme, a position-pair string, to transform a sequence-pair into a chromosome in SEQUENCE, where each gene in a position-pair string is a pair of values representing the two positions of the corresponding department in the sequence-pair. We believe that such an encoding scheme is useful for keeping a "good" pattern during the evolution of generations. The objective function of the MIP-FLP is used to establish the fitness function of SEQUENCE, and the roulette wheel selection rule is used to select parent chromosomes from the last generation. Based on the position-pair encoding scheme, we designed a crossover operator and a mutation operator, as well as a revised elitism operator, to drive SEQUENCE towards the optimal sequence-pair with respect to the MIP-FLP. We determined the parameter settings of SEQUENCE through a factorial experimental design. To further improve the efficiency of SEQUENCE to generate feasible sequence-pairs with respect to the MIP-FLP, we also utilized a penalty function method based on a relaxation of the facility size, where the relaxation amount of the facility size is reduced exponentially as the generations evolve to ensure final solution feasibility.

A series of numerical experiments were conducted to illustrate the effectiveness and efficiency of SEQUENCE for solving the all-rectangular-department continuous-representation-based FLP. We first ran SEQUENCE on all data sets that have been solved to optimality by the MIP-FLP in the literature and compared SEQUENCE's solutions with the optimal solutions for these data sets to show the quality of SEQUENCE's solutions. For 13 of 15 data sets, SEQUENCE achieved the optimal solution with no more than 8 runs. We then conducted numerical experiments for SEQUENCE on some larger-sized data sets widely referred to as benchmark problems in the FLP literature, comparing SEQUENCE's solutions with solutions from nine different heuristics to illustrate the effectiveness of SEQUENCE for solving larger-sized FLPs. For five widely used data sets with the best solution found by continuous-representation-based heuristics, we compared the best SEQUENCE solutions with the solutions from seven other heuristics. We also compared SEQUENCE with two discrete-representation-based heuristics, MULTIPLE and SABLE, to illustrate the advantages of SEQUENCE in terms of both the objective function value and resulting department shapes. To illustrate the effectiveness of SEQUENCE for solving real industrial problems, we also tested SEQUENCE on two large data sets from an industrial application and compared the solutions with other heuristics' solutions. Numerical experiments indicated that SEQUENCE provided better solutions as compared to other heuristics for all test data sets with a justifiable solution time.

In Chapter 5 we further considered applying SEQUENCE to solve the FLP with fixed departments. Through our initial research, we found that for the FLP with fixed departments, many sequence-pairs become infeasible with respect to the fixed department location and dimension restrictions. To address this difficulty, we presented a repair operator to repair a sequence-pair with respect to the fixed departments based on the lower and upper bound of the area of the departments that are allowed to be placed left of, right of, above and below a fixed department in the layout. We utilized these area bounds to determine the potentially feasible range of a fixed department's location in the given sequence-pair and placed the fixed department within its potentially feasible range in the sequence-pair to improve the likelihood of the sequence-pair being feasible after repair. We integrated this repair operator into SEQUENCE in order to solve the FLP with fixed departments more efficiently. Numerical experiments were conducted on different sized data sets with a different number of fixed departments. The effectiveness of the combination of SEQUENCE and the repair operator for solving the FLP with fixed departments was illustrated through a comparison between the best SEQUENCE solutions with two discrete-representation-based heuristics' solutions. The results showed that SEQUENCE with the repair operator provided better solutions in terms of both the objective function value and the department shapes. Furthermore, the impact of the number of fixed departments on the performance of SEQUENCE with the repair operator was also discussed.

In Chapter 6 we addressed the continuous-representation-based FLP with an existing aisle structure (FLPAL). Our research motivation was that in many industrial layout design problems, the impact of an existing aisle structure on the revision of the current layout must be taken into consideration. However, very little research has been conducted in this research domain. We illustrated that in FLPAL a facility is divided into several rectangular-shaped zones by an existing aisle structure and each department can be assigned to only one zone. Based on this analysis, we formulated the FLPAL as an MIP model (MIP-FLPAL). Numerical experiments for the MIP-FLPAL illustrated that similar to the MIP-FLP, the MIP-FLPAL can only be solved for very limited-sized FLPAL problems.

Therefore, we extended our research on the sequence-pair and MIP-based heuristic design to present a genetic algorithm based heuristic, SEQUENCE-AL, to combine the sequence-pair representation and MIP-FLPAL to solve larger-sized FLPAL problems. We first designed a specific zone-based sequence-pair representation, which has two hierarchies: a parent sequence-pair is used to represent the fixed relative location relationship between zones, and for each zone, a child sequence is used to represent relative location relationship between the departments assigned to that zone. We also designed a department assignment operator to transform a regular sequence-pair into a zone-based sequence-pair. Other important issues in the GA-based heuristic design, such as fitness function, selection rule, GA operator design and parameter settings, were also discussed in detail in Chapter 6. Numerical experiments on different sized data sets were conducted to illustrate the effectiveness of SEQUENCE-AL to solve the continuous-representation-based FLPAL, where a comparison with the optimal solutions for small-sized data sets and a comparison with two discrete-representation-based heuristics' solutions for larger-sized data sets were provided. The results of the numerical experiments illustrated that SEQUENCE-AL achieved optimal solutions for 5 of 6 small-sized data sets in 5 runs, and SEQUENCE-AL provided better solutions for all larger-sized data sets in terms of both the objective function value and the department shapes as compared to the other heuristics tested.

In Chapter 7 we studied the facility layout problem with non-rectangular-shaped departments (FLPNR). Although non-rectangular-shaped departments are very typical in industrial layout design applications, very little research is conducted in this research area. We defined one standard orientation from the four different orientations of each non-rectangular department obtained by rotating the department in a counterclockwise manner. We then formulated the FLPNR as an MIP model (MIP-FLPNR) based on a methodology where each non-rectangular department is partitioned into rectangular-shaped sub-departments by vertical borders in its standard orientation and the sub-departments from the same department are connected according to the department's orientation. The locations of the input/output points of the departments and the facility are also included in the MIP-FLPNR. The effect of different factors, such as the facility area utilization, the number of the departments/sub-departments and the number of input/output points, on the performance of the MIP-FLPNR was explored thoroughly through a series of numerical tests. The numerical tests illustrated that although MIP-FLPNR can successfully solve the FLPNR to optimality, the size of the FLPNR problems that can be solved to optimality with an affordable computational effort is limited.

We then presented a genetic algorithm based heuristic, SEQUENCE-NR, to solve larger-sized FLPNR problems. To encode a sequence-pair for the FLPNR as a chromosome in SEQUENCE-NR, we presented a position-pair-orientation encoding scheme, where a position-pair sub-string is used to represent the relative location relationship between sub-departments and an orientation sub-string is used to denote the orientation of departments. Based on this special encoding scheme, we designed a crossover operator, a mutation operator, an orientation adjustment operator, and a diversification operator to be used in SEQUENCE-NR. Given a sequence-pair, we showed that the MIP-FLPNR is simplified to a model with only two types of constraints: a facility size constraint and a sub-department connection constraint. We presented a sufficient and necessary condition for a sequence-pair to be feasible with respect to the facility size constraint. Based on this sufficient and necessary condition, we presented a repair operator to repair the infeasible sequence-pair with respect to the facility size constraint. We also presented a necessary condition for a sequence-pair to be feasible with respect to the sub-department connection constraint and designed a repair operator to repair the infeasible sequence-pair with respect to the sub-department connection constraint based on this necessary condition. The two repair operators were then integrated into SEQUENCE-NR to improve the efficiency of SEQUENCE-NR for solving the FLPNR. A series of numerical tests were conducted on different sized data sets, and the effectiveness of SEQUENCE-NR was illustrated by comparing the best SEQUENCE-NR solutions with both the optimal solutions and another heuristic's solutions. The results showed that SEQUENCE-NR achieved the optimal solutions in 7 of the 10 relatively small-sized data sets and provided better solutions in 6 out of the 9 larger-sized data sets that were tested against a benchmark heuristic.

In general, different types of continuous-representation-based FLPs were studied in this dissertation through a methodology of combining the sequence-pair representation and the MIP-FLP model. We presented a family of heuristics to effectively solve the continuous-representation-based FLP with and without fixed departments, the continuous-representation-based FLP with an existing aisle structure, and the continuous-representation-based FLP with non-rectangular departments. Numerical experiments illustrated the effectiveness of these sequence-pair and MIP-based heuristics for solving the different types of continuous-representation-based FLPs.

We initially hypothesized that a genetic algorithm approach would work well on this family of optimization problems. We believe our results support our initial hypothesis. Now that we have explored this topic more fully, we further hypothesize that the reason that a GA approach worked well is since local information from the gene tells us a great deal about the overall solution to the problem. That is, the variable set related to the relative location of departments is the most critical decision variable set. Note that this is not true for all genetic algorithm representations for all problems. But when it is, like in our case with a position-pair based encoding scheme for the facility layout problem, a genetic algorithm approach can be quite powerful.

8.2 Future Research

Given the capability of the sequence-pair representation to effectively represent all feasible relative location relationships between departments in the mixed-integer programming based layout problem, combining the sequence-pair representation with the MIP model to solve the FLP is a rich research domain with more research directions than we were able to explore in this dissertation.

As a very challenging and complicated problem, there are many different types of FLPs, from block layout design to detailed layout design, from Greenfield layout design to re-layout design, from single-floor layout design to multiple-floor layout design, from centroid-to-centroid distance-based layout evaluation to contour distance-based layout evaluation, and from layout design with all-rectangular departments to layout design with non-rectangular and fixed departments. Each type of FLP has its own special characteristics and these different types of FLPs are not exclusive to each other. That is, there are many layout problems in industry that include features of multiple types of FLPs; e.g., an FLP with fixed non-rectangular departments, an FLP with fixed non-rectangular departments and an existing aisle structure, a multiple-floor FLP with fixed departments, an existing aisle structure and non-rectangular departments, an FLP based on contour-distances and non-rectangular departments and an aisle structure, etc. Further research on extending the sequence-pair and MIP-based heuristics that we developed to solve these different types of FLPs appears to be attractive for both FLP researchers and industrial layout planners. We believe that the research in this dissertation on the layout-sequence-pair representation will provide an excellent foundation for studying these layout problems.

In studying the FLP we adopted the traditional “top-down” methodology to design a layout; i.e., the block layout design is determined before the detailed layout design within each department. However, as recently noted by Meller, Kleiner, and Nussbaum [46], one difficulty with this methodology is that some of the information needed in the block layout design phase can only be accurately derived once the detailed layout design phase is solved. Therefore, Meller, Kleiner, and Nussbaum [46] presented a new model to solve layout problems through a "bottom-up" design methodology, where the detailed layout design is first considered to determine a set of feasible department arrangements that specify the department shape, department area, and locations of input/output points in the department. Then, the layout design for the whole facility is determined by selecting a detailed layout design for each department and optimizing the relative department locations under possible aisle structures.

The bottom-up approach appears to be a very promising new research direction that can greatly improve the practical value of current FLP research. Our research on the FLP with non-rectangular departments partially fell into this research category since in our research the department shape was determined *a priori* and the research objective was to select an appropriate location and orientation for these non-rectangular departments to minimize the material handling cost. However, in our formulation we only considered one arrangement for each department.

Extensions to our research that further support the bottom-up design methodology could be considered through allowing multiple feasible arrangements for each department; e.g., a department can be I-shaped with specific dimensions and a pre-defined arrangement of machines that leads to particular input/output point locations, or L-shaped with a different arrangement of the department area, shape and input/output point locations. The algorithm would then determine the actual arrangement, location and orientation for each department based on the objective of minimizing the total material handling cost. Such an extension can be made in the MIP model and the sequence-pair representation used in MIP-FLPNR does not need to be changed as long as a sequence-pair is used to represent the relative location relationship between departments/sub-departments. However, a new aspect to the chromosome of a solution would need to be considered: the department arrangement selected. Since each department arrangement may have a different number of sub-departments, the chromosome representation would have be considered carefully. Nonetheless, it appears that extending the MIP-FLPNR and SEQUENCE-FLPNR is also a very promising future research direction. Once the MIP-FLPNR and SEQUENCE-FLPNR are extended to the bottom-up design methodology, then other aspects of the FLP, like incorporating an aisle structure and measuring distances with a contour-based aisle approach, would greatly enhance existing FLP research.

As the heuristics developed in this dissertation are extended further to incorporate additional aspects of the FLP, improving the runtime performance of the heuristics will need to be considered as an area of future research. One possible manner in which to improve the performance of the sequence-pair based heuristics is to design more repair operators to efficiently repair or filter infeasible sequence-pairs without actually solving the simplified MIP model. Another possible way to improve the performance of the sequence-pair based heuristics is to study other possible meta-heuristics, such as Simulated Annealing, Tabu Search, Artificial Neural Networks, Ant-Colony Based Approaches, etc., to explore the possibility of designing more efficient sequence-pair based heuristics. Moreover, further research on the properties of the sequence-pair as well as FLP models that explicitly consider the sequence-pair representation in the optimization algorithm may also provide possible opportunities for improving the performance of these sequence-pair and MIP model-based FLP heuristics.

Finally, since the motivation for our research came from the VLSI design literature, our research results can also benefit the research in the VLSI design domain. Although the correspondence between the FLP and VLSI design is not exact, there are similarities between the two research domains. We believe that some of our research results in this dissertation, like the repair operator concept and the methodology for the layout with non-rectangular departments, can be applied to VLSI design. Further research aimed at adopting our results to the VLSI design research domain with the appropriate changes based on the differences between the FLP and VLSI design appears to be another interesting research direction.

Appendix

Appendix A. Summary of Numerical Test Results in Chapter 4

A.1. Numerical Test Results for the Optimality Comparison Test

The following tables summarize the results of the best SEQUENCE solutions for the optimality comparison test.

Data Set M6:

Dept #	Centroids		2 $\times$ Half-Length	
	x	y	x	y
1	13.42	2.50	2.80	5.00
2	11.02	2.50	2.00	5.00
3	9.12	2.50	1.80	5.00
4	7.61	2.50	1.22	4.90
5	1.00	2.50	2.00	5.00
6	4.50	2.50	5.00	5.00

Data Set M7:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	11.42	2.50	2.80	5.00
2	13.82	2.50	2.00	5.00
3	0.90	2.50	1.80	5.00
4	2.41	2.50	1.22	4.90
5	9.02	2.50	2.00	5.00
6	5.52	2.50	5.00	5.00
7	17.32	2.50	5.00	5.00

Data Set FO7:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	1.13	9.47	2.27	7.05
2	3.40	9.47	2.27	7.05
3	6.54	10.99	4.00	4.00
4	6.54	4.50	4.00	8.99
5	3.78	2.97	1.51	5.95
6	2.27	2.97	1.51	5.95
7	0.76	2.97	1.51	5.95

Data Set FO7-1:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	7.43	9.49	2.22	7.02
2	5.21	9.49	2.22	7.02
3	2.05	10.47	4.10	3.80
4	2.05	4.28	4.10	8.57
5	4.84	3.02	1.48	5.92
6	6.32	3.02	1.48	5.92
7	7.80	3.02	1.48	5.92

Data Set FO7-2:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.27	12.06	8.54	1.87
2	4.27	10.19	8.54	1.87
3	4.27	8.32	8.54	1.87
4	4.27	5.27	8.54	4.22
5	2.85	2.37	5.69	1.58
6	2.85	0.79	5.69	1.58
7	7.12	1.58	2.84	3.16

Data Set F8:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	1.07	3.72	2.14	7.44
2	3.21	3.72	2.14	7.44
3	5.36	3.72	2.14	7.44
4	8.85	3.72	4.84	7.44
5	8.07	10.22	6.47	5.56
6	4.03	10.22	1.61	5.56
7	2.42	10.22	1.61	5.56
8	0.81	10.22	1.61	5.56

Data Set F9:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	1.14	9.50	2.29	7.00
2	3.43	9.50	2.29	7.00
3	5.71	9.50	2.29	7.00
4	9.43	9.50	5.14	7.00
5	9.00	3.00	6.00	6.00
6	5.25	3.00	1.50	6.00
7	3.75	3.00	1.50	6.00
8	2.25	3.00	1.50	6.00
9	0.75	3.00	1.50	6.00

Data Set NO7:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	2.96	1.35	5.92	2.70
2	2.96	11.65	5.92	2.70
3	7.23	3.06	2.62	6.11
4	2.96	5.74	5.92	6.08
5	7.23	7.83	2.62	3.44
6	2.96	9.54	5.92	1.52
7	7.23	11.27	2.62	3.44

Data Set NO7-1:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.26	1.19	6.57	2.38
2	0.99	4.21	1.97	7.90
3	5.17	11.84	6.73	2.32
4	5.26	5.05	6.57	5.34
5	5.26	8.46	5.92	1.48
6	0.90	10.58	1.81	4.84
7	5.26	9.94	5.92	1.48

Data Set NO7-2:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.23	1.21	6.62	2.42
2	0.96	4.20	1.92	8.26
3	5.23	11.79	6.62	2.42
4	5.23	5.14	6.62	5.44
5	5.23	8.54	6.62	1.36
6	0.96	10.67	1.92	4.67
7	5.23	9.90	6.62	1.36

Data Set O7:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	3.27	1.23	6.53	2.45
2	7.54	3.98	2.01	7.96
3	6.95	10.48	3.18	5.04
4	3.27	5.21	6.53	5.51
5	2.68	8.80	5.36	1.68
6	2.69	12.16	5.35	1.68
7	2.68	10.48	5.36	1.68

Data Set O7-1:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.07	1.12	6.95	2.24
2	5.64	11.66	5.81	2.68
3	1.37	10.15	2.73	5.71
4	5.07	4.77	6.95	5.05
5	5.64	8.05	5.81	1.51
6	0.80	4.55	1.59	5.50
7	5.64	9.56	5.81	1.51

Data Set O7-2:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.27	2.81	8.54	1.87
2	4.27	0.94	8.54	1.87
3	4.27	12.06	8.54	1.87
4	4.27	5.85	8.54	4.22
5	5.69	8.75	5.69	1.58
6	1.42	9.54	2.84	3.16
7	5.69	10.34	5.69	1.58

Data Set O8:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	2.96	8.95	5.92	2.70
2	2.96	11.65	5.92	2.70
3	8.62	1.50	5.39	2.97
4	2.96	4.56	5.92	6.08
5	8.62	9.66	5.39	6.68
6	8.62	3.82	5.39	1.67
7	2.96	0.76	5.92	1.52
8	8.62	5.49	5.39	1.67

Data Set O9:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	2.94	4.11	5.82	2.75
2	9.74	9.73	4.52	3.54
3	2.92	1.37	5.85	2.74
4	2.99	8.49	5.98	6.02
5	9.74	3.98	4.52	7.96
6	6.73	8.48	1.50	6.00
7	3.00	12.25	6.00	1.50
8	9.00	12.25	6.00	1.50
9	6.67	2.74	1.64	5.48

A.2. Numerical Test Results for the Heuristic Comparison Tests

The following tables summarize the results of the best SEQUENCE solutions for the heuristic comparison tests.

Data Set BM9:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	2.94	4.11	5.82	2.75
2	9.74	9.73	4.52	3.54
3	2.92	1.37	5.85	2.74
4	2.99	8.49	5.98	6.02
5	9.74	3.98	4.52	7.96
6	6.73	8.48	1.50	6.00
7	3.00	12.25	6.00	1.50
8	9.00	12.25	6.00	1.50
9	6.67	2.74	1.64	5.48

Data Set v10:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	2.66	28.70	5.32	44.60
2	15.16	36.93	19.68	5.69
3	12.50	3.20	25.00	6.40
4	16.05	28.50	7.16	11.18
5	9.06	14.66	7.24	16.51
6	8.89	28.50	7.16	11.18
7	22.32	28.50	5.37	11.18
8	15.25	14.66	5.14	16.51
9	15.16	45.39	19.68	11.22
10	21.41	14.66	7.18	16.51

Data Set M11*:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.23	2.69	1.52	1.98
2	2.13	4.84	0.86	2.33
3	0.85	4.83	1.70	2.35
4	4.28	5.27	3.44	1.45
5	2.97	2.69	1.01	1.98
6	4.28	4.11	3.44	0.87
7	1.23	2.84	2.46	1.62
8	1.23	1.01	2.46	2.03
9	5.24	2.69	0.51	1.98
10	5.75	2.69	0.51	1.98
11	4.23	0.85	3.54	1.70

Data Set BM12:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	2.87	2.57	1.75	0.57
2	2.87	4.86	1.75	0.57
3	4.31	7.55	1.11	0.90
4	2.87	5.43	1.75	0.57
5	2.87	3.14	1.75	0.57
6	2.87	3.71	1.75	0.57
7	5.42	7.55	1.11	0.90
8	2.87	4.29	1.75	0.57
9	2.87	1.14	1.75	2.29
10	2.87	6.86	1.75	2.29
11	1.00	4.00	2.00	8.00
12	4.87	3.55	2.25	7.10

Data Set Ba12:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.00	5.50	9.00	1.00
2	5.00	4.50	8.00	1.00
3	5.00	0.50	10.00	1.00
4	5.00	1.50	6.00	1.00
5	5.00	2.50	4.00	1.00
6	8.50	3.50	3.00	1.00
7	8.50	2.50	3.00	1.00
8	5.00	3.50	4.00	1.00
9	2.00	2.50	2.00	1.00
10	2.00	3.50	2.00	1.00
11	0.50	4.50	1.00	1.00
12	1.50	1.50	1.00	1.00

Data Set Ba13:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.10	1.58	7.80	1.15
2	5.10	5.21	7.80	1.03
3	5.10	2.73	7.80	1.15
4	5.10	6.36	7.80	1.28
5	5.10	0.50	6.00	1.00
6	7.33	4.00	2.16	1.39
7	0.60	5.75	1.20	2.50
8	5.17	4.00	2.16	1.39
9	1.92	4.00	1.44	1.39
10	0.60	1.25	1.20	2.50
11	3.36	4.00	1.44	1.39
12	0.70	4.00	1.00	1.00
13	0.70	3.00	1.00	1.00

Data Set Ba14:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	1.65	3.56	1.31	6.87
2	5.82	3.56	1.16	6.87
3	2.96	3.56	1.31	6.87
4	7.13	3.56	1.45	6.87
5	0.50	3.56	1.00	6.00
6	4.43	6.00	1.62	1.85
7	8.43	1.38	1.15	2.61
8	4.43	4.14	1.62	1.85
9	8.43	3.56	1.15	1.75
10	4.43	1.05	1.62	1.85
11	4.43	2.60	1.62	1.24
12	8.35	4.94	1.00	1.00
13	8.35	5.94	1.00	1.00
14	3.93	0.06	7.85	0.13

Data Set M15*:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	3.13	13.80	6.26	2.40
2	8.14	13.67	3.77	2.65
3	8.11	2.87	1.57	5.73
4	6.71	2.87	1.22	5.73
5	3.13	11.88	6.26	1.44
6	12.51	12.49	4.97	5.02
7	11.95	3.68	6.11	4.09
8	12.51	8.47	4.97	3.02
9	0.87	2.87	1.74	5.73
10	3.92	2.87	4.36	5.73
11	11.95	0.82	6.11	1.64
12	3.13	6.93	6.26	2.40
13	12.46	6.35	4.87	1.23
14	3.13	9.65	6.26	3.04
15	8.14	9.04	3.77	6.62

Data Set AB20:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	160.35	183.96	79.31	34.03
2	128.89	239.88	23.08	77.81
3	27.04	191.89	54.07	49.89
4	105.81	239.88	23.08	77.81
5	170.21	216.08	59.57	30.21
6	96.50	289.39	84.85	21.21
7	84.22	256.44	20.10	44.70
8	64.12	256.44	20.10	44.70
9	107.48	183.96	26.42	34.03
10	40.41	127.66	30.52	78.55
11	159.58	129.85	80.84	74.17
12	87.42	133.87	63.48	66.13
13	12.58	35.85	25.15	71.47
14	12.58	119.26	25.15	95.36
15	40.41	44.19	30.52	88.39
16	159.58	46.38	80.84	92.77
17	87.42	50.40	63.48	100.81
18	170.21	265.59	59.57	68.82
19	74.17	200.51	40.20	67.15
20	27.04	258.42	54.07	83.17

Data Set M25*:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	14.09	0.55	1.83	1.10
2	9.62	1.35	1.96	0.51
3	11.50	4.07	2.69	1.86
4	14.06	1.89	1.89	1.59
5	11.70	2.91	2.20	0.45
6	9.62	2.37	1.96	1.53
7	13.92	3.84	2.16	2.32
8	2.01	4.26	2.02	1.48
9	9.62	4.07	1.07	1.86
10	7.20	4.07	0.54	1.86
11	5.39	4.26	2.02	1.48
12	7.87	0.68	1.48	1.35
13	11.86	1.89	2.52	1.59
14	0.50	2.50	1.00	5.00
15	2.56	1.60	3.13	0.64
16	5.26	2.64	2.27	1.76
17	6.77	0.68	0.74	1.35
18	2.56	2.72	3.13	1.60
19	8.28	4.07	1.61	1.86
20	2.56	0.64	3.13	1.28
21	6.67	4.07	0.54	1.86
22	5.26	0.88	2.27	1.76
23	10.89	0.55	4.56	1.10
24	3.70	4.26	1.35	1.48
25	7.52	2.25	2.24	1.78

Data Set SC30:

Dept #	Centroids		2 $\times$ Half-Length	
	x	y	x	y
1	1.80	0.48	3.14	0.95
2	14.51	6.28	0.97	4.08
3	6.51	4.86	4.47	0.89
4	6.51	3.52	8.94	1.79
5	13.39	9.61	1.54	2.59
6	13.39	6.37	1.28	3.90
7	11.21	4.74	3.08	0.65
8	11.21	5.55	3.08	0.97
9	11.21	6.85	3.08	1.62
10	7.98	11.45	5.48	1.10
11	11.21	7.99	3.08	0.65
12	7.98	9.61	9.27	2.59
13	2.76	9.61	1.17	4.29
14	2.69	6.32	1.31	2.29
15	6.51	7.45	6.32	1.74
16	1.09	9.68	2.18	2.75
17	1.02	7.81	2.04	0.98
18	6.51	5.94	6.32	1.26
19	12.63	1.87	2.19	1.82
20	14.36	1.94	1.28	3.89
21	12.35	3.51	2.74	1.46
22	14.58	10.09	0.84	3.55
23	11.26	1.87	0.55	1.82
24	1.02	1.69	2.04	1.47
25	3.89	0.48	1.05	0.95
26	1.02	6.34	2.04	1.96
27	1.02	3.89	2.04	2.94
28	2.69	4.80	1.31	0.76
29	6.51	1.79	8.37	1.67
30	6.51	0.48	4.19	0.95

Data Set SC35:

Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	7.51	1.72	3.00	1.00
2	12.38	2.88	3.83	1.31
3	2.06	11.26	1.00	4.00
4	3.49	11.26	1.87	7.48
5	12.38	6.07	3.83	1.05
6	12.38	4.18	3.83	1.31
7	8.38	8.19	1.14	1.75
8	9.42	8.19	0.93	3.21
9	10.66	8.19	1.56	3.21
10	14.25	8.19	1.87	3.21
11	12.38	5.19	2.83	0.71
12	12.38	8.19	1.87	3.21
13	8.38	11.26	1.14	4.38
14	9.47	11.26	1.03	2.92
15	6.91	11.26	1.80	7.21
16	15.39	12.25	1.22	4.90
17	8.45	14.22	1.29	1.56
18	5.22	11.26	1.58	6.32
19	9.50	3.26	1.93	2.07
20	10.89	1.56	3.75	1.33
21	15.15	3.39	1.71	2.34
22	9.59	5.73	1.74	1.73
23	9.59	4.58	1.74	0.57
24	7.70	5.89	1.05	2.85
25	8.28	3.35	0.50	2.00
26	1.01	1.23	2.01	1.99
27	4.46	0.61	4.90	1.22
28	8.47	5.47	0.50	2.00
29	4.01	3.35	8.03	2.24
30	4.01	1.72	4.00	1.00
31	12.38	13.86	3.94	2.28
32	12.38	11.26	4.80	2.92
33	4.01	5.26	6.32	1.58
34	4.01	6.55	4.00	1.00
35	9.75	13.86	1.31	2.28

A.3. Flow Matrix Data for Data Sets SC30 and SC35

The following tables summarize the flow data for the two new data sets: SC30 and SC35.

Flow Data for SC30:

Dept i	Dept j	Flow f_{ij}	Dept i	Dept j	Flow f_{ij}
1	24	2.95	10	12	38.03
1	25	6.32	11	12	8.84
1	26	1.26	12	13	12.97
1	27	2.11	12	14	4.67
1	28	1.26	12	15	53.42
1	30	13.91	12	16	1.83
2	6	20.38	13	15	12.97
2	19	4.50	14	15	4.67
2	20	3.63	15	4	63.95
2	21	2.93	15	18	190.74
2	22	1.29	16	15	4.58
2	23	1.43	17	15	0.76
4	3	394.11	18	4	190.74
5	11	4.09	19	29	9.18
5	12	33.09	20	29	7.40
6	5	8.92	21	29	5.97
6	7	2.07	22	29	2.63
6	8	4.84	23	29	2.92
6	10	4.56	24	29	5.90
6	12	1.83	25	29	12.65
6	17	0.61	26	29	2.53
7	8	12.97	27	29	4.22
8	9	43.23	28	29	2.53
9	11	4.76	29	4	190.13
9	12	38.47	30	29	59.64

Flow Data for SC35:

Dept i	Dept j	Flow f_{ij}	Dept i	Dept j	Flow f_{ij}
1	24	2.95	11	12	8.84
1	25	6.32	12	32	72.89
1	26	1.26	13	15	12.97
1	27	2.11	14	15	4.67
1	28	1.26	15	4	63.95
1	30	13.91	15	18	190.74
2	6	20.38	16	15	4.58
2	19	4.50	17	15	0.76
2	20	3.63	18	4	190.74
2	21	2.93	19	29	9.18
2	22	1.29	20	29	7.40
2	23	1.43	21	29	5.97
4	3	225.65	22	29	2.63
5	11	4.09	23	29	2.92
5	12	33.09	24	29	5.90
6	5	8.92	25	29	12.65
6	7	2.07	26	29	2.53
6	8	4.84	27	29	4.22
6	10	4.56	28	29	2.53
6	12	1.83	29	33	190.13
6	17	0.61	30	29	59.64
6	31	3.93	31	32	22.92
7	8	12.97	32	13	12.97
8	9	43.23	32	14	4.67
9	11	4.76	32	15	53.42
9	12	38.47	32	16	1.83
10	12	38.03	33	34	168.45

Appendix B. Summary of Numerical Test Results in Chapter 5

B.1. Numerical Test Results for the FLP with a Single Fixed Department

The following tables summarize the results of the best SEQUENCE solutions for the FLP with a single fixed department. The flow data are not changed from the original problem, which can be found either in the literature where the associated data sets were first proposed or in Appendix A.3. (the two new data sets).

Data Set M11:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	4.50	3.17	1.80	1.66
2	No	2.52	1.04	0.96	2.08
3	No	4.50	0.67	3.00	1.33
4	No	1.02	1.22	2.05	2.44
5	No	2.56	3.21	0.89	2.25
6	No	4.50	1.84	3.00	1.00
7	No	1.06	3.39	2.11	1.89
8	No	1.50	5.17	3.00	1.67
9	No	5.70	3.17	0.60	1.66
10	No	3.30	3.17	0.60	1.66
11	Yes	4.50	5.00	3.00	2.00

Data Set Ba12F1:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	3.96	5.21	5.67	1.59
2	No	3.96	3.71	5.66	1.41
3	No	4.14	0.94	5.30	1.88
4	No	8.38	0.94	3.18	1.88
5	No	8.29	3.88	1.00	4.00
6	Yes	3.50	2.50	3.00	1.00
7	No	0.99	1.50	1.00	3.00
8	No	7.29	3.88	1.00	4.00
9	No	5.90	2.44	1.79	1.12
10	No	9.15	3.71	0.71	2.83
11	No	9.75	3.71	0.50	2.00
12	No	0.78	3.71	0.71	1.41

Data Set M15:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	3.50	2.50	7.00	2.14
2	No	3.50	0.71	7.00	1.43
3	No	7.84	2.67	1.68	5.32
4	No	9.34	2.67	1.31	5.32
5	No	6.35	7.12	1.30	6.92
6	No	2.85	5.76	5.70	4.38
7	No	2.83	12.79	5.65	4.42
8	No	2.85	9.27	5.70	2.63
9	No	14.29	3.50	1.43	6.99
10	No	11.79	3.50	3.57	6.99
11	No	8.50	13.33	3.00	3.33
12	No	12.49	8.50	4.98	3.01
13	No	6.33	12.79	1.35	4.42
14	No	8.50	8.50	3.00	6.34
15	Yes	12.50	12.50	5.00	5.00

Data Set M25F1:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	0.43	1.16	0.86	2.32
2	No	8.87	1.12	0.45	2.24
3	No	12.57	4.51	4.87	1.03
4	No	1.50	1.16	1.29	2.32
5	No	10.93	3.15	0.59	1.69
6	No	12.35	1.15	1.30	2.31
7	No	3.23	1.15	2.17	2.31
8	No	1.57	3.89	1.35	2.23
9	No	11.27	1.15	0.87	2.31
10	No	10.61	1.15	0.45	2.24
11	No	12.11	3.15	1.78	1.69
12	No	9.96	3.06	1.34	1.50
13	No	5.18	1.15	1.73	2.31
14	No	4.10	4.33	3.71	1.35
15	No	7.35	0.38	2.60	0.77
16	No	14.00	3.00	2.00	2.00
17	No	8.96	3.06	0.67	1.50
18	No	4.10	2.98	3.71	1.35
19	No	9.74	1.15	1.30	2.31
20	No	7.35	1.54	2.60	1.54
21	No	1.12	2.55	2.24	0.45
22	No	7.29	3.06	2.67	1.50
23	No	8.05	4.40	4.18	1.20
24	No	0.45	3.89	0.90	2.23
25	Yes	14.00	1.00	2.00	2.00

Data Set SC30F1:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	2.28	9.49	0.77	3.87
2	No	3.76	1.54	4.47	0.89
3	No	10.15	10.35	4.47	0.89
4	No	10.15	8.83	7.42	2.16
5	No	9.00	1.54	4.47	0.89
6	No	3.76	0.60	5.00	1.00
7	No	1.00	3.85	1.17	1.70
8	No	2.08	3.91	0.99	3.00
9	No	3.43	3.91	1.70	2.94
10	No	9.00	0.55	5.48	1.10
11	No	4.64	3.81	0.73	2.75
12	Yes	9.00	3.50	8.00	3.00
13	No	13.83	3.50	1.66	3.00
14	No	12.60	1.13	1.73	1.73
15	No	10.15	5.74	7.42	1.48
16	No	14.43	7.63	1.14	5.25
17	No	0.76	1.75	1.53	1.31
18	No	10.15	7.12	6.32	1.26
19	No	3.07	6.26	2.35	1.70
20	No	1.39	9.09	1.00	5.00
21	No	0.45	8.83	0.89	4.47
22	No	0.79	5.64	1.58	1.89
23	No	3.88	2.21	2.24	0.45
24	No	3.46	11.05	1.57	1.90
25	No	3.12	7.33	2.24	0.45
26	No	13.53	11.13	2.29	1.75
27	No	8.94	11.40	4.99	1.20
28	No	5.36	5.42	2.17	0.46
29	No	5.34	8.83	2.20	6.35
30	No	3.46	8.83	1.57	2.54

B.2. Numerical Test Results for the FLP with Multiple Fixed Departments

The following tables summarize the results of the best SEQUENCE solutions for the FLP with multiple fixed departments. The flow data are not changed from the original problem, which can be found either in the literature where the associated data sets were first proposed or in Appendix A.3. (the two new data sets).

Data Set Ba12F2:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	4.50	0.79	5.67	1.59
2	No	4.50	2.29	5.66	1.41
3	No	4.50	5.00	5.00	2.00
4	No	8.50	5.00	3.00	2.00
5	No	8.01	1.53	1.35	2.95
6	Yes	4.50	3.50	3.00	1.00
7	No	0.95	1.95	1.42	2.11
8	No	8.00	3.50	4.00	1.00
9	No	1.50	5.00	1.00	2.00
10	No	9.30	2.18	1.21	1.65
11	Yes	2.50	3.50	1.00	1.00
12	No	1.50	3.50	1.00	1.00

Data Set M25F2:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	5.26	1.60	2.50	0.80
2	No	12.75	4.00	0.50	2.00
3	No	2.00	0.62	4.01	1.25
4	No	5.50	2.50	2.99	1.00
5	No	0.40	3.13	0.80	1.25
6	No	10.84	2.10	1.67	1.80
7	No	2.03	1.88	3.97	1.26
8	No	5.26	0.60	2.50	1.20
9	No	8.76	1.60	2.50	0.80
10	No	8.76	0.60	0.83	1.20
11	Yes	8.50	2.50	3.00	1.00
12	No	12.00	4.00	1.00	2.00
13	No	2.41	3.13	3.21	1.25
14	No	14.17	1.50	1.66	3.00
15	No	5.51	4.67	3.00	0.67
16	No	8.01	4.00	2.00	2.00
17	No	11.25	4.00	0.50	2.00
18	No	12.51	1.50	1.66	3.00
19	No	10.43	0.60	2.50	1.20
20	No	5.51	3.67	3.00	1.33
21	No	7.93	0.60	0.83	1.20
22	No	10.01	4.00	2.00	2.00
23	No	2.00	4.38	4.01	1.25
24	No	7.01	1.00	1.00	2.00
25	Yes	14.00	4.00	2.00	2.00

Data Set SC30F2:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	13.82	1.90	0.79	3.80
2	No	2.63	3.97	3.70	1.08
3	No	8.95	2.76	4.47	0.89
4	No	8.95	4.11	8.94	1.79
5	No	2.26	8.50	0.89	4.47
6	No	2.36	5.30	3.17	1.58
7	No	0.39	5.27	0.77	2.58
8	No	0.39	8.50	0.77	3.87
9	No	1.29	8.50	1.03	4.83
10	No	3.32	8.50	1.24	4.83
11	No	2.26	11.23	3.16	0.63
12	No	5.66	8.50	3.43	7.00
13	No	10.00	9.59	5.00	1.00
14	No	10.00	10.48	3.87	0.77
15	No	10.00	8.05	5.26	2.09
16	No	10.02	11.43	5.29	1.13
17	No	13.37	10.21	1.41	1.41
18	Yes	10.00	6.00	4.00	2.00
19	No	2.54	2.84	3.39	1.18
20	No	2.00	0.62	4.00	1.25
21	No	2.00	1.75	4.00	1.00
22	No	5.48	2.61	2.48	1.21
23	No	0.42	2.84	0.85	1.18
24	No	14.61	1.90	0.79	3.80
25	No	12.07	2.28	1.77	0.57
26	No	14.21	5.70	1.58	2.54
27	No	13.81	8.24	2.37	2.53
28	No	14.21	4.12	1.58	0.63
29	Yes	7.50	1.00	7.00	2.00
30	No	12.00	1.00	2.00	2.00

Data Set SC30F3:

Dept #	Fixed?	Centroids		2 × Half-Length	
		x	y	x	y
1	No	2.53	3.94	1.00	2.99
2	No	3.46	7.72	3.02	1.32
3	No	10.00	10.74	4.47	0.89
4	No	10.00	9.39	8.94	1.79
5	No	6.57	5.70	2.85	1.40
6	No	3.49	6.25	3.07	1.63
7	No	14.33	7.75	1.33	1.50
8	No	14.00	5.50	2.00	1.50
9	No	14.00	3.50	2.00	2.50
10	No	12.50	1.00	3.00	2.00
11	No	4.68	3.58	0.63	3.16
12	Yes	9.00	3.50	8.00	3.00
13	No	6.30	11.14	2.92	1.71
14	No	13.11	11.14	1.75	1.71
15	No	10.00	7.75	7.33	1.50
16	No	3.31	11.02	3.06	1.96
17	No	1.07	10.75	1.41	1.41
18	Yes	10.00	6.00	4.00	2.00
19	No	3.70	3.94	1.34	2.99
20	No	3.46	9.21	3.02	1.66
21	No	1.01	1.00	2.00	2.00
22	No	0.98	9.27	1.95	1.54
23	No	5.28	7.39	0.50	1.98
24	No	1.60	3.72	0.87	3.43
25	No	3.25	2.22	2.24	0.45
26	No	0.58	3.72	1.16	3.43
27	No	0.98	6.97	1.95	3.07
28	No	5.25	9.39	0.56	1.79
29	Yes	7.50	1.00	7.00	2.00
30	No	3.00	1.00	2.00	2.00

Appendix C. Summary of Numerical Test Results in Chapter 6

C.1. Numerical Test Results for the Optimality Comparison Test

The following tables summarize the results of the best SEQUENCE-AL solutions for the optimality comparison test. Since SEQUENCE-AL achieves the optimal solutions for all data sets except Data Set O9a, we only report the optimal solutions (which are also the best SEQUENCE-AL solutions) for all data sets except O9a. For O9a, we report both the optimal solution and the best SEQUENCE-AL solution. The flow data are not changed from the original problem, which can be found in [61].

Data Set F7a-1:

Zone Data				
Zone #	Centroids		$2 \times$ Half-Length	
	x	y	x	y
1	8.00	6.00	16.00	4.00
2	4.50	2.00	9.00	4.00
3	12.50	2.00	7.00	4.00

Optimal Solution				
Dept #	Centroids		$2 \times$ Half-Length	
	x	y	x	y
1	4.00	1.00	8.00	2.00
2	4.00	3.00	8.00	2.00
3	3.89	6.00	4.00	4.00
4	10.39	6.00	9.00	4.00
5	10.39	2.00	2.24	4.00
6	12.63	2.00	2.24	4.00
7	14.88	2.00	2.24	4.00

Data Set FO7a-2:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	8.00	6.00	16.00	4.00
2	4.50	2.00	9.00	4.00
3	12.50	2.00	7.00	4.00
Optimal Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.00	1.00	8.00	2.00
2	4.00	3.00	8.00	2.00
3	3.89	6.00	4.00	4.00
4	10.39	6.00	9.00	4.00
5	10.39	2.00	2.24	4.00
6	12.63	2.00	2.24	4.00
7	14.88	2.00	2.24	4.00

Data Set O7a-1:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	8.00	6.00	16.00	4.00
2	4.50	2.00	9.00	4.00
3	12.50	2.00	7.00	4.00
Optimal Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.50	6.75	6.40	2.50
2	13.24	2.00	4.00	4.00
3	10.90	6.75	6.40	2.50
4	4.50	2.00	9.00	4.00
5	10.12	2.00	2.24	4.00
6	4.50	4.75	6.00	1.50
7	10.50	4.75	6.00	1.50

Data Set O7a-2:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	8.00	6.00	16.00	4.00
2	4.50	2.00	9.00	4.00
3	12.50	2.00	7.00	4.00
Optimal Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.50	6.59	6.42	2.49
2	13.24	2.00	4.00	4.00
3	10.89	6.74	6.36	2.52
4	4.50	2.00	9.00	4.00
5	10.12	2.00	2.24	4.00
6	4.50	4.67	6.71	1.34
7	10.89	4.74	6.07	1.48

Data Set O8a:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	8.00	6.00	16.00	4.00
2	4.50	2.00	9.00	4.00
3	12.50	2.00	7.00	4.00
4	18.50	4.00	5.00	8.00
Optimal Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.00	1.00	8.00	2.00
2	4.00	3.00	8.00	2.00
3	3.89	6.00	4.00	4.00
4	10.39	6.00	9.00	4.00
5	10.39	2.00	2.24	4.00
6	12.63	2.00	2.24	4.00
7	14.88	2.00	2.24	4.00

Data Set O9a:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	3.00	3.00	6.00	6.00
2	10.50	3.00	9.00	6.00
3	3.50	9.50	7.00	7.00
4	11.00	9.50	8.00	7.00
Optimal Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.07	3.93	3.85	4.15
2	11.21	9.29	2.42	6.59
3	13.71	9.11	2.57	6.22
4	10.34	3.93	8.68	4.15
5	4.11	9.11	5.78	6.22
6	9.25	9.11	1.50	6.00
7	10.34	1.10	6.00	1.50
8	1.40	3.00	1.50	6.00
9	7.75	9.11	1.50	6.00
SEQUENCE-AL Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	8.56	8.57	3.11	5.14
2	1.67	3.00	2.66	6.00
3	11.67	8.57	3.11	5.14
4	3.50	8.57	7.00	5.14
5	9.00	3.00	6.00	6.00
6	3.75	3.00	1.50	6.00
7	3.50	11.89	6.00	1.50
8	14.11	8.53	1.78	5.06
9	5.25	3.00	1.50	6.00

C.2. Numerical Test Results for the Heuristic Comparison Test

The following tables summarize the results of the best SEQUENCE-AL solutions for the heuristic comparison test. The flow data are not changed from the original problem, which can be found either in the literature where the associated data sets were first proposed or in Appendix A.3. (for Data Set SC30a).

Data Set M11a:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	3.00	4.50	6.00	3.00
2	1.50	1.50	3.00	3.00
3	4.50	1.50	3.00	3.00

SEQUENCE-AL Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	3.53	1.59	1.06	2.83
2	5.12	1.59	0.71	2.83
3	5.12	5.07	1.61	1.86
4	3.24	5.07	2.15	1.86
5	2.65	1.59	0.71	2.83
6	4.41	1.59	0.71	2.83
7	0.76	1.59	1.06	2.83
8	0.67	4.50	1.33	3.00
9	2.04	1.59	0.50	2.00
10	1.54	1.59	0.50	2.00
11	3.53	3.57	4.39	1.14

Data Set BM12a:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	3.00	6.50	6.00	3.00
2	2.00	2.50	4.00	5.00
3	5.00	2.50	2.00	5.00

SEQUENCE-AL Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.75	2.00	0.50	2.00
2	4.50	4.50	1.00	1.00
3	5.50	4.50	1.00	1.00
4	4.50	3.50	1.00	1.00
5	4.25	2.00	0.50	2.00
6	4.50	0.50	1.00	1.00
7	5.67	5.75	0.67	1.49
8	5.67	7.24	0.67	1.49
9	5.50	2.00	1.00	4.00
10	2.00	4.50	4.00	1.00
11	2.67	6.50	5.33	3.00
12	2.00	2.00	4.00	4.00

Data Set M15a:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.00	12.00	10.00	6.00
2	3.00	4.50	6.00	9.00
3	8.00	4.50	4.00	9.00
4	12.50	10.00	5.00	10.00
5	12.50	2.50	5.00	5.00

SEQUENCE-AL Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	1.43	3.95	2.87	4.53
2	1.43	7.61	2.87	2.79
3	12.45	5.92	4.90	1.84
4	12.45	4.29	4.90	1.43
5	3.54	4.47	1.34	6.71
6	5.41	13.97	9.19	2.07
7	12.33	10.97	2.48	8.07
8	8.35	10.97	3.30	3.93
9	11.58	1.99	3.16	3.16
10	8.83	4.29	2.33	8.57
11	14.28	10.97	1.41	7.07
12	6.77	4.47	1.55	7.75
13	10.55	10.97	1.10	5.48
14	5.11	4.47	1.79	8.94
15	3.52	10.97	6.35	3.93

Data Set M25a:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.00	2.50	10.00	5.00
2	12.50	3.50	5.00	3.00
3	12.50	1.00	5.00	2.00

SEQUENCE-AL Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	12.69	0.84	3.87	0.77
2	7.27	4.09	0.55	1.81
3	8.32	4.04	1.56	1.92
4	12.69	1.61	3.87	0.77
5	8.32	2.76	1.56	0.64
6	7.45	0.45	3.31	0.91
7	12.69	3.20	2.07	2.41
8	1.73	1.20	2.14	0.94
9	7.45	1.22	3.16	0.63
10	5.15	2.06	1.29	0.77
11	4.30	0.50	2.99	1.00
12	3.23	2.68	2.15	0.93
13	10.83	3.20	1.66	2.41
14	1.08	2.91	2.15	1.39
15	5.65	3.56	2.69	0.74
16	4.30	1.34	2.99	0.67
17	3.23	3.37	2.15	0.47
18	1.08	4.30	2.15	1.39
19	7.45	1.99	3.31	0.91
20	5.65	4.30	2.69	0.74
21	3.58	1.94	1.85	0.54
22	3.23	4.30	2.15	1.39
23	9.55	2.76	0.89	4.47
24	1.73	1.94	1.85	0.54
25	5.65	2.82	2.69	0.74

Data Set SC30a:

Zone Data				
Zone #	Centroids		2 × Half-Length	
	x	y	x	y
1	5.00	8.50	10.00	7.00
2	12.50	8.50	5.00	7.00
3	3.00	2.50	6.00	5.00
4	10.50	2.50	9.00	5.00

SEQUENCE-AL Solution				
Dept #	Centroids		2 × Half-Length	
	x	y	x	y
1	4.20	1.25	3.60	0.83
2	8.54	3.18	1.10	3.64
3	3.65	5.45	4.47	0.89
4	3.65	6.85	7.30	1.92
5	9.55	9.40	0.89	4.47
6	9.78	3.18	1.38	3.64
7	12.13	3.38	1.39	1.43
8	12.13	4.55	3.33	0.90
9	12.13	5.59	4.27	1.17
10	14.42	9.40	1.15	5.20
11	11.92	6.49	3.16	0.63
12	11.92	9.40	3.85	5.20
13	8.59	9.57	1.03	4.86
14	7.69	9.78	0.77	3.87
15	3.65	9.78	7.07	1.41
16	3.65	11.04	5.48	1.10
17	8.95	6.67	2.09	0.95
18	3.65	8.44	6.32	1.26
19	7.44	3.18	1.10	3.64
20	8.65	5.37	2.70	0.74
21	6.45	2.76	0.89	4.47
22	7.99	0.68	2.20	1.36
23	8.42	5.96	2.24	0.45
24	4.20	0.42	3.60	0.83
25	0.75	2.11	1.12	0.89
26	10.95	2.05	0.97	4.10
27	1.20	0.83	2.40	1.67
28	7.60	7.02	0.60	1.66
29	3.54	3.78	4.92	2.44
30	3.54	2.11	4.47	0.89

Appendix D. Summary of Numerical Test Results in Chapter 7

D.1. Numerical Test Results for the Optimality Comparison Test

The following tables summarize the results of the best SEQUENCE-NR solutions for the optimality comparison test.

Data Set I7:

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
1	1	1.00	4.00	2.00	8.00	1.00	0.00	1.00	8.00
2	1	6.00	7.67	8.00	2.00	2.00	7.67	10.00	7.67
3	1	9.00	3.67	2.00	6.00	9.00	6.67	9.00	0.67
4	1	11.00	2.67	2.00	4.00	11.00	0.67	11.00	4.67
5	1	11.00	7.17	2.00	5.00	11.00	4.67	11.00	9.67
6	1	6.00	9.67	8.00	2.00	10.00	9.67	2.00	9.67
7	1	11.00	11.67	1.00	4.00	11.00	9.67	11.00	13.67

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	1.33	1.33
2	3	1	2.00	2.00
2	5	1	4.00	4.00
3	4	1	2.00	2.00
4	5	1	0.00	0.00
5	6	1	1.00	1.00
5	7	1	0.00	0.00
Total				10.33

Data Set I8:

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
1	1	3.00	4.50	6.00	2.00	0.00	4.50	6.00	4.50
2	1	8.50	4.50	5.00	3.00	6.00	4.50	11.00	4.50
3	1	9.00	1.50	6.00	3.00	12.00	1.50	6.00	1.50
4	1	8.00	7.00	4.00	2.00	6.00	7.00	10.00	7.00
5	1	11.00	7.50	2.00	3.00	11.00	6.00	11.00	9.00
6	1	9.00	10.50	6.00	3.00	12.00	10.50	6.00	10.50
7	1	8.00	8.50	4.00	1.00	10.00	8.50	6.00	8.50
8	1	3.50	10.50	5.00	3.00	6.00	10.50	1.00	10.50

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	0.00	0.00
1	4	1	2.50	2.50
2	3	1	4.00	4.00
2	5	1	1.50	1.50
3	4	1	5.50	5.50
4	5	1	2.00	2.00
5	6	1	2.50	2.50
5	7	1	1.50	1.50
6	8	1	0.00	0.00
7	8	1	2.00	2.00
Total				21.50

Data Set I9:

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
1	1	5.00	1.50	6.00	2.00	2.00	1.50	8.00	1.50
2	1	10.50	1.50	5.00	3.00	8.00	1.50	13.00	1.50
3	1	10.00	7.50	6.00	3.00	13.00	7.50	7.00	7.50
4	1	10.00	4.00	4.00	2.00	8.00	4.00	12.00	4.00
5	1	13.00	4.50	2.00	3.00	13.00	3.00	13.00	6.00
6	1	10.00	10.50	6.00	3.00	13.00	10.50	7.00	10.50
7	1	5.00	8.00	4.00	1.00	7.00	8.00	3.00	8.00
8	1	4.00	6.00	5.00	3.00	6.50	6.00	1.50	6.00
9	1	1.50	10.00	3.00	4.00	1.50	8.00	1.50	12.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	0.00	0.00
1	4	1	2.50	2.50
2	3	1	6.00	6.00
2	5	1	1.50	1.50
3	4	1	4.50	4.50
3	7	1	0.50	0.50
4	5	1	2.00	2.00
5	3	1	1.50	1.50
5	6	1	4.50	4.50
5	8	1	6.50	6.50
6	7	1	2.50	2.50
7	8	1	5.50	5.50
7	9	1	1.50	1.50
8	9	1	2.00	2.00
Total				41.00

Data Set I10:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	1.00	12.00	2.00	6.00	1.00	15.00	1.00	9.00
2	1	4.50	11.50	5.00	3.00	2.00	11.50	7.00	11.50
3	1	8.50	8.50	3.00	6.00	8.50	11.50	8.50	5.50
4	1	3.00	8.00	4.00	2.00	1.00	8.00	5.00	8.00
5	1	6.00	8.50	2.00	3.00	6.00	10.00	6.00	7.00
6	1	4.00	5.50	6.00	3.00	7.00	5.50	1.00	5.50
7	1	8.50	3.50	1.00	4.00	8.50	5.50	8.50	1.50
8	1	11.50	1.50	5.00	3.00	9.00	1.50	14.00	1.50
9	1	6.00	1.50	4.00	3.00	8.00	1.50	4.00	1.50
10	1	2.00	1.50	4.00	3.00	4.00	1.50	0.00	1.50

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	3.50	3.50
1	4	1	1.00	1.00
2	3	1	1.50	1.50
2	5	1	2.50	2.50
3	6	1	1.50	1.50
3	7	1	0.00	0.00
4	5	1	3.00	3.00
5	6	1	2.50	2.50
6	4	1	2.50	2.50
6	7	1	7.50	7.50
7	8	1	0.50	0.50
7	9	1	0.50	0.50
9	10	1	0.00	0.00
Total				26.50

Data Set L4:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	1.50	8.00	3.00	6.00	1.50	11.00	–	–
1	2	6.00	6.00	6.00	2.00	–	–	9.00	6.00
2	1	11.00	6.50	4.00	3.00	9.00	6.50	–	–
2	2	12.00	10.00	2.00	4.00	–	–	12.00	12.00
3	1	8.50	12.00	4.00	2.00	10.50	12.00	–	–
3	2	7.50	9.00	2.00	4.00	–	–	7.50	7.00
4	1	7.50	2.50	3.00	5.00	7.50	5.00	–	–
4	2	12.00	1.50	6.00	3.00	–	–	15.00	1.50

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	0.50	0.50
1	4	1	2.50	2.50
2	3	1	1.50	1.50
3	1	1	10.00	10.00
3	4	1	2.00	2.00
Total				16.50

Data Set L5:

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
1	1	13.00	10.00	6.00	3.00	16.00	10.00	–	–
1	2	11.00	5.50	2.00	6.00	–	–	11.00	2.50
2	1	8.50	4.50	3.00	4.00	8.50	2.50	–	–
2	2	5.00	5.50	4.00	2.00	–	–	3.00	5.50
3	1	5.00	7.50	4.00	2.00	3.00	7.50	–	–
3	2	6.00	10.50	2.00	4.00	–	–	6.00	12.50
4	1	2.50	12.50	5.00	3.00	5.00	12.50	–	–
4	2	1.50	8.00	3.00	6.00	–	–	1.50	5.00
5	1	1.50	2.50	3.00	5.00	1.50	5.00	–	–
5	2	5.00	1.00	4.00	2.00	–	–	7.00	1.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	2.50	2.50
2	3	1	2.00	2.00
2	5	1	2.00	2.00
3	4	1	1.00	1.00
4	5	1	0.00	0.00
Total				7.50

Data Set L6:

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
1	1	1.50	3.50	3.00	6.00	1.50	6.50	–	–
1	2	6.00	1.50	6.00	2.00	–	–	9.00	1.50
2	1	11.00	1.50	4.00	3.00	9.00	1.50	–	–
2	2	12.00	5.00	2.00	4.00	–	–	12.00	7.00
3	1	8.50	12.00	2.00	4.00	8.50	10.00	–	–
3	2	5.50	13.00	4.00	2.00	–	–	3.50	13.00
4	1	3.50	9.50	3.00	5.00	3.50	12.00	–	–
4	2	8.00	8.50	6.00	3.00	–	–	11.00	8.50
5	1	13.50	8.50	5.00	3.00	11.00	8.50	–	–
5	2	15.00	12.00	2.00	4.00	–	–	15.00	14.00
6	1	12.50	14.00	2.00	4.00	12.50	12.00	–	–
6	2	9.50	15.00	4.00	2.00	–	–	7.50	15.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	0.00	0.00
2	3	1	6.50	6.50
2	5	1	2.50	2.50
3	4	1	1.00	1.00
4	5	1	0.00	0.00
4	6	1	5.00	5.00
5	6	1	4.50	4.50
Total				19.50

Data Set U4:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	12.00	13.00	2.00	6.00	12.00	10.00	–	–
1	2	9.00	15.00	4.00	2.00	–	–	–	–
1	3	6.00	13.00	2.00	6.00	–	–	6.00	10.00
2	1	3.00	8.50	6.00	2.00	6.00	8.50	–	–
2	2	1.00	5.50	2.00	4.00	–	–	–	–
2	3	3.00	2.50	6.00	2.00	–	–	6.00	2.50
3	1	12.50	2.50	5.00	3.00	10.00	2.50	–	–
3	2	14.00	5.50	2.00	3.00	–	–	–	–
3	3	12.50	8.50	5.00	3.00	–	–	10.00	8.50
4	1	8.00	8.50	4.00	3.00	10.00	8.50	–	–
4	2	7.00	5.00	2.00	4.00	–	–	–	–
4	3	8.00	1.50	4.00	3.00	–	–	10.00	1.50

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	1.50	1.50
1	4	1	5.50	5.50
2	3	1	4.00	4.00
3	1	1	3.50	3.50
3	4	1	0.00	0.00
Total				14.50

Data Set M5:

Dept #	Sub-Dept #	Centroids x	Centroids y	Length x	Length y	Input x	Input y	Output x	Output y
1	1	1.00	3.00	2.00	6.00	1.00	6.00	–	–
1	2	3.50	1.00	3.00	2.00	–	–	–	–
1	3	6.00	3.00	2.00	6.00	–	–	6.00	6.00
2	1	6.00	9.00	2.00	6.00	6.00	12.00	–	–
2	2	9.00	7.00	4.00	2.00	–	–	11.00	7.00
3	1	12.50	4.50	3.00	5.00	12.50	7.00	12.50	2.00
4	1	8.50	3.00	3.00	6.00	8.50	6.00	–	–
4	2	12.00	1.00	4.00	2.00	–	–	14.00	1.00
5	1	17.00	1.50	6.00	3.00	14.00	1.50	–	–
5	2	19.00	5.00	2.00	4.00	–	–	–	–
5	3	17.00	8.50	6.00	3.00	–	–	14.00	8.50

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	6.00	6.00
1	4	1	2.50	2.50
2	3	1	1.50	1.50
2	4	1	3.50	3.50
3	5	1	2.00	2.00
4	5	1	0.50	0.50
Total				16.00

Data Set M6:

Dept #	Sub-Dept #	Centroids x	Centroids y	Length x	Length y	Input x	Input y	Output x	Output y
1	1	19.00	10.00	2.00	6.00	19.00	7.00	–	–
1	2	16.50	12.00	3.00	2.00	–	–	–	–
1	3	14.00	10.00	2.00	6.00	–	–	14.00	7.00
2	1	14.00	4.00	2.00	6.00	14.00	1.00	–	–
2	2	11.00	6.00	4.00	2.00	–	–	9.00	6.00
3	1	7.50	8.50	3.00	5.00	7.50	6.00	7.50	11.00
4	1	11.50	10.00	3.00	6.00	11.50	7.00	–	–
4	2	8.00	12.00	4.00	2.00	–	–	6.00	12.00
5	1	3.00	11.00	6.00	3.00	6.00	11.00	–	–
5	2	1.00	7.50	2.00	4.00	–	–	–	–
5	3	3.00	4.00	6.00	3.00	–	–	6.00	4.00
6	1	7.50	3.00	3.00	6.00	7.50	0.00	7.50	6.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	6.00	6.00
1	4	1	2.50	2.50
2	3	1	1.50	1.50
2	4	1	3.50	3.50
3	5	1	1.50	1.50
4	5	1	1.00	1.00
6	3	1	0.00	0.00
6	6	1	6.00	6.00
Total				22.00

D.2. Numerical Test Results for the Heuristic Comparison Test

The following tables summarize the results of the best SEQUENCE-NR solutions for the heuristic comparison test.

Data Set M10-1:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	17.00	19.30	6.00	2.00	20.00	19.30	–	–
1	2	15.00	16.80	2.00	3.00	–	–	–	–
1	3	17.00	14.30	6.00	2.00	–	–	20.00	14.30
2	1	17.00	12.30	6.00	2.00	20.00	12.30	–	–
2	2	15.00	9.30	2.00	4.00	–	–	15.00	7.30
3	1	11.50	8.30	3.00	5.00	11.50	10.80	11.50	5.80
4	1	16.00	5.80	6.00	3.00	13.00	5.80	–	–
4	2	18.00	9.30	2.00	4.00	–	–	18.00	11.30
5	1	1.50	3.00	3.00	6.00	1.50	6.00	–	–
5	2	5.00	1.00	4.00	2.00	–	–	–	–
5	3	8.50	3.00	3.00	6.00	–	–	8.50	6.00
6	1	8.50	9.00	3.00	6.00	8.50	6.00	8.50	12.00
7	1	7.50	15.00	3.00	6.00	7.50	12.00	7.50	18.00
8	1	5.50	19.00	4.00	2.00	7.50	19.00	–	–
8	2	4.50	16.00	2.00	4.00	–	–	4.50	14.00
9	1	12.50	13.00	3.00	1.00	11.00	13.00	–	–
9	2	13.50	14.50	1.00	2.00	–	–	–	–
9	3	12.50	16.00	3.00	1.00	–	–	11.00	16.00
10	1	10.00	14.00	2.00	4.00	10.00	16.00	10.00	12.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	2.00	2.00
2	3	1	2.50	2.50
3	4	1	0.00	0.00
5	6	1	1.50	1.50
6	7	1	3.00	3.00
7	8	1	1.50	1.50
9	10	1	3.50	3.50
10	3	1	0.50	0.50
10	7	1	2.50	2.50
Total				17.00

Data Set M10-2:

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
1	1	6.00	9.00	2.00	6.00	6.00	6.00	–	–
1	2	3.50	11.00	3.00	2.00	–	–	–	–
1	3	1.00	9.00	2.00	6.00	–	–	1.00	6.00
2	1	1.00	3.00	2.00	6.00	1.00	6.00	–	–
2	2	4.00	1.00	4.00	2.00	–	–	6.00	1.00
3	1	8.50	10.80	3.00	5.00	8.50	8.30	8.50	13.30
4	1	8.00	14.80	6.00	3.00	5.00	14.80	–	–
4	2	10.00	18.30	2.00	4.00	–	–	10.00	20.30
5	1	7.50	3.00	3.00	6.00	7.50	6.00	–	–
5	2	11.00	1.00	4.00	2.00	–	–	–	–
5	3	14.50	3.00	3.00	6.00	–	–	14.50	6.00
6	1	14.50	9.00	3.00	6.00	14.50	6.00	14.50	12.00
7	1	13.50	15.00	3.00	6.00	13.50	12.00	13.50	18.00
8	1	16.00	18.30	2.00	4.00	16.00	16.30	–	–
8	2	13.00	19.30	4.00	2.00	–	–	11.00	19.30
9	1	17.50	3.00	3.00	1.00	16.00	3.00	–	–
9	2	18.50	4.50	1.00	2.00	–	–	–	–
9	3	17.50	6.00	3.00	1.00	–	–	16.00	6.00
10	1	12.00	8.00	2.00	4.00	12.00	6.00	12.00	10.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
FI #1	1	1	10.00	10.00
FI #1	5	1	11.50	11.50
1	2	1	0.00	0.00
2	3	1	9.80	9.80
3	4	1	5.00	5.00
5	6	1	0.00	0.00
6	7	1	1.00	1.00
7	8	1	4.20	4.20
9	10	1	4.00	4.00
10	3	1	5.20	5.20
10	7	1	3.50	3.50
4	FO #1	1	0.00	0.00
8	FO #1	1	2.00	2.00
Total				56.20

Data Set M10-3:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	3.00	12.00	6.00	2.00	0.00	12.00	–	–
1	2	5.00	14.50	2.00	3.00	–	–	–	–
1	3	3.00	17.00	6.00	2.00	–	–	0.00	17.00
2	1	1.00	8.00	2.00	6.00	1.00	11.00	–	–
2	2	4.00	6.00	4.00	2.00	–	–	6.00	6.00
3	1	7.50	8.50	3.00	5.00	7.50	6.00	7.50	11.00
4	1	9.00	14.80	6.00	3.00	6.00	14.80	–	–
4	2	11.00	18.30	2.00	4.00	–	–	11.00	20.30
5	1	14.00	1.50	6.00	3.00	11.00	1.50	–	–
5	2	16.00	5.00	2.00	4.00	–	–	–	–
5	3	14.00	8.50	6.00	3.00	–	–	11.00	8.50
6	1	12.50	11.50	6.00	3.00	9.50	11.50	15.50	11.50
7	1	17.00	13.30	3.00	6.00	17.00	10.30	17.00	16.30
8	1	17.00	18.30	2.00	4.00	17.00	16.30	–	–
8	2	14.00	19.30	4.00	2.00	–	–	12.00	19.30
9	1	7.00	4.50	1.00	3.00	7.00	6.00	–	–
9	2	8.50	3.50	2.00	1.00	–	–	–	–
9	3	10.00	4.50	1.00	3.00	–	–	10.00	6.00
10	1	10.00	8.00	2.00	4.00	10.00	6.00	10.00	10.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
FI #1	1	12	10.00	120.00
FI #1	5	10	11.50	115.00
1	2	6	7.00	42.00
2	3	6	1.50	9.00
3	4	6	5.30	31.80
5	6	10	4.50	45.00
6	7	20	2.70	54.00
7	8	20	0.00	0.00
9	10	10	0.00	0.00
10	3	4	6.50	26.00
10	7	6	7.30	43.80
4	FO #1	18	1.00	18.00
8	FO #1	5	3.00	15.00
Total				519.60

Data Set M15-1:

Dept #	Sub-Dept #	Centroids x	Centroids y	Length x	Length y	Input x	Input y	Output x	Output y
1	1	10.00	3.00	2.00	6.00	10.00	6.00	–	–
1	2	12.50	1.00	3.00	2.00	–	–	–	–
1	3	15.00	3.00	2.00	6.00	–	–	15.00	6.00
2	1	18.00	9.00	2.00	6.00	18.00	6.00	–	–
2	2	15.00	11.00	4.00	2.00	–	–	13.00	11.00
3	1	8.50	11.00	5.00	3.00	11.00	11.00	6.00	11.00
4	1	3.00	5.50	6.00	3.00	6.00	5.50	–	–
4	2	1.00	2.00	2.00	4.00	–	–	1.00	0.00
5	1	22.00	6.50	6.00	3.00	19.00	6.50	–	–
5	2	24.00	10.00	2.00	4.00	–	–	–	–
5	3	22.00	13.50	6.00	3.00	–	–	19.00	13.50
6	1	16.00	13.50	6.00	3.00	19.00	13.50	13.00	13.50
7	1	17.50	18.50	3.00	6.00	17.50	21.50	17.50	15.50
8	1	24.00	17.50	2.00	4.00	24.00	15.50	–	–
8	2	21.00	18.50	4.00	2.00	–	–	19.00	18.50
9	1	11.50	18.50	3.00	1.00	13.00	18.50	–	–
9	2	10.50	17.00	1.00	2.00	–	–	–	–
9	3	11.50	15.50	3.00	1.00	–	–	13.00	15.50
10	1	12.00	12.00	2.00	4.00	12.00	14.00	12.00	10.00
11	1	14.00	8.50	6.00	3.00	11.00	8.50	17.00	8.50
12	1	5.00	16.50	2.00	4.00	5.00	18.50	–	–
12	2	8.00	15.50	4.00	2.00	–	–	10.00	15.50
13	1	14.50	15.50	3.00	1.00	13.00	15.50	–	–
13	2	15.50	17.00	1.00	2.00	–	–	–	–
13	3	14.50	18.50	3.00	1.00	–	–	13.00	18.50
14	1	3.00	9.50	6.00	3.00	0.00	9.50	6.00	9.50
15	1	7.50	7.50	3.00	4.00	7.50	9.50	7.50	5.50

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	3.00	3.00
2	3	1	2.00	2.00
3	4	1	5.50	5.50
5	6	1	0.00	0.00
6	3	1	4.50	4.50
6	10	1	1.50	1.50
7	8	1	6.50	6.50
8	9	1	6.00	6.00
9	10	1	2.50	2.50
10	11	1	2.50	2.50
12	13	1	3.00	3.00
13	9	1	0.00	0.00
14	15	1	1.50	1.50
15	4	1	1.50	1.50
Total				40.00

Data Set M15-2:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	1.00	5.00	2.00	6.00	1.00	8.00	–	–
1	2	3.50	3.00	3.00	2.00	–	–	–	–
1	3	6.00	5.00	2.00	6.00	–	–	6.00	8.00
2	1	13.00	10.50	6.00	2.00	10.00	10.50	–	–
2	2	15.00	13.50	2.00	4.00	–	–	15.00	15.50
3	1	16.50	17.00	5.00	3.00	14.00	17.00	19.00	17.00
4	1	22.00	14.00	6.00	3.00	19.00	14.00	–	–
4	2	24.00	17.50	2.00	4.00	–	–	24.00	19.50
5	1	1.50	15.00	3.00	6.00	1.50	18.00	–	–
5	2	5.00	13.00	4.00	2.00	–	–	–	–
5	3	8.50	15.00	3.00	6.00	–	–	8.50	18.00
6	1	11.00	19.50	6.00	3.00	8.00	19.50	14.00	19.50
7	1	12.00	1.50	6.00	3.00	9.00	1.50	15.00	1.50
8	1	14.00	5.00	2.00	4.00	14.00	3.00	–	–
8	2	11.00	6.00	4.00	2.00	–	–	9.00	6.00
9	1	5.50	11.50	3.00	1.00	7.00	11.50	–	–
9	2	4.50	10.00	1.00	2.00	–	–	–	–
9	3	5.50	8.50	3.00	1.00	–	–	7.00	8.50
10	1	14.00	8.50	4.00	2.00	12.00	8.50	16.00	8.50
11	1	22.00	8.50	6.00	3.00	19.00	8.50	25.00	8.50
12	1	7.00	1.00	4.00	2.00	5.00	1.00	–	–
12	2	8.00	4.00	2.00	4.00	–	–	8.00	6.00
13	1	8.50	8.50	3.00	1.00	7.00	8.50	–	–
13	2	9.50	10.00	1.00	2.00	–	–	–	–
13	3	8.50	11.50	3.00	1.00	–	–	7.00	11.50
14	1	17.50	3.00	3.00	6.00	17.50	0.00	17.50	6.00
15	1	17.50	12.00	3.00	4.00	17.50	10.00	17.50	14.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
FI #1	1	1	12.00	12.00
FI #1	5	1	21.50	21.50
FI #1	7	1	5.50	5.50
FI #1	12	1	1.00	1.00
FI #1	14	1	12.50	12.50
1	2	1	6.50	6.50
2	3	1	2.50	2.50
3	4	1	3.00	3.00
5	6	1	2.00	2.00
6	3	1	2.50	2.50
6	10	1	13.00	13.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
7	8	1	2.50	2.50
8	9	1	7.50	7.50
9	10	1	5.00	5.00
10	11	1	3.00	3.00
12	13	1	3.50	3.50
13	9	1	0.00	0.00
14	15	1	4.00	4.00
15	4.00	1.00	1.50	1.50
4	FO #1	1	2.5	2.5
11	FO #1	1	9.5	9.5
Total				121.00

Data Set M15-3:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	8.00	4.00	6.00	2.00	5.00	4.00	–	–
1	2	10.00	6.50	2.00	3.00	–	–	–	–
1	3	8.00	9.00	6.00	2.00	–	–	5.00	9.00
2	1	7.00	11.00	6.00	2.00	4.00	11.00	–	–
2	2	9.00	14.00	2.00	4.00	–	–	9.00	16.00
3	1	12.50	14.50	5.00	3.00	10.00	14.50	15.00	14.50
4	1	18.00	16.50	6.00	3.00	15.00	16.50	–	–
4	2	20.00	20.00	2.00	4.00	–	–	20.00	22.00
5	1	8.50	19.00	3.00	6.00	8.50	16.00	–	–
5	2	5.00	21.00	4.00	2.00	–	–	–	–
5	3	1.50	19.00	3.00	6.00	–	–	1.50	16.00
6	1	2.50	13.00	3.00	6.00	2.50	16.00	2.50	10.00
7	1	8.00	1.50	6.00	3.00	5.00	1.50	11.00	1.50
8	1	13.00	4.00	4.00	2.00	11.00	4.00	–	–
8	2	14.00	7.00	2.00	4.00	–	–	14.00	9.00
9	1	18.00	10.50	1.00	3.00	18.00	9.00	–	–
9	2	16.50	11.50	2.00	1.00	–	–	–	–
9	3	15.00	10.50	1.00	3.00	–	–	15.00	9.00
10	1	17.00	8.00	4.00	2.00	15.00	8.00	19.00	8.00
11	1	23.50	11.00	3.00	6.00	23.50	8.00	23.50	14.00
12	1	3.00	1.00	4.00	2.00	1.00	1.00	–	–
12	2	4.00	4.00	2.00	4.00	–	–	4.00	6.00
13	1	20.50	6.50	3.00	1.00	19.00	6.50	–	–
13	2	21.50	8.00	1.00	2.00	–	–	–	–
13	3	20.50	9.50	3.00	1.00	–	–	19.00	9.50
14	1	20.50	3.00	3.00	6.00	20.50	0.00	20.50	6.00
15	1	17.00	13.50	4.00	3.00	19.00	13.50	15.00	13.50

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
FI #1	1	10	4.00	40.00
FI #1	5	4	19.50	78.00
FI #1	7	15	1.50	22.50
FI #1	12	4	5.00	20.00
FI #1	14	4	15.50	62.00
1	2	8	3.00	24.00
2	3	10	2.50	25.00
3	4	8	2.00	16.00
5	6	4	1.00	4.00
6	3	4	12.00	48.00
6	10	4	14.50	58.00
7	8	15	2.50	37.50
8	9	20	4.00	80.00
9	10	20	1.00	20.00
10	11	15	4.50	67.50
12	13	4	15.50	62.00
13	9	2	1.50	3.00
14	15	8	9.00	72.00
15	4.00	8.00	3.00	24.00
4	FO #1	5	9	45
11	FO #1	10	5.5	55
Total				863.50

Data Set M20-1:

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
1	1	9.00	9.00	2.00	6.00	9.00	6.00	–	–
1	2	6.50	11.00	3.00	2.00	–	–	–	–
1	3	4.00	9.00	2.00	6.00	–	–	4.00	6.00
2	1	13.00	5.00	6.00	2.00	10.00	5.00	–	–
2	2	15.00	8.00	2.00	4.00	–	–	15.00	10.00
3	1	12.00	8.50	3.00	5.00	12.00	11.00	12.00	6.00
4	1	8.50	3.00	3.00	6.00	8.50	6.00	–	–
4	2	12.00	1.00	4.00	2.00	–	–	14.00	1.00
5	1	5.00	16.00	3.00	6.00	5.00	19.00	–	–
5	2	8.50	14.00	4.00	2.00	–	–	–	–
5	3	12.00	16.00	3.00	6.00	–	–	12.00	19.00
6	1	15.00	20.50	6.00	3.00	12.00	20.50	18.00	20.50
7	1	18.00	8.00	3.00	6.00	18.00	11.00	18.00	5.00
8	1	23.00	2.00	4.00	2.00	21.00	2.00	–	–
8	2	24.00	5.00	2.00	4.00	–	–	24.00	7.00
9	1	9.00	19.50	3.00	1.00	10.50	19.50	–	–
9	2	8.00	18.00	1.00	2.00	–	–	–	–

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
9	3	9.00	16.50	3.00	1.00	–	–	10.50	16.50
10	1	13.00	12.00	4.00	2.00	11.00	12.00	15.00	12.00
11	1	15.00	16.00	3.00	6.00	15.00	13.00	15.00	19.00
12	1	2.50	20.00	4.00	2.00	4.50	20.00	–	–
12	2	1.50	17.00	2.00	4.00	–	–	1.50	15.00
13	1	19.50	18.50	3.00	1.00	18.00	18.50	–	–
13	2	20.50	20.00	1.00	2.00	–	–	–	–
13	3	19.50	21.50	3.00	1.00	–	–	18.00	21.50
14	1	15.00	23.50	6.00	3.00	18.00	23.50	12.00	23.50
15	1	1.50	13.00	3.00	4.00	1.50	15.00	1.50	11.00
16	1	21.50	6.00	3.00	6.00	21.50	3.00	21.50	9.00
17	1	21.50	11.00	2.00	4.00	21.50	9.00	–	–
17	2	18.50	12.00	4.00	2.00	–	–	16.50	12.00
18	1	23.50	14.50	1.00	3.00	23.50	13.00	–	–
18	2	22.00	15.50	2.00	1.00	–	–	–	–
18	3	20.50	14.50	1.00	3.00	–	–	20.50	13.00
19	1	9.00	23.50	6.00	3.00	12.00	23.50	6.00	23.50
20	1	4.50	23.00	3.00	4.00	4.50	25.00	4.50	21.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
1	2	1	7.00	7.00
2	3	1	4.00	4.00
3	4	1	3.50	3.50
5	6	1	1.50	1.50
6	7	1	9.50	9.50
7	8	1	6.00	6.00
9	10	1	5.00	5.00
10	11	1	1.00	1.00
11	12	1	11.50	11.50
12	15	1	0.00	0.00
13	14	1	2.00	2.00
14	3	1	12.50	12.50
14	6	1	3.00	3.00
14	19	1	0.00	0.00
16	17	1	0.00	0.00
17	3	1	5.50	5.50
17	7	1	2.50	2.50
18	7	1	4.50	4.50
18	11.00	1.00	5.50	5.50
19	20	1	3	3
20	12	1	1	1
Total				88.50

Data Set M20-2:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	8.00	3.00	2.00	6.00	8.00	6.00	–	–
1	2	10.50	1.00	3.00	2.00	–	–	–	–
1	3	13.00	3.00	2.00	6.00	–	–	13.00	6.00
2	1	15.00	8.00	2.00	6.00	15.00	5.00	–	–
2	2	12.00	10.00	4.00	2.00	–	–	10.00	10.00
3	1	8.50	8.50	3.00	5.00	8.50	11.00	8.50	6.00
4	1	22.00	6.00	6.00	3.00	19.00	6.00	–	–
4	2	24.00	9.50	2.00	4.00	–	–	24.00	11.50
5	1	4.00	1.50	6.00	3.00	1.00	1.50	–	–
5	2	6.00	5.00	2.00	4.00	–	–	–	–
5	3	4.00	8.50	6.00	3.00	–	–	1.00	8.50
6	1	10.00	12.50	6.00	3.00	7.00	12.50	13.00	12.50
7	1	11.50	17.00	3.00	6.00	11.50	14.00	11.50	20.00
8	1	16.50	17.00	2.00	4.00	16.50	19.00	–	–
8	2	19.50	16.00	4.00	2.00	–	–	21.50	16.00
9	1	1.50	20.00	3.00	1.00	0.00	20.00	–	–
9	2	2.50	21.50	1.00	2.00	–	–	–	–
9	3	1.50	23.00	3.00	1.00	–	–	0.00	23.00
10	1	1.00	17.50	2.00	4.00	1.00	19.50	1.00	15.50
11	1	6.50	15.50	6.00	3.00	3.50	15.50	9.50	15.50
12	1	21.00	10.00	4.00	2.00	19.00	10.00	–	–
12	2	22.00	13.00	2.00	4.00	–	–	22.00	15.00
13	1	5.50	10.50	3.00	1.00	4.00	10.50	–	–
13	2	6.50	12.00	1.00	2.00	–	–	–	–
13	3	5.50	13.50	3.00	1.00	–	–	4.00	13.50
14	1	6.00	18.50	6.00	3.00	3.00	18.50	9.00	18.50
15	1	22.00	19.00	3.00	4.00	22.00	17.00	22.00	21.00
16	1	17.50	8.00	3.00	6.00	17.50	5.00	17.50	11.00
17	1	18.00	13.00	2.00	4.00	18.00	11.00	–	–
17	2	15.00	14.00	4.00	2.00	–	–	13.00	14.00
18	1	0.50	12.50	1.00	3.00	0.50	14.00	–	–

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
18	2	2.00	11.50	2.00	1.00	–	–	–	–
18	3	3.50	12.50	1.00	3.00	–	–	3.50	14.00
19	1	16.00	22.50	6.00	3.00	13.00	22.50	19.00	22.50
20	1	19.00	19.00	3.00	4.00	19.00	21.00	19.00	17.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
FI #1	1	1	9.00	9.00
FI #1	5	1	5.50	5.50
FI #1	13	1	11.50	11.50
FI #2	9	1	15.00	15.00
FI #2	16	1	17.50	17.50
FI #2	18	1	9.50	9.50
1	2	1	3.00	3.00
2	3	1	2.50	2.50
3	4	1	10.50	10.50
5	6	1	10.00	10.00
6	7	1	3.00	3.00
7	8	1	6.00	6.00
9	10	1	4.50	4.50
10	11	1	2.50	2.50
11	12	1	15.00	15.00
12	15	1	2.00	2.00
13	14	1	6.00	6.00
14	3	1	8.00	8.00
14	6.00	1.00	8.00	8.00
14	19	1	8	8
16	17	1	0.5	0.5
17	3	1	7.5	7.5
17	7	1	1.5	1.5
18	7	1	8	8
18	11	1	1.5	1.5
19	20	1	1.5	1.5
20	12	1	7	7
4	FO #1	1	4.5	4.5
8	FO #1	1	4.5	4.5
Total				193.50

Data Set M20-3:

Dept	Sub-Dept	Centroids		Length		Input		Output	
#	#	x	y	x	y	x	y	x	y
1	1	17.00	6.00	6.00	2.00	14.00	6.00	–	–
1	2	19.00	8.50	2.00	3.00	–	–	–	–
1	3	17.00	11.00	6.00	2.00	–	–	14.00	11.00
2	1	23.00	22.00	2.00	6.00	23.00	19.00	–	–
2	2	20.00	24.00	4.00	2.00	–	–	18.00	24.00
3	1	16.00	17.50	3.00	5.00	16.00	21.00	16.00	14.00
4	1	19.00	13.50	6.00	3.00	16.00	13.50	–	–
4	2	21.00	17.00	2.00	4.00	–	–	21.00	20.00
5	1	7.00	1.50	6.00	3.00	4.00	1.50	–	–
5	2	9.00	5.00	2.00	4.00	–	–	–	–
5	3	7.00	8.50	6.00	3.00	–	–	4.00	8.50
6	1	7.00	11.50	6.00	3.00	3.00	11.50	11.00	11.50
7	1	13.00	13.50	6.00	3.00	10.00	13.50	16.00	13.50
8	1	20.00	20.00	4.00	2.00	22.00	20.00	–	–
8	2	19.00	17.00	2.00	4.00	–	–	19.00	15.00
9	1	0.50	1.50	1.00	3.00	0.50	3.00	–	–
9	2	2.00	0.50	2.00	1.00	–	–	–	–
9	3	3.50	1.50	1.00	3.00	–	–	3.50	3.00
10	1	12.00	4.00	4.00	2.00	10.00	4.00	14.00	4.00
11	1	12.50	8.00	3.00	6.00	12.50	5.00	12.50	11.00
12	1	23.00	6.00	4.00	2.00	21.00	6.00	–	–
12	2	24.00	9.00	2.00	4.00	–	–	24.00	11.00
13	1	3.50	17.00	1.00	3.00	3.50	18.50	–	–
13	2	5.00	16.00	2.00	1.00	–	–	–	–
13	3	6.50	17.00	1.00	3.00	–	–	6.50	18.50
14	1	10.00	18.50	6.00	3.00	7.00	18.50	13.00	18.50
15	1	23.50	13.00	3.00	4.00	23.50	11.00	23.50	15.00
16	1	7.50	23.00	3.00	6.00	7.50	20.00	7.50	26.00
17	1	4.00	26.00	4.00	2.00	6.00	26.00	–	–
17	2	3.00	23.00	2.00	4.00	–	–	3.00	21.00

Dept #	Sub-Dept #	Centroids		Length		Input		Output	
		x	y	x	y	x	y	x	y
18	1	8.50	16.50	3.00	1.00	10.00	16.50	–	–
18	2	7.50	15.00	1.00	2.00	–	–	–	–
18	3	8.50	13.50	3.00	1.00	–	–	10.00	13.50
19	1	15.00	21.50	6.00	3.00	12.00	21.50	18.00	21.50
20	1	21.50	9.00	3.00	4.00	21.50	11.00	21.50	7.00

Dept i	Dept j	Flow f_{ij}	Distance d_{ij}	Flow Distance $f_{ij}d_{ij}$
FI #1	1	5	15.00	75.00
FI #1	5	15	2.50	37.50
FI #1	13	4	20.00	80.00
FI #2	9	20	2.50	50.00
FI #2	16	3	22.50	67.50
FI #2	18	3	21.50	64.50
1	2	10	17.00	170.00
2	3	8	5.00	40.00
3	4	14	0.50	7.00
5	6	20	4.00	80.00
6	7	12	3.00	36.00
7	8	12	12.50	150.00
9	10	20	7.50	150.00
10	11	20	2.50	50.00
11	12	10	13.50	135.00
12	15	20	0.50	10.00
13	14	12	0.50	6.00
14	3	4	5.50	22.00
14	6.00	2.00	17.00	34.00
14	19	6.00	4	24
16	17	6	1.5	9
17	3	4	13	52
17	7	2	14.5	29
18	7	9	0	0
18	11	3	11	33
19	20	6	14	84
20	12	6	1.5	9
4	FO #1	12	9	108
8	FO #1	24	6	144
15	FO #1	20	1.5	30
Total				1786.50

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Vita

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Qi Liu went to the United States in August, 2001 to pursue a Ph.D. degree in the Grado Department of Industrial and Systems Engineering at Virginia Polytechnic Institute and State University (Virginia Tech) under the guidance of Dr. Russell D. Meller. During his Ph.D. studies at Virginia Tech, he worked as a research assistant for the Center for High Performance Manufacturing (CHPM) to develop a decision-support software package, LayoutVT, for the facility layout problem. He also worked as a research assistant for Ingersoll-Rand on two consulting projects: a distribution center relocation project and a facility re-layout project. Qi Liu was awarded the Grado Fellowship in 2002, the Dover Scholarship in 2003, and the Robert R. Reisinger Honor Scholarship from the Material Handling Education Foundation in 2004 due to his performance as a student and his area of research. His research interests include the facility layout problem, the facility location problem, material handling system design, and production and inventory management system design.