HIERARCHICAL MAXIMAL COVERING LOCATION PROBLEM WITH REFERRAL IN THE PRESENCE OF PARTIAL COVERAGE

A THESIS SUBMITTED TO
THE GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
OF
MIDDLE EAST TECHNICAL UNIVERSITY

BY

ÖZGÜN TÖREYEN

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR
THE DEGREE OF MASTER OF SCIENCE
IN
OPERATIONAL RESEARCH

SEPTEMBER 2007

Approval of the thesis:

HIERARCHICAL MAXIMAL COVERING LOCATION PROBLEM IN THE PRESENCE OF PARTIAL COVERAGE

submitted by **ÖZGÜN TÖREYEN** in partial fulfillment of the requirements for the degree of **Master of Science in Operational Research, Industrial Engineering Department, Middle East Technical University** by,

Prof. Dr. Canan ÖZGEN _____
Dean, Graduate School of **Natural and Applied Sciences**

Prof. Dr. Çağlar GÜVEN _____
Head of Department, **Industrial Engineering**

Assist.Prof. Dr. Esra KARASAKAL _____
Supervisor, **Industrial Engineering Dept., METU**

Examining Committee Members:

Prof. Dr. Ömer KIRCA _____
Industrial Engineering Dept., METU

Assist.Prof. Dr. Esra KARASAKAL _____
Industrial Engineering Dept., METU

Assoc. Prof. Dr. Haldun SÜRAL _____
Industrial Engineering Dept., METU

Assoc.Prof. Dr. Canan SEPİL _____
Industrial Engineering Dept., METU

Dr. Orhan KARASAKAL _____
R&D Dept., TUN

Date: 06.09.2007

I hereby declare that all information in this document has been obtained and presented in accordance with academic rules and ethical conduct. I also declare that, as required by these rules and conduct, I have fully cited and referenced all material and results that are not original to this work.

Name, Last name : Özgün TÖREYEN

Signature :

ABSTRACT

HIERARCHICAL MAXIMAL COVERING LOCATION PROBLEM WITH REFERRAL IN THE PRESENCE OF PARTIAL COVERAGE

TÖREYEN, Özgün

M. Sc., Department of Industrial Engineering
Supervisor: Assist. Prof. Dr. Esra KARASAKAL

September 2007, 158 pages

We consider a hierarchical maximal covering location problem to locate *p* health centers and *q* hospitals in such a way that maximum demand is covered, where health centers and hospitals have successively inclusive hierarchy. Demands are 3 types: demand requiring low-level service only, demand requiring high-level service only, and demand requiring both levels of service at the same time. All types of requirements of a demand point should be either covered by hospital providing both levels of service or referred to hospital via health center since a demand point is not covered unless all levels of requirements are satisfied. Thus, a health center cannot be opened unless it is suitable to refer its covered demand to a hospital. Referral is defined as coverage of health centers by hospitals.

We also added partial coverage to this complex hierarchic structure, that is, a demand point is fully covered up to the minimum critical distance, non-covered after the maximum critical distance and covered with a decreasing quality while increasing distance to the facility between minimum and maximum critical distances.

We developed an MIP formulation to solve the Hierarchical Maximal Covering Location Problem with referral in the presence of partial coverage. We solved small-size problems optimally using GAMS. For large-size problems we developed a Genetic Algorithm that gives near-optimal results quickly. We tested our Genetic Algorithm on randomly generated problems of sizes up to 1000 nodes.

Keywords: Hierarchical Maximal Covering Location Problem, partial coverage, referral, Genetic Algorithm.

ÖZ

KISMİ KAPSAMANIN OLDUĞU DURUMDA SEVK ETMELİ HİYERARŞİK MAKSİMUM KAPSAMA YERLEŞİM PROBLEMİ

TÖREYEN, Özgün

Yüksek Lisans, Endüstri Mühendisliği Bölümü
Tez Yöneticisi: Y. Doç. Dr. Esra KARASAKAL

Eylül 2007, 158 Sayfa

Maksimum talebi karşılamak için aralarında ardıl dahil bir hiyerarşi bulunan p sağlık merkezi ve q hastaneyi yerleştirme problemini ele aldık. 3 tür talep vardır: yalnızca alt-seviye hizmete ihtiyaç duyan talep, yalnızca üst seviye hizmete ihtiyaç duyan talep ve hizmetlerin ikisine birden aynı zamanda ihtiyaç duyan talep. Bir talep noktasındaki bütün talep bölünmeksizin iki yoldan biriyle karşılanabilir; talep ya iki seviye hizmeti de sağlayan hastane tarafından karşılanacaktır ya da sağlık merkezi üzerinden hastaneye sevk edilecektir. Bunun nedeni, bir talep noktasının bütün seviyelerdeki hizmet ihtiyaçları karşılanmadıkça, kapsanmamış sayılmasıdır. Bu zorunluluğun diğer tarafı ise bir sağlık merkezinin üzerinde toplanan talebi hastaneye sevk etmeye uygun olmaması durumunda, sağlık merkezinin kurulamayacak olmasıdır. Sevk, hastanelerin sağlık merkezlerini kapsaması olarak tanımlanmıştır.

Biz bu karmaşık hiyerarşik yapıya aynı zamanda kısmi kapsama ekledik; şöyle ki talep minimum kritik uzaklığa kadar tamamıyle kapsanır, maksimum kritik uzaklıktan sonra hiç kapsanmaz ve bu iki uzaklık arasında uzaklık arttıkça düşen bir kaliteyle kapsanır.

Kısmi kapsamanın olduğu durumda sevk etmeli hiyerarşik maksimum kapsama yerleşim problemi adını verdiğimiz problem için bir karışık tamsayı programlama formülasyonu geliştirdik. Küçük ölçekli problemleri GAMS ile optimal olarak çözdük. Büyük ölçekli problemler için ise, hızlı ve kaliteli sonuç veren bir Genetik Algoritma geliştirdik. Geliştirdiğimiz Genetik Algoritma'yı büyüklüğü 1000 noktaya kadar çıkan rastgele oluşturulmuş problemlerde test ettik.

Anahtar Kelimeler: Hiyerarşik Maksimum Kapsama Yerleşim Problemi, kısmi kapsama, sevk, Genetik Algoritma.

To My Precious Family

ACKNOWLEDGMENTS

I would like to thank to my supervisor Assist. Prof. Dr. Esra Karasakal and co-supervisor Dr. Orhan Karasakal for their guidance, patience, encouragements and insight throughout the research.

I would like to express my deepest gratitude to my family for their endless moral support and patience; especially to my sister for her continuous motivation with her sayings “Are you still studying?”.

I would especially like to thank to Taner Gülez, Şafak Baykal, Cemal Samur and Nuri Mutlu for their valuable contributions.

Thanks are also due to my superiors and my very special friends in ASELSAN who never gave up believing in me.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

ALS	Advanced Life Support
B&B	Branch-and-Bound
BLS	Basic Life Support
GA	Genetic Algorithm
GMCLP	Generalized Maximal Covering Location Problem
GRASP	Greedy Adding Procedure with Random Substitution
HMCLP	Hierarchical Maximal Covering Location Problem
HMCLP(R)-P	Hierarchical Maximal Covering Location Problem with Referral in Presence of Partial Coverage
IP	Integer Programming
LB	Lower Bound
LP	Linear Programming
MCLP	Maximal Covering Location Problem
MCLP-P	Maximal Covering Location Problem in Presence of Partial Coverage
MIP	Mixed Integer Programming
MPSX	Mathematical Programming System Extended
SCP	Set Covering Problem
UB	Upper Bound
VS	Vertex Substitution

CHAPTER 1

INTRODUCTION

The Maximal Covering Location Problem (MCLP) has been used frequently to make the decision of locating a limited number of emergency service systems in order to cover maximum amount of demand. The Hierarchical MCLP (HMCLP) has taken one step and extended the types of facilities, constructing a hierarchy amongst them. In HMCLP, there are different types of facilities supplying different levels of service; low-level facilities are eligible only to meet the requirements of low-level demand whereas high-level facilities are eligible to supply both low and high-levels of service.

Although introduction of hierarchy was a major step, when health services are focused amongst other emergency services, HMCLP may be insufficient to represent the requirements of the health systems. We extended the problem with the possibility that categorization of demand –requiring either low-level or high-level service– may not be apparent in advance. Demand may be assigned to a health center first, and then after expert categorization it either stays in the health center or is referred to a hospital. Referral of demand from a health center to a hospital is modeled by coverage of the health center by the hospital, since we deal with coverages.

Coverage of demand is generally modeled using binary variables; as coverage if the distance between facility and demand is less than a pre-determined distance –called critical distance–, and non-coverage if the distance is greater than the critical distance. Another extension we have taken into account is the partial

coverage of demand. By defining a second critical distance, the crispy fall down of quality of coverage on the critical distance border is enlarged to the area between two critical distances and the fall down is modeled to be inversely proportional with distance.

We call the resulting problem Hierarchical Maximal Covering Location Problem with referral in presence of partial coverage and abbreviate it as HMCLP(R)-P and propose a concise mixed-integer programming (MIP) formulation. However, the problem is NP-hard. Optimal solutions can be found up to node size of 50 with GAMS. For the problems with size larger than 50 nodes, we propose a Genetic Algorithm (GA) that gives near-optimal solutions quickly.

The organization of the thesis is as follows: Literature is summarized in Section 2 to enlighten the previous work in this area. Problem is described and formulated in Section 3 and GA solution is proposed in Section 4. Results are evaluated in Section 5 and concluding remarks and further research directions are presented in Section 6.

CHAPTER 2

LITERATURE SURVEY

2.1 HIERARCHICAL MAXIMAL COVERING LOCATION PROBLEM

Set Covering Problem (SCP) proposed by Toregas et al. (1971) is the first and basic emergency service locating problem, which can be regarded as the origin of the covering location problems. The problem is to minimize the total number of emergency facilities required to cover whole demand, where coverage is possible only if the distance between demand and facility is less than a pre-determined distance, which is generally called critical distance in literature.

Church and ReVelle (1974) develop a dual approach to SCP. They propose a linear programming (LP) formulation that maximizes coverage of total weighted demand with fixed number of facilities. The dual problem has been called the Maximal Covering Location Problem and has evaded high attention with its wide application areas, which are examined interestingly by Chen-Hua Chung (1986).

In order to take the differentiated demand requirements and hierarchy of servers into account, Moore and ReVelle (1982) modify MCLP to Hierarchical Maximal Covering Location Problem (HMCLP). The objective is to cover all levels of demand requirements with pre-determined numbers of different service providing facilities which have hierarchic relationships in between. The hierarchic relationships are well-categorized by Eitan, Narula and Tien (1991) and Şahin and Süral (2007). The primary facility hierarchies are mentioned as successively

inclusive facility hierarchy and successively exclusive facility hierarchy. If a *k*-level facility provides only the services unique to itself, it is categorized as successively exclusive facility hierarchy. However, if a *k*-level facility provides the services one lower level (*k-1*-level) facility provides in addition to the services unique to it, it is categorized as successively inclusive facility hierarchy. Another occasionally-encountered hierarchy mentioned is locally inclusive facility hierarchy in which a *k*-level facility provides all services to demand located close and only the services unique to it to demand located further.

Moore and ReVelle (1982) propose a successively inclusive facility hierarchy. Their objective is to minimize the total population which lacks access to any level of service with a given number of facilities for each level. They define different critical distances for satisfaction of low-level demand by low-level facility, satisfaction of low-level demand by high-level facility and satisfaction of high-level demand by high-level facility. Since the model is successively inclusive, satisfaction of low-level demand is possible both by low-level facilities and by high-level facilities, whereas high-level demand can be satisfied only by high-level facilities.

Hierarchy has been considered differently by Charnes and Storbeck (1980). Back-up coverage is used as a hierarchy relationship in their goal programming formulation which objects to satisfy both critical calls and non-critical calls by locating pre-determined numbers of different vehicles; called Basic Life Support (BLS) and Advanced Life Support (ALS) vehicles. ALS vehicles provide service to meet the critical calls whereas BLS vehicles both provide back-up coverage to critical calls in the case ALS vehicles are insufficient and provide service to meet non-critical calls. Coverage of critical demand by ALS vehicles, back-up coverage of critical demand by BLS vehicles and coverage of non-critical demand by BLS vehicles are regarded as goals and the total weighted under-attainment is minimized by the objective function.

The concept of referral has come out with *p*-median hierarchical location-allocation problems by Narula and Ogbu (1978). In addition to allocation of demand to health centers and to hospitals, allocation of demand at health centers to hospitals, which is named as referral is considered. A pre-determined portion of demand accumulated at a health center has to be referred to a hospital. The objective is to locate fixed numbers of capacitated health centers and hospitals such that the total distance traveled is minimized.

Referral is adapted to HMCLP by Marianov and Serra (2001) in the presence of congestion. They consider nested, non-nested and coherent hierarchies which include referral. They describe the classification which is similar to the categorization of Eitan, Narula and Tien (1991). They call a hierarchy nested if a high-level server provides also low-level service. If servers provide different services, it is categorized as non-nested hierarchy which corresponds to successively exclusive hierarchy of Eitan, Narula and Tien (1991). A coherent hierarchical system is defined as a system in which all customers served by the same low-level server have to be served by the same high-level server.

For non-nested systems, demand has to be allocated to both health centers and hospitals; it has to be referred from a health center to a hospital even though they are located in the same place. The objective is to maximize total weighted referral with pre-determined numbers of low and high-level servers. Requirement of high-level servers providing low-level service is added for the nested case. For coherent systems, low-level servers are matched with high-level servers for referral, while the objective remains the same.

When the 0-1 coverage assumption of MCLP is relinquished, generalized coverage emerges. Berman and Krass (2002) model a Generalized Maximal Covering Location Problem (GMCLP) where coverage is modeled as a non-increasing step function of the distance between the demand point and the nearest facility. Berman, Krass and Drezner (2003) consider the case where each demand

can be covered fully, partially or not at all. They describe two critical distances, in between of which, a gradual decrease occurs in coverage from full coverage to non-coverage which they name coverage decay function. Drezner, Wesolowsky and Drezner (2004) formulate the problem as minimization of non-coverage where they define non-coverage up to first critical distance as 0 and non-coverage after first critical distance as factors of weight, where factors are defined proportional to remoteness. Karasakal and Karasakal (2004) define the partial coverage between the minimum critical distance and the maximum critical distance as a general function of distance. They formulate MCLP with partial coverage (MCLP-P) and conduct sensitivity analyses to reflect effects of MCLP-P from MCLP.

When solution procedures proposed in these studies are considered, since HMCLP is NP-Hard, exact methods for large-scaled problems can not be encountered in literature. Moore and ReVelle (1982) solve a 144-node problem by Mathematical Programming System Extended (MPSX). Marianov and Serra (2001) propose a two-phase heuristic algorithm that they test problems of size 50 nodes. In the first phase Greedy Adding Procedure with random substitution (GRASP) is used to find the first hierarchical level facilities. Then, in the second phase vertex substitution (VS) heuristic is applied. Espejo, Galvão and Boffey (2003) propose a combined Lagrangean-Surrogate relaxation which deviates maximum of 3.3% from upper bound (UB) in average for problem sizes of 55 to 700 nodes.

Berman and Krass (2002) test their MCLP-P model on problems of size 20 to 400 nodes with IP, LP-relaxation and greedy heuristic. The maximum of deviation averages of greedy heuristic from optimal recorded is 1.4% for the network topology of 300 nodes. Drezner, Wesolowsky and Drezner (2004) develop a lower bound (LB) and solve problems of sizes 10-10000 nodes utilizing the LB in Branch-and-Bound (B&B) algorithm they coded. Karasakal and Karasakal (2004)

utilized Lagrangean Relaxation to solve randomly-generated problems of sizes 200 to 1000 nodes.

2.2 GENETIC ALGORITHM

Genetic Algorithm (GA) is proposed by Holland (1975) where Darwin's theory of evolution is inspired. GA's have been utilized extensively for the solution of combinatorial optimization problems which are thoroughly explained by Goldberg (1989) and Beasley et al. (1993). GA is a meta-heuristic, based on the principals and mechanisms of natural selection. The algorithm starts with generation of a population composed of chromosomes that represent solutions. The chromosomes are evaluated with respect to performance criteria and given fitness values. The higher the fitness value, the higher the probability to remain to next generations for that chromosome since chromosomes are selected according to their fitness values and mated to form new offspring. Offspring may or may not be replaced with parent chromosomes depending on the structure of the algorithm. The chromosomes of the resulting generation are then exposed to mutation that alters portions of their chromosomal structure. These operations – named as selection, cross-over and mutation in literature, take place at each iteration. The aim of the algorithm is to attain fit offspring in sufficient number of iterations.

Direct applications of GA to HMCLP are not present in literature; however, other covering location problem applications enlightened the path of this study. Jaramillo, Bhadury and Batta (2002) apply GA to MCLP as well as to uncapacitated and capacitated facility location, centroid and medianoid problems. They utilize a binary representation scheme of size n_f where n_f designates the number of potential facility sites. Fitness function values for each chromosome are calculated with respect to the MCLP objective function. Parents are selected according to Binary Tournament Selection Method, where a pair of individuals is

selected from the population at random and the better one is taken to the mating pool. An iterative process is followed for mating in order not to generate offspring that are identical to their parents. Fitness-based fusion cross-over, which focuses on the differences of the structures of two parents, is repeated until differentiated offspring are obtained. Then mutation is performed by selecting randomly one of the opened facilities and moving it to another site. Mutation rate is suggested to be increased parallel to convergence of GA, by Beasley and Chu (1996). Incremental replacement method, explained by Beasley et al. (1993), is applied for the population replacement. Replacing less fit members of the population with child solutions is called incremental replacement, since average fitness of the population increases if the child solutions have better fitness values than those of the solutions being replaced. Another commonly used method is the generational replacement where new population of children replaces the whole parent population unconditionally. The tests are conducted on 88- and 150-vertex networks. GA followed by substitution procedure, which takes a solution and attempts to improve it using a greedy heuristic, is compared with Lagrangean heuristic followed by a substitution procedure. Although GA followed by substitution procedure is computationally relatively expensive, the quality of solutions is better.

Li et al. (2004) apply GA to MCLP as well as *p*-median and multi-objective problems. They represent the solutions with a string length of *2n* where *n* is the number of facilities to be located. The string is composed of column and row numbers of *n* facilities within the spatial dimensions of *N*x*N* cells. The coordinates are then converted into binary format. Initial population is generated using a random procedure and fitness values of strings are evaluated according to MCLP objective function. They use 1-point cross-over where cutting point for separating the genes is randomly decided, and a standard mutation operator that randomly flips bits from 0 to 1 or from 1 to 0. Offspring are replaced with existing individuals according to their fitness values. The procedure is repeated until the improvement in the best fitness is insignificant. They test their findings

on real-data representing the urban districts of Hong Kong of 150x150 cells and cell size of 300 m^2. They compare results of GA with Neighborhood Search Heuristic and Simulated Annealing. GA outperforms other methods in quality and computation time is found to be 29.4% of Simulated Annealing.

CHAPTER 3

HIERARCHICAL MAXIMAL COVERING LOCATION PROBLEM WITH REFERRAL IN PRESENCE OF PARTIAL COVERAGE

3.1 BACKGROUND

Classical MCLP decides fixed number of facility location points in order to maximize coverage of total weighted demand. Coverage of demand node by facility is represented using binary variables; as covered or uncovered, according to a pre-determined distance. This distance has been called critical distance – *S* in literature. Each facility is treated to have a virtual circular area around it, which has a radius of *S* and demand points which locate inside this area are said to be covered.

In Figure 3.1, two facilities are located and their service areas with radii of *S* are indicated transparently. The demand points that are within critical distances of facilities are covered. The points that are further are uncovered.

MCLP is modeled by Church and ReVelle (1974) as follows:

$$Max \quad \sum_{i \in I} a_i y_i \qquad (1)$$

s.t.

$$\sum_{j \in N_i} x_j \geq y_i \qquad \forall i \in I \qquad (2)$$

$$\sum_{j \in J} x_j = p \qquad (3)$$

$$x_j, y_i \in \{0,1\} \qquad \forall i \in I, \forall j \in J \qquad (4)$$

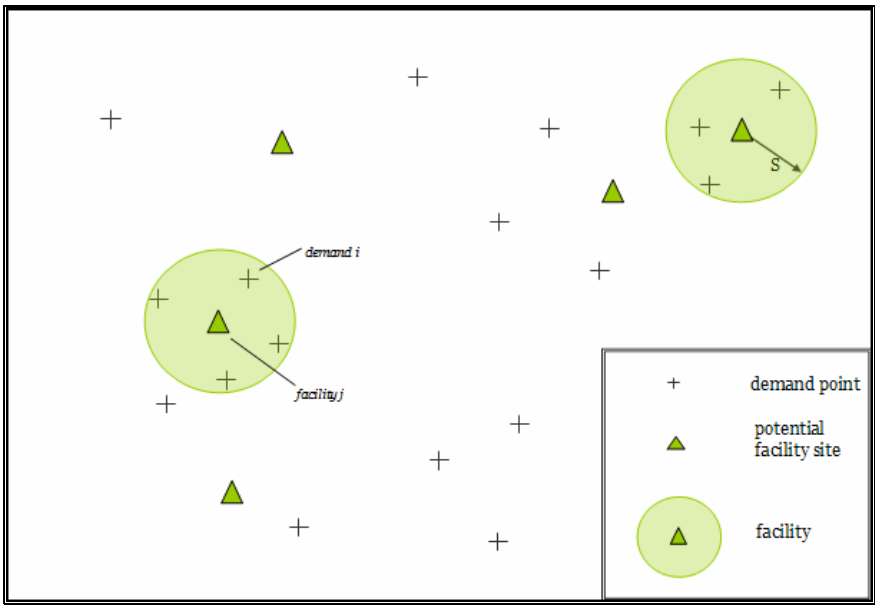


Figure 3.1 – Illustration of MCLP

where

I : set of demand nodes

J : set of facility sites

S : critical distance

d_{ij} : shortest distance from node i to node j

x_j : $\begin{cases} 1, \text{ if a facility is opened at site } j \\ 0, \text{ otherwise} \end{cases}$

N_i : the set of facility sites that are eligible to cover demand point *i*,

$$N_i = \left\{ j \in J \middle| d_{ij} \leq S \right\}$$

$$y_i : \begin{cases} 1, \text{ if demand at } i \text{ is covered} \\ 0, \text{ otherwise} \end{cases}$$

a_i : population at demand node *i*

p : number of facilities to be located

Objective (1) maximizes the number of people covered within the critical distance. Constraint set (2) allows coverage of demand point *i* if one or more facilities are established within critical distance. Constraint (3) limits the number of established facilities to *p*. Constraint set (4) ensures all variables to be binary.

HMCLP extends classical MCLP by differentiating levels of service demanded and levels of service provided and also setting hierarchical relationships between the differentiated servers. In HMCLP, more than one level of service is required, where levels are categorized according to the complexity of service they provide. High-level service is supplied by high-level facilities whereas low-level service is supplied by both low-level and high-level facilities.

In Figure 3.2, demand points require both low and high-level services, and the facilities are discriminated to meet these differentiated service requirements. Critical distances of high-level facilities – S^2 are larger than critical distances of low-level facilities – S^1, since high level facilities has been thought to be more capable and equipped, in literature.

Both levels of demand requirements are satisfied for the demand points inside the larger circular areas (demand i_2 for instance) whereas only the low-level deman d requirements are satisfied for the ones inside the smaller circular areas (demand i_1

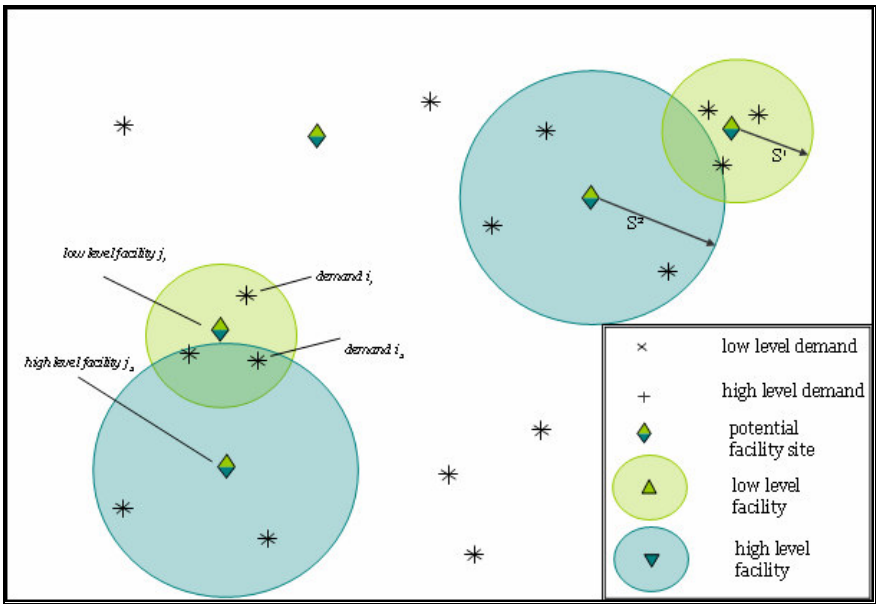


Figure 3.2 – Illustration of HMCLP

for instance). High-level demand requirements of those demand points are unsatisfied. Demand points that are outside of any of the circles above are uncovered at all.

HMCLP is modeled as follows by Moore and ReVelle (1982):

$$Max \sum_{j \in J} f_j x_j \qquad (5)$$

s.t.

$$\sum_{i \in I} a_{ij} y_i + \sum_{i \in I} b_{ij} z_i - x_j \geq 0 \qquad \forall j \in J \qquad (6)$$

$$\sum_{i \in I} c_{ij} z_i - x_j \geq 0 \qquad \forall j \in J \qquad (7)$$

$$\sum_{i \in I} y_i = p \qquad (8)$$

$$\sum_{i \in I} z_i = q \qquad (9)$$

$$x_j, y_i, z_i \in \{0,1\} \qquad \forall j \in J, \forall i \in I \qquad (10)$$

where

I : set of potential facility sites

J : set of demand areas

a_{ij} : { 1, if demand area j can be covered by level-1 service offered at a lower-level facility located at $i \in I$; 0, otherwise

b_{ij} : { 1, if demand area j can be covered by level-1 service offered at a higher-level facility located at $i \in I$; 0, otherwise

c_{ij} : { 1, if demand area j can be covered by level-2 service offered at a higher-level facility located at $i \in I$; 0, otherwise

x_j : { 1, if demand area j is covered; 0, otherwise

y_i : { 1, if a lower-level facility is located at site $i \in I$; 0, otherwise

z_i : { 1, if a higher-level facility is located at site $i \in I$; 0, otherwise

f_j :population of demand area j

p : number of lower-level facilities to be located

q : number of higher-level facilities to be located

Objective function (5) maximizes the total population covered by both level-1 and level-2 services. Constraint set (6) states that a demand area $j \in J$ is covered by level-1 service if there is at least either one lower-level facility or one higher-level facility within its corresponding critical distance. Constraint set (7) states that a demand area $j \in J$ is covered by level-2 service if there is at least one higher-level facility within its corresponding critical distance. Constraint (8) limits the number

of lower-level facilities in the solution to p; whereas constraint (9) limits the number of higher-level facilities in the solution to q. Finally, constraint sets (10) define 0–1 nature of the decision variables.

Demand points include demand requiring low-level service and demand-requiring high-level service at the same time. In some cases, demand has to be covered by low-level facility first and then covered by high-level facility. The role low-level facility executes is called referral in literature.

Referral has first been studied in p-median problems in literature; where all demand is assumed to have access to facilities and the total distance traveled in order to access is the main concern. The 2-hierarchical uncapacitated p-median formulation with referral by Narula and Ogbu (1983) is as follows:

$$Min \sum_{i=1}^{n}\sum_{j=1}^{n}(X_{ij}^{01} + X_{ij}^{02} + X_{ij}^{12})d_{ij} \qquad (11)$$

s.t.

$$\sum_{j=1}^{n}(X_{ij}^{01} + X_{ij}^{02}) = W_i \qquad i = 1,...,n \qquad (12)$$

$$\sum_{j=1}^{n} X_{ij}^{12} = \theta\sum_{j=1}^{n} X_{ji}^{01} \qquad i = 1,...,n \qquad (13)$$

$$\sum_{i=1}^{n} X_{ij}^{01} \le MY_j^1 \qquad j = 1,...,n \qquad (14)$$

$$\sum_{i=1}^{n} X_{ij}^{02} + \sum_{i=1}^{n} X_{ij}^{12} \le MY_j^2 \qquad j = 1,...,n \qquad (15)$$

$$\sum_{j=1}^{n} Y_j^1 = p_1 \qquad (16)$$

$$\sum_{j=1}^{n} Y_j^2 = p_2 \qquad (17)$$

$$Y_j^1 + Y_j^2 \le 1 \qquad j = 1,...,n \qquad (18)$$

$$0 \le X_{ij}^{01} \le W_i,\ 0 \le X_{ij}^{02} \le W_i,\ 0 \le X_{ij}^{12} \le \theta M$$

$$i = 1,...,n\ ;\ j = 1,...,n \quad (19)$$

$$Y_j^1, Y_j^2 \in \{0,1\} \qquad j = 1,...,n \quad (20)$$

where

X_{ij}^{01}: 1, if the demand at location i with no facility located there, is allocated to a level-1 facility at location j; 0, otherwise

X_{ij}^{02}: 1, if the demand at location i with no facility located there, is allocated to a level-2 facility at location j; 0, otherwise

X_{ij}^{12}: 1, if the demand at location i with level-1 facility located there, is referred to a level-2 facility at location j; 0, otherwise

Y_j^1: 1, if a level-1 facility is located at location j; 0, otherwise

Y_j^2: 1, if a level-2 facility is located at location j; 0, otherwise

p_1 : number of level-1 facilities to be located

p_2 : number of level-2 facilities to be located

n : number of potential locations

W_i : demand at location i; where $M = \sum_{i=1}^{n} W_i$

θ : fraction of demand referred from a level-1 facility to level-2 facility; where $0 \le \theta \le 1$

d_{ij} : minimum travel distance between locations i and j

Objective function (11) minimizes the total distance traveled for demand assigned to level-1 facilities, demand assigned to level-2 facilities and demand referred to

level-2 facilities from level-1 facilities. Constraint set (12) ensures that demand at each location is allocated to a facility. Constraint set (13) states that a fraction θ of total demand accumulated at level-1 facilities is referred to level-2 facilities. Constraint sets (14) and (15) ensure that allocations are made only to locations with facilities. Constraints (16) and (17) state that p_1 level-1 facilities and p_2 level-2 facilities can be opened. Constraint set (18) ensures that at most one facility can be opened in each location.

Another critical distance S^3; that is the maximum distance; referral of demand from low-level facilities to high-level facilities is possible, is defined in addition to critical distances for coverage of demand by low-level facilities S^1 and coverage of demand by high-level facilities S^2.

Thus, the low-level facilities within S^3 distance to high-level facilities are said to be covered by high-level facilities. This implies that demand points covered by these low-level facilities are also covered by high-level facilities, although demand points are not within S^2 distance of high-level facilities.

In Figure 3.3, low-level facilities have low-level demand service area (of radii S^1) whereas high-level facilities have both high-level demand service area (of radii S^2) and referral area (of radii S^3).

Demand points only within S^1 distance of low-level facilities (demand i_1 for instance), would be uncovered by high-level facilities if there were no referral. However, in this case, since low-level facility j_1 is within S^3 distance of high-level facility j_2, demand i_1 is also covered. High-level demand at point i_1 is satisfied by high-level facility at j_2 via referral.

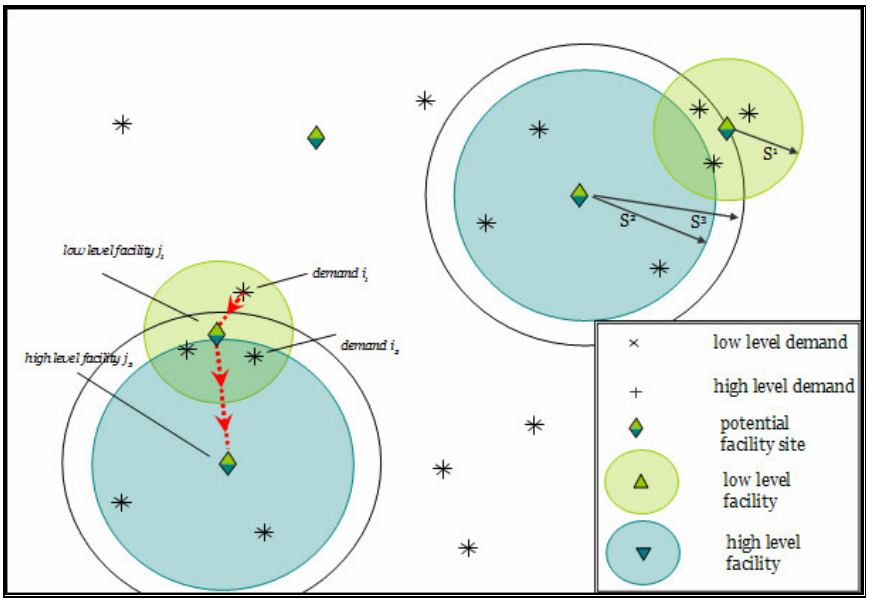


Figure 3.3 – Illustration of MCLP with referral

Partial coverage is another relaxation to the classical MCLP that extends classical concept of binary coverage by defining one more critical distance. Binary coverage models assume that coverage is 100% till the critical distance and fall crisply down to 0% after critical distance. Difference of coverages in two sides of borders is softened by introducing the second critical distance. Henceforth, the first critical distance is called the minimum critical distance – *S* and the second critical distance is called the maximum critical distance – *T*.

The coverage concept, therefore, is modified and concept of quality is introduced. Demand points that are within *S* distance to a facility are said to be covered, points that are further than *T* distance are said to be uncovered, and the points that are located between *S*-*T* distances are partially covered; that is the quality of service decreases as distance to the center increases. Coverage takes continuous values between 0 and 1 to represent quality.

The MCLP-P is modeled by Karasakal and Karasakal (2004) as follows:

$$Max \sum_{i \in I} \sum_{j \in M_i} c_{ij} x_{ij} \qquad (21)$$

s.t.

$$\sum_{j \in J} y_j = P \qquad (22)$$

$$x_{ij} \le y_j \qquad \forall i \in I, j \in M_i \qquad (23)$$

$$\sum_{j \in M_i} x_{ij} \le 1 \qquad \forall i \in I \qquad (24)$$

$$y_j \in \{0,1\} \qquad \forall j \in J \qquad (25)$$

$$x_{ij} \in \{0,1\} \qquad \forall i \in I, j \in M_i \qquad (26)$$

where

I : index set of demand points,

J : index set of potential facility sites,

P: number of facilities to be sited,

M_i : set of facility sites that can either fully or partially cover the demand point i,

S: the maximum full coverage distance,

T: the maximum partisl coverage distance, $(T > S)$,

D_{ij} : the travel distance between the facility j and demand point i,

C_{ij} : the level of coverage provided by the facility j to the demand point i,

$$C_{ij}: \begin{cases} 1, \text{ if } D_{ij} \le S \\ f(D_{ij}), \text{ if } S < D_{ij} \le T, \ (0 < f(D_{ij}) < 1) \\ 0, \text{ otherwise} \end{cases}$$

$$y_j: \begin{cases} 1, \text{ if a facility is sited at } j, \\ 0, \text{ otherwise} \end{cases}$$

$$x_{ij}: \begin{cases} 1, \text{ if the demand at point } i \text{ is either partially or fully covered by a facility at } j, \\ 0, \text{ otherwise} \end{cases}$$

Objective function (21) maximizes the coverage level within the maximum critical distance *T*. Constraint (22) limits the number of facilities to be sited to *P*. Constraint set (23) ensures that if a facility is not sited at *j*, then demand at *i* can not be covered by *j*. Constraint set (24) ensures that all demand points can be covered by at most one facility. If there are more than one facilities covering a demand point, the facility that provides the maximum coverage will be selected which is forced by the objective function. Constraint sets (25) and (26) impose binary restriction on the decision variables.

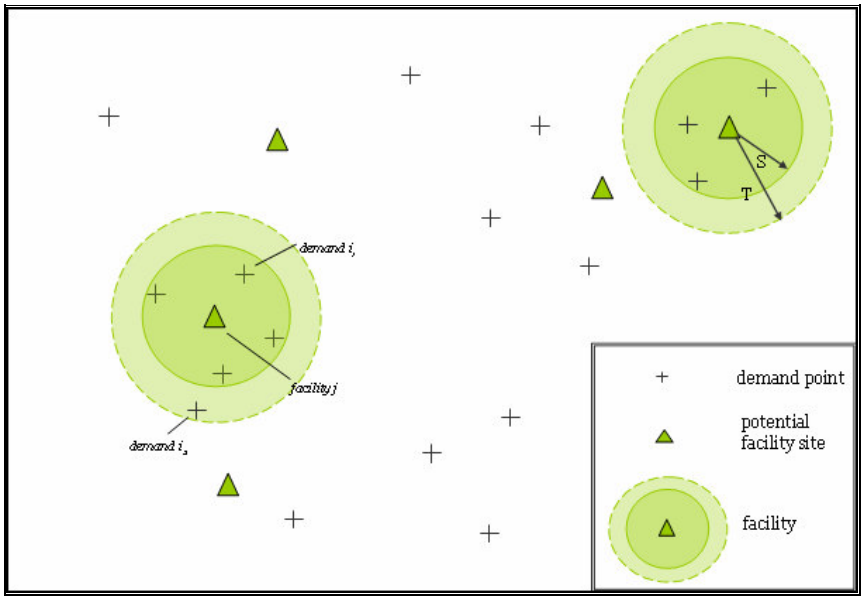


Figure 3.4 – Illustration of partial coverage

In Figure 3.4, the demand points within circular area framed by continuous lines (demand point i_1 for instance) are 100% covered whereas the points inside dashed lines but outside the continuous lines (demand point i_2 for instance) are partially covered. Coverage is inversely proportional with the distance between the

demand and the facility nodes. Points outside all of the circular areas are totally uncovered.

The revealed model, thus, can be represented as in Figure 3.5.

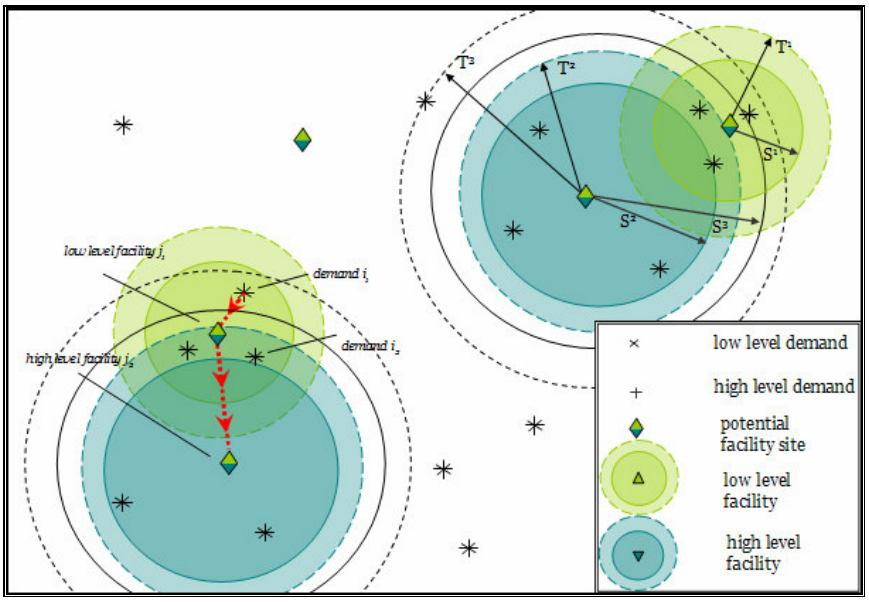


Figure 3.5 – Illustration of HMCLP with referral in the presence of partial coverage

In the above figure, all demand points require both low and high-level service. The potential facility sites are appropriate for establishment of both types of facilities. Frames of binary coverage and partial coverage are indicated with continuous and dashed lines, sequentially.

Demand i_2 is covered by high-level facility j_2 and low level facility j_1; therefore both low and high-level service requirements are satisfied. High-level service

requirement is either directly partially satisfied by high-level facility j_2 or it is indirectly satisfied by high-level facility j_2 via referral from low-level facility j_1.

Demand i_1 is covered by low-level facility j_1. Although it is not covered by any high-level facility, both low and high-level service requirements of it is also satisfied, since low-level facility j_1 is covered by high-level facility j_2.

3.2 MOTIVATION

Consider a health service system. If you have a complaint of sore throat, you go to a health center, since you know that this level of service is provided by a health center. If you have a heart attack, you are directly taken to a hospital, since it is known that heart attack is emergency situation and a health center is not equipped enough to manage necessary operations for a heart attack.

However, if you have a headache; the reason may be that you are too tired and you need just vitamins, but on the other hand it may be that you have a serious tumor in the membrane of your brain and you should have a very critical surgery that carries 80% risk of death. In such a situation, you need a preliminary evaluation. If the reason of the headache is tiredness, then you should remain in the health center, but if the reason is a tumor, then you should be referred to a hospital.

Another example may be from the battlefield. Suppose that we have a battery-headquarters that commands 3 batteries. If target is considered to be within the capacity of the batteries by the forward observer then the target is handled by the battery headquarter. If the target can not be destroyed by the batteries, it is handled by the upper-headquarters and determined to be destroyed by rocket missiles.

However, if the target can not be evaluated by the forward observer, then it should be evaluated in the battery-headquarters. After evaluation, if decision is finalized as batteries destroy the target then operation stays in the battery-headquarters. If battery-headquarters decide that batteries are not capable, then the decision of with which weapon to destroy should be referred to the upper-headquarters.

In these two cases, the question of "If the upper level service provider gives both types of services, then why do not we directly assign demand to the upper level instead of creating another level?" may arise. The reason is assigning whole demand directly to the hospital or all targets directly to the upper-headquarters is costly since giving a low-level service by a high-level server is costly and undesirable. Carrying out the procedure in such a way is less complicated and more efficient.

So referral in a hierarchical service system which includes both referral from low-level to high-level server and direct assignment to high-level server is motivated by the third type of demand that has preliminary evaluation about its characteristic. In addition to referral, we need to explain the motivation under the partial coverage.

Partial coverage is directly related to the quality of service, but it should not be thought as probability. Consider a hospital that provides ambulances in case of emergency. Say that, the critical time for access of ambulance to the demand point is determined as 3 minutes. If an ambulance can reach the point within 3 minutes, then it can prevent death of a person having a heart attack, but if the demand point is further than 3 minutes, the person can not have emergency service from this hospital.

Suppose there is another person within 4 minutes of this hospital. If he has a heart attack and he expects service from this hospital, then he would not take it.

However, what if this person has gastric bleeding? Then it may be acceptable to serve this person within 4 minutes. It is true that, the hospital can not prevent his heart attack, but it can prevent his gastric bleeding. If he is further, say within 5 minutes range of the hospital, the hospital can not prevent this person's gastric bleeding in this case, but only his appendicitis.

If we look at the problem from a different angle, consider a person having gastritis within 5 km of a hospital. If he had a heart-related problem or he had to have a surgery, he would tolerate making 5 km way to hospital. However, for gastridis he would tolerate at most 4 km but not 5 km and may give up the idea of visiting hospital.

Drezner, Wesolowsky and Drezner (2004) describe very interesting applications of partial coverage concept. They consider a public facility such as a post office for objective of customer satisfaction. If people are within l distance, they are very satisfied with the service, that they only walk to the facility. People who live within a distance of between l and u have a linearly decreasing satisfaction, that they drive to the facility. People who live beyond a distance u are very dissatisfied because they may not even use the facility at all. Maximizing the satisfaction is in fact what MCLP-P formulation is.

They consider another scenario which is valid in medical facilities. They interpret partial coverage as the rate of survival for the heart attack victims. Up to a determined time (distance l), survival rate is 100%. Then survival rate decreases with the time taken to reach the patient, and after a certain time (distance u) survival rate reaches a constant value because the patient either did not survive by that time or his condition is stabilized and he will survive even with very late help.

They explained other scenarios such as delivery problem, competitive location, dense competition and radio/TV/cellular transmitter.

Applications are also found in military. Suppose there is an observer airplane that observes ships. Up to 5 miles, the plane can observe ships of 20 m long; but in 6 miles, the precision of sight deteriorates and it observes ships if they are at least 30 m long.

In all the applications, there is a decrease in quality. Within the maximum critical distance (u or T) the facilities can not be regarded as supplying the same service that they supply within the minimum critical distance (l or S), but they can not also be regarded as supplying no service. There is sacrifice from quality (such as not being able to prevent death of person having heart attack 4 minutes away the hospital, not being able to see 20 m long ships within 6 miles distance), but also an advantage (such as not being obliged to establish another hospital to prevent gastric bleeding of the person in 4 minutes, not being obliged to charge another observing plane to detect 30 m long ships).

3.3 PROBLEM DEFINITION

Given a set of demand points and a set of potential facility sites, the objective is to maximize the total amount of demand covered with a pre-determined number of successively inclusive hierarchical facilities; where coverage is defined as being within a pre-determined critical distance. This general concept of hierarchical facilities is reduced to health centers and hospitals in our problem.

Demand has both low-level and high-level requirements that have to be satisfied. In addition to this, it may have a characteristic that can not be categorized in advance. Thus, people of the same demand point may need low-level service only, high-level service only or both levels of services at the same time; where demand point is regarded uncovered unless all levels of service requirements are

satisfied. However, demand at a demand point can not be fractioned; that is demand can not be allocated to different facilities.

High-level service can only be provided by hospitals whereas low-level service can be provided by both health centers and hospitals, since hierarchy is successively inclusive. This hierarchic structure obliges demand to be covered by hospital directly or indirectly or not to be covered at all; that is either demand is covered by a hospital that is supplying both low and high-level services or it is referred to a hospital via a health center covering it or it is not covered at all. All service requirements of a covered demand point are satisfied; that is there exists no demand point covered only by health centers. Referral here represents coverage of demand by a health center that is covered by a hospital. This enables whole low-level and high-level demand to be satisfied. Low-level demand is satisfied by health center or hospital directly. High-level demand, on the other hand, is satisfied by hospital directly or by referral indirectly.

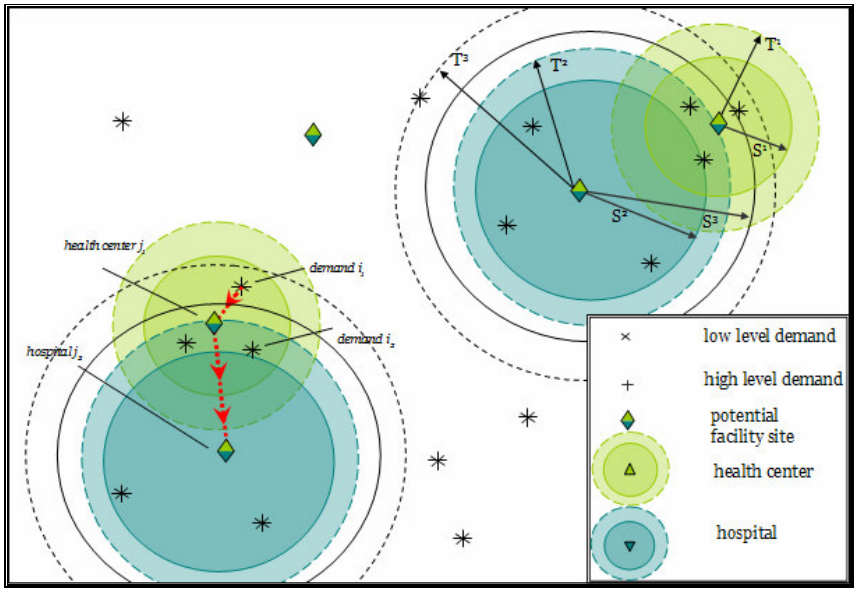


Figure 3.6 – Illustration of the problem

In Figure 3.6, low-level demand at node i_1 is fully covered by health center at node j_1. Low-level demand at node i_2 can either be fully covered by health center at node j_1 or be partially covered by hospital at node j_2. High-level demand at node i_2 is partially covered by hospital at node j_2. High-level demand at node i_1 is non-covered unless demand is referred. In the above graph, since demand at node i_1 is covered by health center at node j_1 and health center at node j_1 is also covered by hospital at node j_2; high-level demand at node i_1 is said to be covered via referral.

In addition to the classical coverage concept, coverage here is modeled with a decreasing function rather than binary, by defining minimum and maximum critical distances. Coverage is considered as full-coverage before minimum critical distance *S* and as non-coverage after maximum critical distance *T*. In between, it is considered as a linearly decreasing function that is inversely proportional with distance; representing partial coverage or in other words, the quality of coverage.

In Figure 3.7, coverage is 1 until minimum critical distance, linearly converges to 0 from minimum critical distance to maximum critical distance, and is 0 after maximum critical distance.

In classical HMCLP models, weight of demand at a demand point is separated into d_i^1 - demand requiring low level service and d_i^2 - demand requiring high level service; provided that $d_i^1 + d_i^2 = d_i$ where d_i is the total weight. Coverage is used to be calculated using these weights. However; in our model, demand is not needed to be separated.

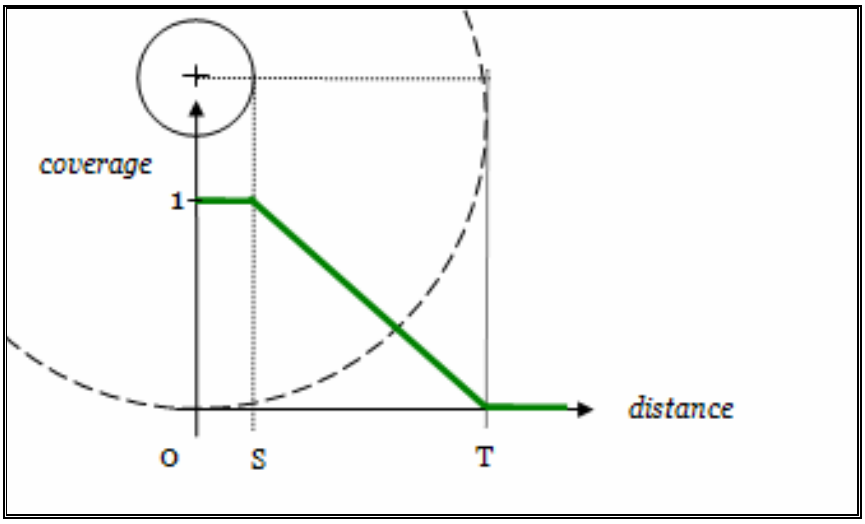


Figure 3.7– Coverage vs. distance function

In classical hierarchical approach, a demand point is either covered by low-level facility only or high-level facility only or covered by both or not covered at all. In the case that demand point is covered only by a low-level facility, the portion of demand that requires high-level service stays unsatisfied. To subtract this portion from coverage calculations, it is needed to discriminate weights of demands. Thus, each demand type should contribute separately to coverage calculations.

In our case, however; such a situation is never encountered; that is in any demand point it is impossible to satisfy demand requiring low-level service but unsatisfy demand requiring high-level service; because of our obligatory hierarchic assignment using referral. In our model, since every demand point has either to be covered by hospital (directly or via referral) or not to be covered at all; it is not needed to consider low-level demand weights, thus to discriminate weights of demands.

3.4 ASSUMPTIONS

1. Given a set of nodes and a set of edges that combine these nodes; demand points are assumed to be accumulated only at nodes.

2. Given a set of nodes and a set of edges, facilities are assumed to be established only at nodes.

3. The decrease in the quality of coverage between critical distances *S* and *T* is assumed to follow a linear pattern.

4. A health center can be opened only if it can be referable to a hospital. If a health center is not within referable critical distance of hospitals, it is not allowed to be opened.

5. Demand can not be split at assignment; it is assigned to at most one facility. If it is assigned to a health center, a pre-determined percent δ of it is referred to the corresponding hospital that is matched with the health center. In experimentation, it is assumed that $\delta = 1$, all demand assigned to health centers is referred to hospitals.

6. At a demand point, demand requiring low-level service and demand requiring high-level service are not differentiated. The total demand is designated by d_i. Each demand point requires both high-level and low-level services.

7. There is no differentiation considered in critical distances of high-level facility providing high-level service and low-level service, as in some studies in literature. We assume that both high- and low-level requirements are satisfied when demand is covered by high-level facilities. It is identical to utilization of minimum of critical distances of high-level

facility providing low-level service and high-level facility providing high-level service for both coverages.

8. There exists no restriction about opening health centers and hospitals in the same place.

3.5 MATHEMATICAL FORMULATION

3.5.1 MODEL

$$Max\ w_1 \sum_{i\in I}\sum_{j\in J} d_i\, c_{ij}^1 x_{ij}^1 + w_2 \sum_{i\in I}\sum_{j\in J} d_i\, c_{ij}^2 x_{ij}^2 + w_3 \sum_{j\in J}\sum_{k\in J} \delta\left(\sum_{i\in I} d_i\, c_{ij}^1 x_{ij}^1\right) c_{jk}^3 y_{jk} \qquad (27)$$

s.t.

$$\sum_{i\in J} z_i = q \qquad (28)$$

$$\sum_{i\in I}\sum_{j\in J} y_{ij} \le p \qquad (29)$$

$$x_{ij}^1 \le a_{ij}^1 \sum_{k\in J} y_{jk} \qquad \forall i\in I, j\in J \qquad (30)$$

$$x_{ij}^2 \le a_{ij}^2 z_j \qquad \forall i\in I, j\in J \qquad (31)$$

$$\sum_{j\in J} (x_{ij}^1 + x_{ij}^2) \le 1 \qquad \forall i\in I \qquad (32)$$

$$y_{ij} \le a_{ij}^3 z_j \qquad \forall i\in J, j\in J \qquad (33)$$

$$\sum_{j\in J} y_{ij} \le 1 \qquad \forall i\in J \qquad (34)$$

$$x_{ij}^1 \in \{0,1\} \qquad \forall i\in I, j\in J \qquad (35)$$

$$x_{ij}^2 \in \{0,1\} \qquad \forall i\in I, j\in J \qquad (36)$$

$$y_{ij} \in \{0,1\} \qquad \forall i\in J, j\in J \qquad (37)$$

$$z_i \in \{0,1\} \qquad \forall i\in J \qquad (38)$$

where

I: set of demand points

J: set of potential facility sites to open health center and/or hospital, $J \subset I$

d_i : demand at i (weight of node i)

a_{ij}^1 : 1, if demand at node i is within T^1 distance of health center at node j

0, otherwise

a_{ij}^2 : 1, if demand at node i is within T^2 distance of hospital at node j

0, otherwise

a_{ij}^3 : 1, if health center at node i is within T^3 distance of hospital at node j

0, otherwise

c_{ij}^1 : 1, if demand at node i is within S^1 distance of health center at node j

$(T^1 - dist_{ij}) / (T^1 - S^1)$, if demand at node i is between S^1 and T^1 distance of health center at node j

0, otherwise

c_{ij}^2 : 1, if demand at node i is within S^2 distance of hospital at node j

$(T^2 - dist_{ij}) / (T^2 - S^2)$, if critical demand at node i is between S^2 and T^2 distance of hospital at node j

0, otherwise

c_{ij}^3: 1, if health center at node i is within S^3 distance of hospital at node j

$(T^3 - dist_{ij}) / (T^3 - S^3)$, if health center at node i is between S^3 and T^3 distance of hospital at node j

0, otherwise

$dist_{ij}$: distance between nodes i and j

S^1: minimum critical distance for demand-by-health center coverage

S^2: minimum critical distance for demand-by-hospital coverage

S^3: minimum critical distance for health center-by-hospital coverage

T^1: maximum critical distance for demand-by-health center coverage

T^2: maximum critical distance for demand-by-hospital coverage

T^3: maximum critical distance for health center-by-hospital coverage

x_{ij}^1: 1, if demand at node i is covered by a health center at node j

0, otherwise

x_{ij}^2: 1, if demand at node i is covered by a hospital at node j

0, otherwise

y_{ij}: 1, if health center at node i is opened and covered by a hospital at node j

0, otherwise

z_i: 1, if hospital is opened at node i

0, otherwise

w_1: weight of first term of objective function, importance deemed to coverage of demand by health centers

w_2: weight of second term of objective function, importance deemed to coverage of demand by hospitals

w_3: weight of third term of objective function, importance deemed to referral of demand to hospitals via health centers

δ: fraction of demand that has to be referred to hospitals via health centers

Objective (27) maximizes the total demand covered; total of weighted coverage provided by health centers to demand points, weighted coverage provided by hospitals to demand points and weighted coverage provided by hospitals to demand referred via health centers. Note that the objective function is nonlinear.

Constraint set (28) fixes the number of hospitals to be opened at *q*. Constraint set (29) limits the number of referrals -assignments from health centers to hospitals- with *p*. This constraint set in fact, limits the number of opened and covered health centers, together with constraint set (34). Referral is required to be considered in order to limit the number, because if a health center is not able to refer its demand it is not allowed to be opened. The constraint should be less than or equal to, otherwise infeasibility may occur depending on the problem instance.

Constraint set (30) ensures that demand at node *i* can be covered by a health center at node *j* only if demand at node *i* is within T^1 critical distance of health center at node *j* and health center at node *j* is assigned to a hospital. Constraint set (31) ensures that demand at node *i* can be covered by a hospital at node *j* only if demand at node *i* is within T^2 critical distance of an opened hospital at node *j*. Constraint set (32) restricts demand at node *i* to be covered by only one facility or not covered at all.

Constraint set (33) ensures that health center at node *i* can be covered by a hospital at node *j* only if health center at node *i* is within T^3 critical distance of an opened hospital at node *j*. Constraint set (34) restricts health center at node *i* to be covered by at most one hospital. Coverage in this relationship can also be considered as assignment or matching as well.

Constraint sets (35)-(38) ensure all variables to be binary.

Complexity of the model is O(| I || J |)., since

# of variables: $2*|I|*|J|+|J|^2+|J|=|J|*(2|I|+|J|+1)$: O(| I || J |) and

# of constraints: $2*|I|*|J|+|I|+|J|^2+|J|$: O(| I || J |).

The model also includes a quadratic element in the third term of the objective function which is needed to be removed. The linearization is carried out in two different ways.

3.5.2 LINEARIZED MODELS

3.5.2.1 LINEARIZED MODEL 1

Objective function is changed as follows

$$Max\ w_1\sum_{i\in I}\sum_{j\in J} d_i\, c_{ij}^1 x_{ij}^1 + w_2\sum_{i\in}\sum_{j\in J} d_i\, c_{ij}^2 x_{ij}^2 + w_3\delta\sum_{j\in J}\sum_{k\in J}\sum_{i\in I} d_i\, c_{ij}^1 c_{jk}^3 u_{ijk} \qquad (27a)$$

and the following constraints are added,

$$u_{ijk} \le \frac{1}{2}\left(x_{ij}^1 + y_{jk}\right) \qquad \forall i\in I, j\in J, k\in J \qquad (39)$$

$$u_{ijk} \in \{0,1\} \qquad \forall i\in I, j\in J, k\in J \qquad (40)$$

where

u_{ijk} : { 1, if demand at node i is referred to hospital at node k via health center at node j ; 0, otherwise

Objective function (27a) is the linearized form of objective function (27) by introduction of decision variable u_{ijk}. Constraint set (39) ensures that referral from demand point *i* to hospital *k* via health center *j* is possible only when demand point *i* is covered by health center *j* (i.e. $x_{ij} = 1$) and health center *j* is covered by hospital *k* (i.e. $y_{jk} = 1$). Constraint set (40) ensures that u_{ijk} are binary.

Complexity of the model is increased to $O(|I||J|^2)$, since

# of variables: $2*|I|*|J|+|J|^2+|J|+|I|*|J|^2 =$

$|J|*(2|I|+|J|+1+|I||J|)$: $O(|I||J|^2)$ and

# of constraints: $2*|I|*|J|+|I|+|J|^2+|J|+|I|*|J|^2$: $O(|I||J|^2)$.

3.5.2.2 LINEARIZED MODEL 2

Objective function is changed as follows

$$Max\ w_1\sum_{i\in I}\sum_{j\in J} d_i\, c_{ij}^1 x_{ij}^1 + w_2\sum_{i\in I}\sum_{j\in J} d_i\, c_{ij}^2 x_{ij}^2 + w_3\sum_{j\in J}\sum_{k\in J} u_{jk} \qquad (27b)$$

and the following constraints are added,

$$u_{jk} \le \delta\left(\sum_{i\in I} d_i\, c_{ij}^1 x_{ij}\right) c_{jk}^3 \qquad \forall j\in J, k\in J \qquad (41)$$

$$u_{jk} \le M y_{jk} \qquad \forall j\in J, k\in J \qquad (42)$$

$$u_{jk} \in \{0,1\} \qquad \forall j\in J, k\in J \qquad (43)$$

where

u_{jk}: total weight accumulated in health center at node *j* to be referred to hospital at node *k*

M: a large number

Objective function (27b) is the linearized form of objective function (27) by the introduction of decision variable u_{jk}. Constraint set (41) limits the weight referred from health center *j* to hospital *k* by coverage weighted total demand accumulated in health center *j*, that is the total weight of demand point *i*'s covered by health center *j*. Constraint set (42) sets the weighted coverage at node *j* to zero if no coverage is provided from node *k.* In case of coverage, the constraint set does not put bounds on the amount. Constraint set (43) ensures that u_{jk} are binary.

Complexity of the model is stayed at O($|I||J|$) in this linearization, since

# of variables: $2*|I|*|J|+|J|^2+|J|+|J|^2=|J|*(2|I|+|J|+1+|J|)$: O($|I||J|$) and

# of constraints: $2*|I|*|J|+|I|+|J|^2+|J|+|J|^2$: O($|I||J|$).

The problem is NP-hard; that is complexity increases exponentially with problem size. In most of the uncapacitated covering problems assignment is not needed. The information of whether a demand point is covered or not is sufficient, it is not required to keep which facility covers which demand point. However, introduction of partial coverage requires assignment, since coverage is calculated using distances between demand and facility nodes.

The following sets are defined in order to reduce problem size.

$M_{ij}^1 = \{ij \ni i \in I \wedge j \in J \wedge a_{ij}^1 = 1\}$: set of demand point-health center pairs that are in T^1 distance to each other

$M_{ij}^2 = \{ij \ni i \in I \wedge j \in J \wedge a_{ij}^2 = 1\}$: set of demand point-hospital pairs that are in T^2 distance to each other

$M_{ij}^3 = \{ij \ni i \in J \wedge j \in J \wedge a_{ij}^3 = 1\}$: set of health center-hospital pairs that are in T^3 distance to each other

3.5.3 LINEARIZED REDUCED MODELS

3.5.3.1 LINEARIZED REDUCED MODEL 1

$$Max \sum_{ij \in M_{ij}^1} d_i \, c_{ij}^1 x_{ij}^1 + \sum_{ij \in M_{ij}^2} d_i \, c_{ij}^2 x_{ij}^2 + \sum_{ijk \in M_{ij}^1 \wedge M_{jk}^3} d_i \, c_{ij}^1 c_{jk}^3 u_{ijk}$$

s.t.

$$\sum_{i \in J} z_i = q$$

$$\sum_{ij \in M_{ij}^3} y_{ij} \le p$$

$$x_{ij}^1 \le a_{ij}^1 \sum_{k \in M_{jk}^3} y_{jk} \qquad \forall ij \in M_{ij}^1$$

$$x_{ij}^2 \le a_{ij}^2 z_j \qquad \forall ij \in M_{ij}^2$$

$$\sum_{j \in M_{ij}^1} x_{ij}^1 + \sum_{j \in M_{ij}^2} x_{ij}^2 \le 1 \qquad \forall i \in I$$

$$y_{ij} \le a_{ij}^3 z_j \qquad \forall ij \in M_{ij}^3$$

$$\sum_{j \in M_{ij}^3} y_{ij} \le 1 \qquad \forall i \in J$$

$$u_{ijk} \le \frac{1}{2}\left(x_{ij}^1 + y_{jk}\right) \qquad \forall ijk \in M_{ij}^1 \wedge M_{jk}^3$$

$$x_{ij}^1 \in \{0,1\} \qquad \forall ij \in M_{ij}^1, \; x_{ij}^2 \in \{0,1\} \quad \forall ij \in M_{ij}^2$$

$$y_{ij} \in \{0,1\} \qquad \forall ij \in M_{ij}^3,$$

$$z_i \in \{0,1\} \qquad \forall i \in J, \; u_{ijk} \in \{0,1\} \qquad \forall ijk \in M_{ij}^1 \wedge M_{jk}^3$$

3.5.3.2 LINEARIZED REDUCED MODEL 2

$$Max \sum_{ij \in M_{ij}^1} d_i \, c_{ij}^1 x_{ij}^1 + \sum_{ij \in M_{ij}^2} d_i \, c_{ij}^2 x_{ij}^2 + \sum_{jk \in M_{jk}^3} u_{jk}$$

s.t.

$$\sum_{i \in J} z_i = q$$

$$\sum_{ij \in M_{ij}^3} y_{ij} \le p$$

$$x_{ij}^1 \le a_{ij}^1 \sum_{k \in M_{jk}^3} y_{jk} \qquad \forall ij \in M_{ij}^1$$

$$x_{ij}^2 \le a_{ij}^2 z_j \qquad \forall ij \in M_{ij}^2$$

$$\sum_{j \in M_{ij}^1} x_{ij}^1 + \sum_{j \in M_{ij}^2} x_{ij}^2 \le 1 \qquad \forall i \in I$$

$$y_{ij} \le a_{ij}^3 z_j \qquad \forall ij \in M_{ij}^3$$

$$\sum_{j \in M_{ij}^3} y_{ij} \le 1 \qquad \forall i \in J$$

$$u_{jk} \le \left(\sum_{i \in M_{ij}^1} d_i \, c_{ij}^1 x_{ij} \right) c_{jk}^3 \qquad \forall jk \in M_{jk}^3$$

$$u_{jk} \le M y_{jk} \qquad \forall jk \in M_{jk}^3$$

$$x_{ij}^1 \in \{0,1\} \qquad \forall ij \in M_{ij}^1, \; x_{ij}^2 \in \{0,1\} \quad \forall ij \in M_{ij}^2$$

$$y_{ij} \in \{0,1\} \qquad \forall ij \in M_{ij}^3,$$

$$z_i \in \{0,1\} \qquad \forall i \in J, \; u_{jk} \in \{0,1\} \qquad \forall jk \in M_{jk}^3$$

3.6 AN EXAMPLE AND SENSITIVITY ANALYSIS

The formulation developed for HMCLP(R)-P is illustrated on a 50-node example problem. Suppose the budget gives opportunity to establish 14 health centers and 6 hospitals.

The parameters are set at $S^1 = 30$, $S^2 = 60$, $S^3 = 80$, $T^1 = 50$, $T^2 = 80$, $T^3 = 100$ and $w^1 = 1$, $w^2 = 1$, $w^3 = 1$, $\delta = 1$ initially. The optimal configuration is presented in Figure 3.8.

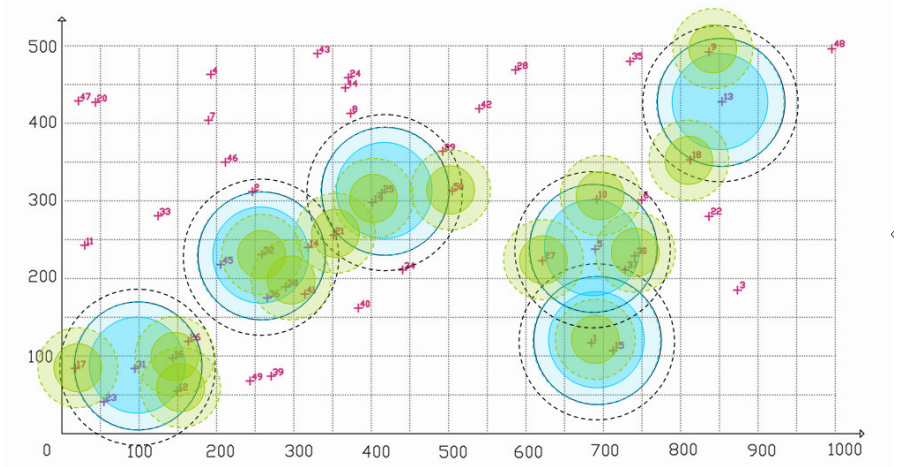
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
original problem	$S^1 = 30$ $S^2 = 60$ $S^3 = 80$ $T^1 = 50$ $T^2 = 80$ $T^3 = 100$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 1$	*1-1* *9-9* *10-10* *12-12* *14-21* *15-1* *16-16* *17-17* *18-18* *19-19* *21-21* *25-19* *26-16* *27-27* *30-30* *32-32* *36-38* *37-30* *38-38* *41-38* *50-50*	*5-5* *13-13* *23-31* *31-31* *45-32*	*1-1* *9-13* *10-5* *12-31* *16-31* *17-31* *18-13* *19-25* *21-25* *27-5* *30-5* *32-32* *38-32* *50-25*	*1* *5* *13* *25* *31* *32*	*611.71*	*346*
							

Figure 3.8 – Optimal configurations of facilities for the original problem

The setting for critical distances may be narrower or larger as presented in figure 3.9.

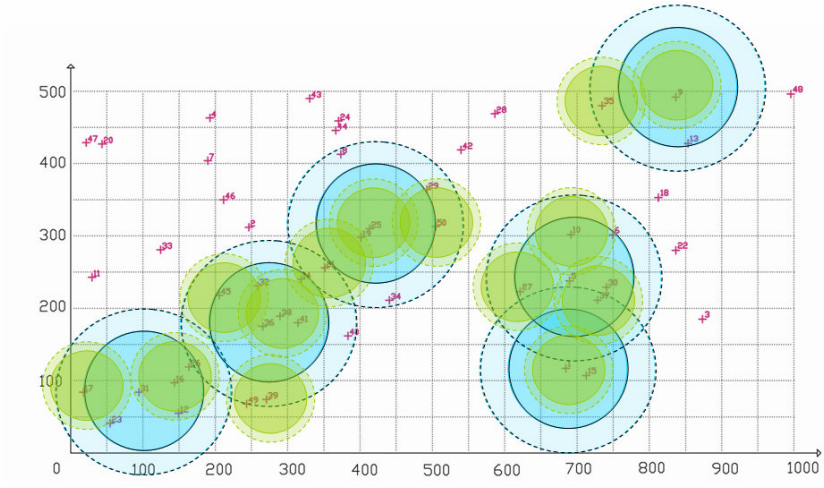
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
1	$S^1 = 50$ $S^2 = 80$ $S^3 = 80$ $T^1 = 60$ $T^2 = 120$ $T^3 = 120$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 1$	*1-1* *5-37* *9-9* *10-10* *12-16* *14-21* *15-1* *16-16* *17-17* *19-25* *21-21* *25-25* *26-16* *27-27* *29-50* *30-37* *31-16* *32-38* *35-35* *36-38* *37-37* *38-38* *39-39* *41-38* *45-45* *49-39* *50-50*	*6-5* *8-25* *13-9* *23-31* *34-25* *40-36*	*1-1* *9-9* *10-5* *16-31* *17-31* *21-25* *25-25* *27-5* *35-9* *37-5* *38-36* *39-36* *45-36* *50-25*	*1* *5* *9* *25* *31* *36*	*703,20*	*401*
							

Figure 3.9 – Changes in optimal configurations of facilities with changes in all critical distances

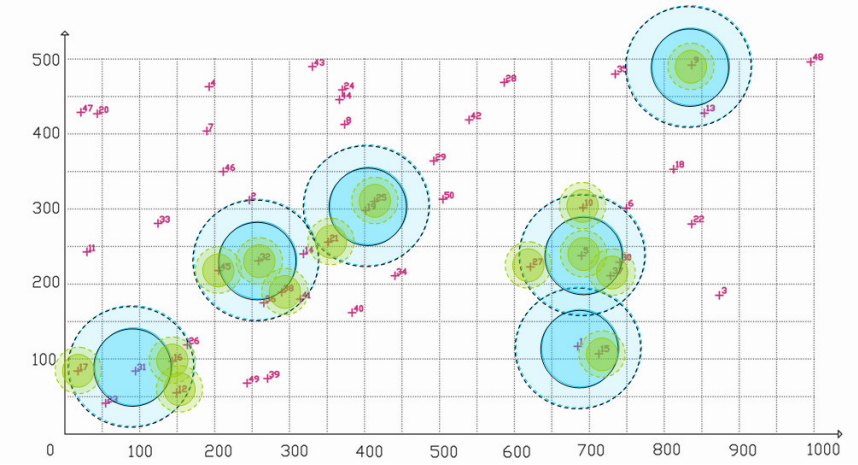
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
2	$S^1 = 20$ $S^2 = 60$ $S^3 = 60$ $T^1 = 30$ $T^2 = 90$ $T^3 = 90$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 1$	*5-5* *9-9* *10-10* *12-12* *15-15* *16-16* *17-17* *19-25* *21-21* *25-25* *27-27* *30-37* *32-32* *37-37* *38-38* *41-38* *45-45*	*1-1* *2-32* *6-5* *13-9* *14-32* *23-31* *26-31* *31-31* *36-32*	*5-5* *9-9* *10-5* *12-31* *15-1* *16-31* *17-31* *21-19* *25-19* *27-5* *32-32* *37-5* *38-32* *45-32*	*1* *5* *9* *19* *31* *32*	*551.28*	*328*
							

Figure 3.9 (continued) – Changes in optimal configurations of facilities with changes in all critical distances

Figure 3.9 indicates that even small adjustments in parameter settings may alter the settlement of the facilities. Therefore, the characteristics of the region, the

health culture and the experimented quality that can be supplied should be treated as important factors in determination of the parameters.

In Figure 3.8, there is another issue that we need to discuss. Although it is not restricted by the formulation to establish a health center and a hospital at the same site, in the optimal solution it is not expected to have such a case since establishing both facilities in the same site is inefficient. If there is an extra facility, it should be established in a different site to cover additional demand. However, in the above configuration, both a health center and a hospital are placed in node 32.

The importance of setting parameters comes into scene at this point. Although the model explained in Section 3.5 is verified; without correct setting of parameters it does not reflect entire requirements. The expectation is having a configuration as dispersed as possible. Then the reason behind locating both facilities at the same site should be analyzed.

The constraint of “health centers can be opened only if they can be referred to hospitals” causes hospitals in the middle with batches of health centers around them, which are within the referral critical distances of the hospitals. This accumulation can be prevented by enlarging the referral critical distances. However, that technical requirement coincides with real life. Hospitals frequently serve people coming from distant places because of their special capabilities or abilities of their doctors. Thus, having coverage for distant places even if coverage level is low sounds reasonable.

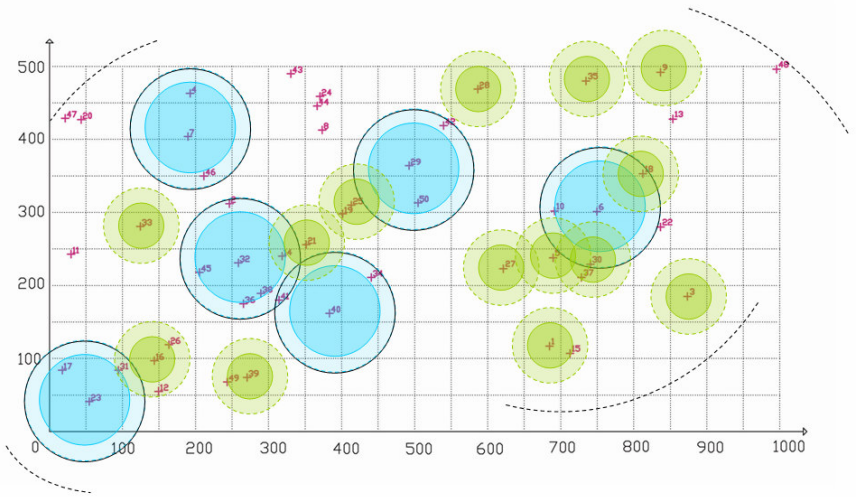
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
3	$S^1 = 50$ $S^2 = 80$ $S^3 = 80$ $T^1 = 60$ $T^2 = 120$ $T^3 = \max_{ij}\{dist_{ij}\}$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 1$	*1-1* *3-3* *5-5* *9-9* *12-16* *14-21* *15-1* *16-16* *18-18* *19-25* *21-21* *25-25* *16-16* *27-27* *28-28* *30-30* *33-33* *35-35* *37-30* *39-39* *49-39*	*4-7* *6-6* *7-7* *10-6* *17-23* *23-23* *29-29* *31-23* *32-32* *34-40* *36-32* *38-32* *40-40* *41-40* *42-29* *45-32* *46-7* *50-29*	*1-6* *3-6* *5-6* *9-6* *16-23* *18-6* *21-32* *25-29* *27-6* *28-29* *30-6* *33-7* *35-6* *39-40*	*6* *7* *23* *29* *32* *40*	*726.83*	*479*
							

Figure 3.10 – Changes in optimal configurations of facilities with changes in referral critical distances

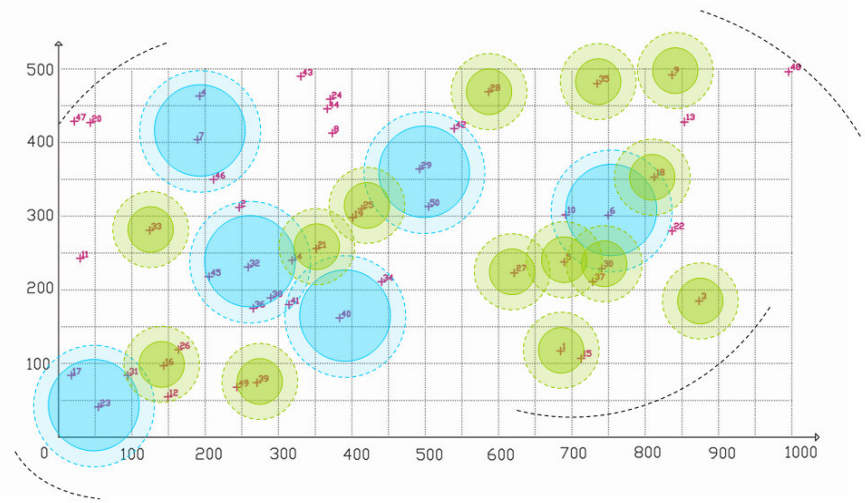
	Changed Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
4	$S^1 = 30$ $S^2 = 60$ $S^3 = 0$ $T^1 = 50$ $T^2 = 80$ $T^3 = \max_{ij}\{dist_{ij}\}$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 1$	*1-1* *3-3* *5-5* *9-9* *12-16* *14-21* *15-1* *16-16* *18-18* *19-25* *21-21* *25-25* *26-16* *27-27* *28-28* *30-30* *33-33* *35-35* *37-30* *39-39* *49-39*	*4-7* *6-6* *7-7* *10-6* *17-23* *23-23* *29-29* *31-23* *32-32* *34-40* *36-32* *38-32* *40-40* *41-40* *42-29* *45-32* *46-7* *50-29*	*1-6* *3-6* *5-6* *9-6* *16-23* *18-6* *21-32* *25-29* *27-6* *28-29* *30-6* *33-7* *35-6* *39-40*	*6* *7* *23* *29* *32* *40*	*706.48*	*479*
							

Figure 3.10 (continued) – Changes in optimal configurations of facilities with changes in referral critical distances

In Figure 3.10, the referral critical distances are adjusted. Enlargement of maximum critical distance for referral provides the desired effect of homogeneous dispersal of health centers and hospitals. Since any health center in any district

can be referred to any hospital, establishing health centers and hospitals in different places earns meaning.

The configurations are consistent with the 'Total People Covered' values presented in last columns. It calculates the total coverage without the consideration of partial coverage; that is the total weight within colored coverage areas. This eliminates the consideration of quality but dwells on quantity. Increasing the maximum critical distance of referral to infinity -which is identical to the maximum distance between any nodes-, yields maximum amount of net coverage.

The fraction of people referred from health centers to hospitals (δ) is another important parameter. If the referral rate is small, the amount directly assigned to hospitals increases. This is same with having the weight of the third term of the objective function (w^3) as 0.1.

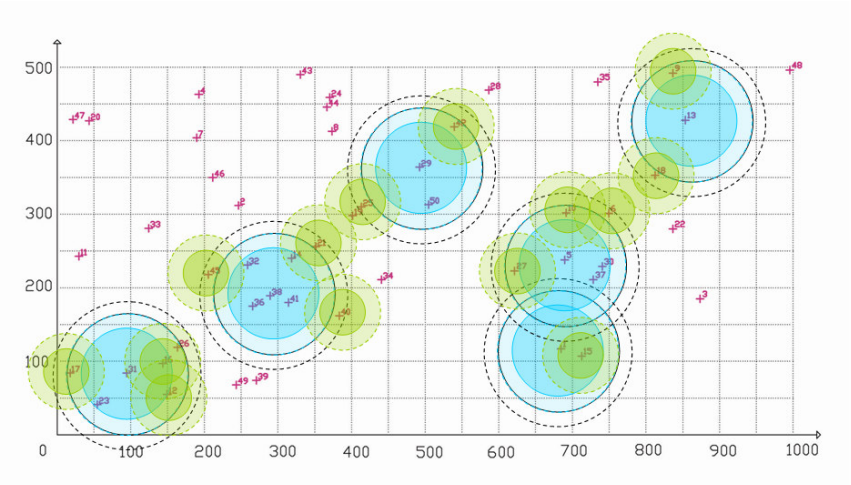
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
5	$S^1 = 30$ $S^2 = 60$ $S^3 = 80$ $T^1 = 50$ $T^2 = 80$ $T^3 = 100$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 0.1$	*1-15* *6-6* *9-9* *10-10* *12-12* *15-15* *16-16* *17-17* *18-18* *19-25* *21-21* *25-25* *26-16* *27-27* *40-40* *42-42* *45-45*	*5-5* *13-13* *14-38* *23-31* *29-29* *30-5* *31-31* *32-38* *36-38* *37-5* *38-38* *41-38* *50-29*	*6-5* *9-13* *10-5* *12-31* *15-1* *16-31* *17-31* *18-13* *21-38* *25-29* *27-5* *40-38* *42-29* *45-38*	*1* *5* *13* *29* *31* *38*	*392.72*	*374*
							

Figure 3.11 – Changes in optimal configurations of facilities with changes in referred fraction

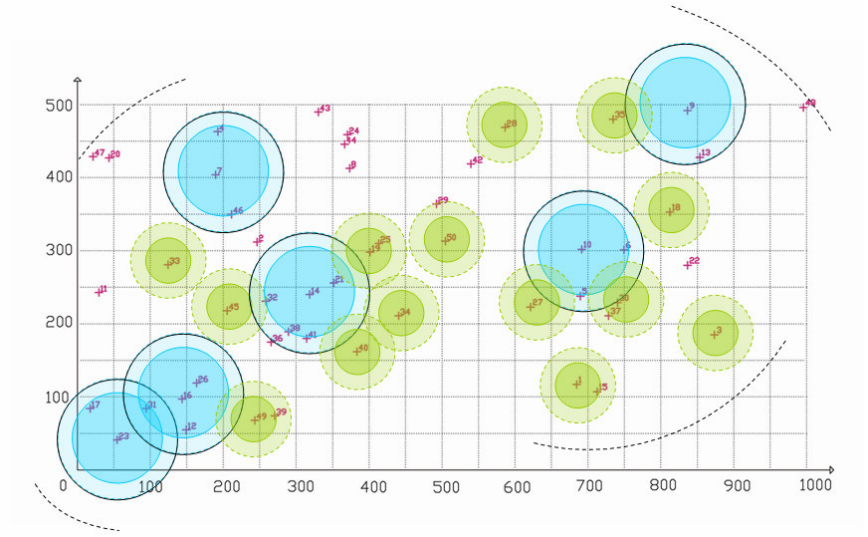
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
6	$S^1 = 30$ $S^2 = 60$ $S^3 = 80$ $T^1 = 50$ $T^2 = 80$ $T^3 = \max_{ij}\{dist_{ij}\}$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 0.1$	*1-1* *3-3* *15-1* *18-18* *19-19* *25-19* *27-27* *28-28* *30-30* *33-33* *34-34* *35-35* *37-30* *39-49* *40-40* *45-45* *49-49* *50-50*	*4-7* *5-10* *6-10* *7-7* *9-9* *10-10* *12-16* *13-9* *14-14* *16-16* *17-23* *21-14* *23-23* *26-26* *31-23* *32-14* *38-14* *41-14* *46-7*	*1-10* *3-10* *18-10* *19-14* *27-10* *28-10* *30-10* *33-7* *34-14* *35-9* *40-14* *45-14* *49-16* *50-10*	*7* *9* *10* *14* *16* *23*	*496.11*	*479*
							

Figure 3.11 (continued) – Changes in optimal configurations of facilities with changes in referred fraction

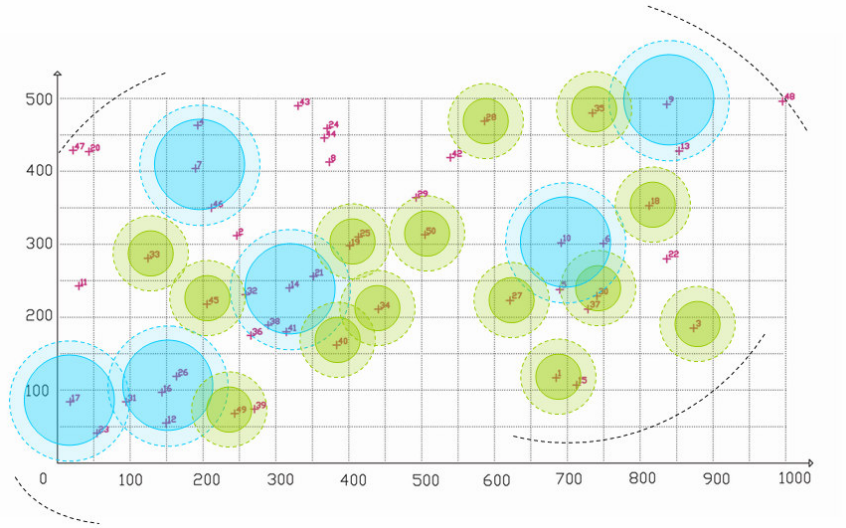
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
7	$S^1 = 30$ $S^2 = 60$ $S^3 = 0$ $T^1 = 50$ $T^2 = 80$ $T^3 = \max_{ij}\{dist_{ij}\}$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 0.1$	*1-1* *3-3* *15-1* *18-18* *19-19* *25-19* *27-27* *28-28* *30-30* *33-33* *34-34* *35-35* *37-30* *39-49* *40-40* *45-45* *49-49* *50-50*	*4-7* *5-10* *6-10* *7-7* *9-9* *10-10* *12-16* *13-9* *14-14* *16-16* *17-17* *21-14* *23-17* *26-16* *31-16* *32-14* *38-14* *41-14* *46-7*	*1-10* *3-10* *18-10* *19-14* *27-10* *28-10* *30-10* *33-7* *34-14* *35-9* *40-14* *45-14* *49-16* *50-10*	*7* *9* *10* *14* *16* *17*	*494.32*	*479*
							

Figure 3.11 (continued) – Changes in optimal configurations of facilities with changes in referred fraction

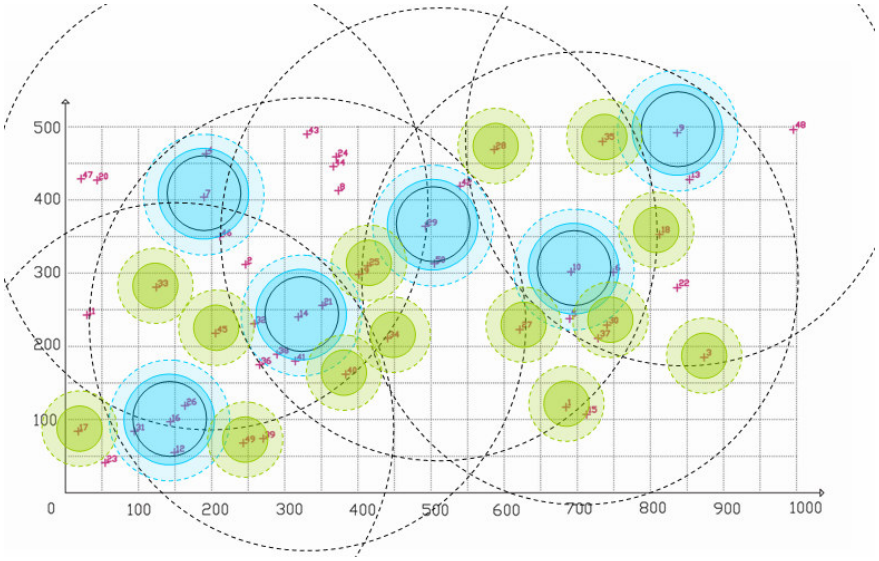
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
8	$S^1 = 30$ $S^2 = 60$ $S^3 = 50$ $T^1 = 50$ $T^2 = 80$ $T^3 = 300$ $w^1 = 1$ $w^2 = 1$ $w^3 = 1$ $\delta = 0.1$	*1-1* *3-3* *15-1* *17-17* *18-18* *19-25* *25-25* *27-27* *28-28* *30-30* *33-33* *34-34* *35-35* *37-30* *39-49* *40-40* *45-45* *49-49*	*4-7* *5-10* *6-10* *7-7* *9-9* *10-10* *12-16* *13-9* *14-14* *16-16* *21-14* *26-16* *29-29* *31-16* *32-14* *38-14* *41-14* *42-29* *46-7* *50-29*	*1-10* *3-10* *17-16* *18-10* *25-29* *27-10* *28-29* *30-10* *33-7* *34-14* *35-9* *40-14* *45-14* *49-16*	*7* *9* *10* *14* *16* *29*	*489.10*	*482*
							

Figure 3.11 (continued) – Changes in optimal configurations of facilities with changes in referred fraction

The referral rate affects the configuration. When referral rate is large, demand is forced to be assigned to health centers first and then to be referred to hospitals. In this way, it is counted by both the first and the third terms of the objective function. Figure 3.11 demonstrates that the largest effect is obtained with the referral critical distances of 50 and 300. Consistently, the value of 'Total People Covered' is the highest amongst all.

Determination of objective function is another critical factor for application of the model. The current objective function reflects desire of achievement of three objectives

- low-level coverage of demand nodes by health centers,
- high-level coverage of demand nodes via referral that are already covered by health centers, and
- low and high-level coverage of demand nodes by hospitals

with equal importance, since these objectives are combined with weights of 1 ($w^1 = w^2 = w^3 = 1$). However, the preference for different objectives may be different.

Figure 3.11 also demonstrates the situation of weight of the third term of the objective function (w^3) being 0.1 whereas rate of referral (δ) is 1.

Another modification that equalizes the importance of direct coverage by hospital and coverage via referral is changing the weight of coverage of low-level demand by health centers (w^1) to 0. The intuition behind this modification is that, there is a double coverage counting for the demand points that are firstly covered by health centers and then referred to hospitals, when $\delta = 1$. The low-level coverage and high-level coverage contribute to objective function separately with equal importance. However, since there is no possibility that low-level demand of a demand point is remained unsatisfied while high-level demand of that demand point is satisfied; satisfaction of high-level demand via referral guarantees satisfaction of low-level demand by health centers. Since the desire is to cover all levels of as much as possible demand, and covering high-level ensures covering

all levels; the objective function can be re-defined as combination of coverage of high-level demand by hospitals and coverage of high-level demand via referral. Figure 3.12 demonstrates the effect of change in w^1.

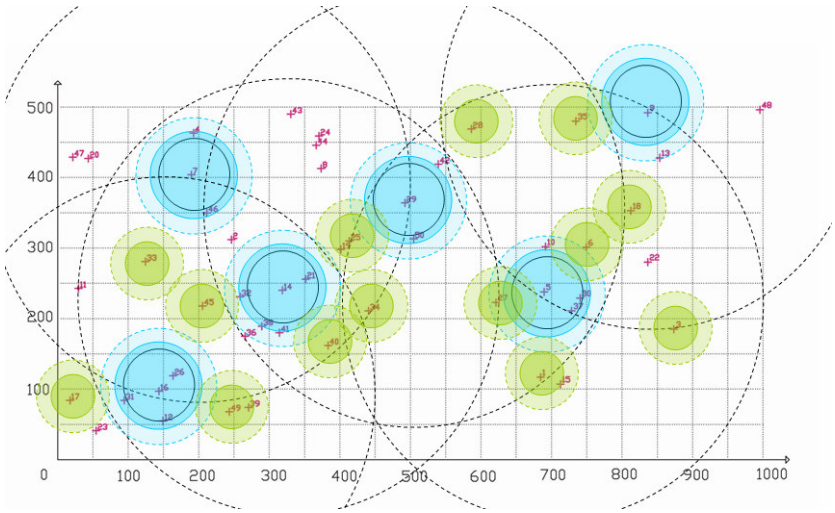
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
9	$S^1 = 30$ $S^2 = 60$ $S^3 = 50$ $T^1 = 50$ $T^2 = 80$ $T^3 = 300$ $w^1 = 0$ $w^2 = 1$ $w^3 = 1$ $\delta = 1$	*1-1* *3-3* *6-6* *15-1* *17-17* *18-18* *19-25* *25-25* *27-27* *28-28* *33-33* *34-34* *35-35* *39-49* *40-40* *45-45* *49-49*	*4-7* *5-5* *7-7* *9-9* *10-5* *12-16* *13-9* *14-14* *16-16* *21-14* *26-16* *29-29* *30-5* *31-16* *32-14* *37-5* *38-14* *41-14* *42-29* *46-7* *50-29*	*1-5* *3-5* *6-5* *17-16* *18-9* *25-29* *27-5* *28-29* *33-7* *34-14* *35-9* *40-14* *45-14* *49-16*	*5* *7* *9* *14* *16* *29*	*407.60*	*482*
							

Figure 3.12 – Change in optimal configuration of facilities with changes in weight of first term in objective function

The configuration does not differ substantially from the trial of same critical distances with referral rate or third term weight of 0.1. The value of 'Total People Covered' is the same. These two configurations are alternative solutions in fact.

The reason of improvement in dispersal when one of weights of first and third terms are changed is that in the objective function even though it is guaranteed that if a demand point is assigned to a health center, it is certainly referred to a hospital and the vice versa that if a demand point is referred to a hospital then it certainly is covered by a health center; appearance of both of these terms in the objective function makes covering demand by health centers and referring them two times more important than covering demand by hospitals. So, in the optimal configuration, hospitals are found out to be located closer to the health centers in order to achieve the two times more important covering rather than being located in different zones.

Increasing the objective function weight of coverage of demand by hospitals to 2 reveals exactly the same configuration with decreasing the objective function weight of coverage of demand by health centers to 0, as demonstrated in Figure 3.13.

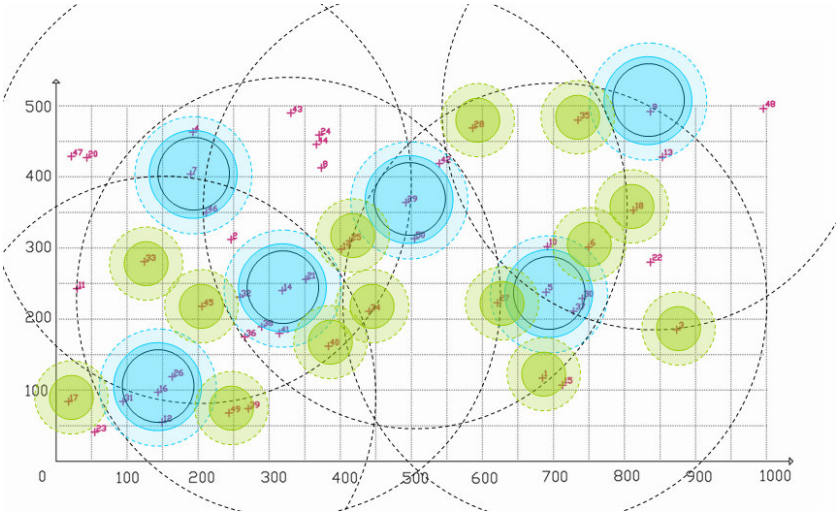
	Problem Parameters	Assignment of Demand to Health Centers (Demand-Health Center)	Assignment of Demand to Hospitals (Demand-Hospital)	Refer of Health Centers to Hospitals (Health Center-Hospital)	Opened Hospitals	Optimal Result	Total People Covered
10	$S^1 = 30$ $S^2 = 60$ $S^3 = 50$ $T^1 = 50$ $T^2 = 80$ $T^3 = 300$ $w^1 = 1$ $w^2 = 2$ $w^3 = 1$ $\delta = 1$	*1-1* *3-3* *6-6* *15-1* *17-17* *18-18* *19-25* *25-25* *27-27* *28-28* *33-33* *34-34* *35-35* *39-49* *40-40* *45-45* *49-49*	*4-7* *5-5* *7-7* *9-9* *10-5* *12-16* *13-9* *14-14* *16-16* *21-14* *26-16* *29-29* *30-5* *31-16* *32-14* *37-5* *38-14* *41-14* *42-29* *46-7* *50-29*	*1-5* *3-5* *6-5* *17-16* *18-9* *25-29* *27-5* *28-29* *33-7* *34-14* *35-9* *40-14* *45-14* *49-16*	*5* *7* *9* *14* *16* *29*	*879.10*	*482*
							

Figure 3.13 – Change in optimal configuration of facilities with changes in weight of second term in objective function

These should be considered while setting the aforementioned parameters of the model. Weights, referral rate and critical distances play an important role in the resulting configuration.

In any case, in order to reflect the real situation more successfully, it is adequate to use large radius for referral maximum critical distance. However, large referral minimum critical distance would not be adequate to every case. It has to be analyzed regarding quality.

Weights of objectives should also be determined carefully. Covering demand by health centers and referring those covered demand to hospitals may be two separate objectives in equal importance or they may be combined to form a single objective that has equal importance with covering demand by hospitals. In the case of combining coverage by health centers and referral, the disadvantage of eliminating the importance of the first term and equalizing the importance of covering demand directly by hospitals and covering them by referral via health centers should be noted. If coverage of demand by health centers and via referral are not counted separately, direct assignment to hospitals increases. Directly assigning people requiring low-level demand to hospitals that are eligible to supply high-level demand is less-desirable, in fact, than referring them to hospital via health centers. Hierarchical structure is preserved and used more efficiently in the latter case. Thus, double counting referred demand may be an alternative. In experimentation, we used this double-counting setting.

Another 50-node example is presented in Figures 3.14 and 3.15 to illustrate the effect of partial coverage. With allowance of partial coverage, the total demand area covered is enlarged, since sacrifice from quality of coverage for some demand nodes brings providing service to a higher number of nodes.

Opened Health Centers	Nodes Covered by Health Centers	Opened Hospitals	Nodes Covered by Hospitals	Optimal Result	Total People Covered
2 34 5 36 6 37 17 40 25 41 26 44 31 48	2 34 5 35 6 36 15 37 17 40 21 41 25 43 26 44 31 48	4 11 12 19 21 47	4 11 12 19 27 29 32 47	541	306

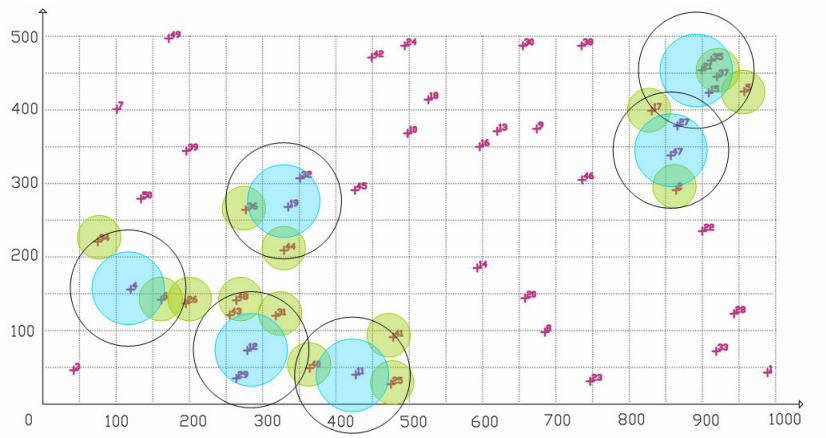


Figure 3.14 – Optimal configuration of facilities in HMCLP with referral without partial coverage

Opened Health Centers	Nodes Covered by Health Centers	Opened Hospitals	Nodes Covered by Hospitals	Optimal Result	Total People Covered
2 14 16 17 19 24 26 31 34 36 37 40 41 48	*2 5 6 13 14 15 16 17 19 21 24 26 31 32 34 35 36 37 40 41 42 43 48*	*4 11 18 20 27 44*	*4 8 10 11 18 20 25 27 44 47*	*583.72 (460 fully-covered, 123.72 partially-covered)*	*380 (263 fully-covered, 117 partially covered)*

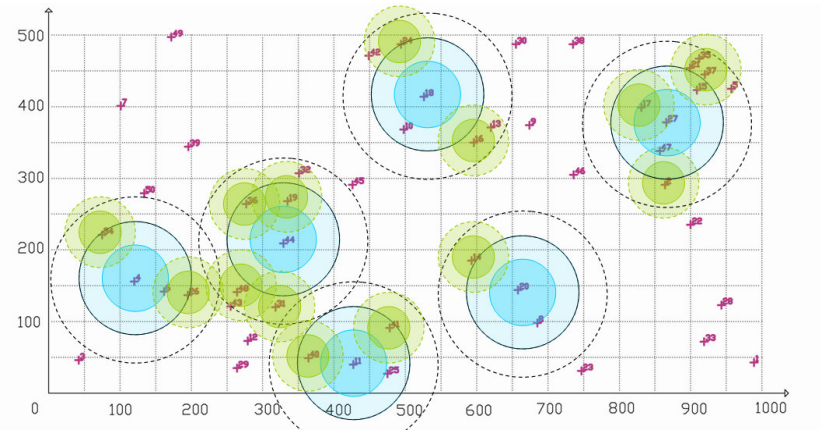


Figure 3.15 – Optimal configuration of facilities in HMCLP with referral in the presence of partial coverage

Partial coverage is not considered in Figure 3.14. The optimal configuration includes large sections which are not covered at all; such as the middle part from top to bottom, the top-left and bottom-right parts. However, when partial coverage is considered as in Figure 3.15, sacrifice is made in order to serve to more number of demand points even though the quality reduces, reveals a more diverse configuration. The maximal critical distances are about 1.5 multiple of manimum critical distances. The amount of demand covered increases about 25%, from 306 people to 380 people whereas the fully-covered portion is decreased only by 14% from 306 to 263.

The trade-off should be determined carefully. In some cases, it may be encountered that the amount partially covered is increased substantially so that the resulting objective function is also increased even though the amount covered fully is reduced too much. It should be noted that quality is sacrificed when partial coverage is considered. The reduction in the amount fully covered should not descend substantially.

If the discussion in Section 3.2 is revisited, it should be asked which is desirable; whether to survive 100 people having heart attack with 60% rate or to survive 59 people with 100% rate. The first is what MCLP-P formulation suggests and the latter is what MCLP formulation suggests. Certainly, the first suggestion is more desirable.

On the other hand, the answer of question may vague in some cases. It should be determined that whether it is more desirable to control all the critical points with capability of observing 30 m long ships and not to control any of the critical points with capability of observing 20 m long ships.

CHAPTER 4

GENETIC ALGORITHM

4.1 BACKGROUND

Genetic Algorithm (GA) is an evolutionary meta-heuristic algorithm that is inspired from evolution theory.

In nature, every individual is formed of chromosomes which individual takes its characteristics from. Chromosomes are formed of genes which are the smallest fragments of the genetic structure that can be exchanged and altered. Fertilization -that is exchange of genes- takes place between two individuals of species in order to generate fitter offspring that has stronger characteristics than his parents that makes him more robust to environmental conditions, since the offspring that is better adapted to environment sustain his life whereas weak offspring is destined to come to an end of existence. Mutation sometimes takes place randomly to alter the genetic structure. At the end, amongst the offspring the ones that are stronger continue their existence. The others vanish.

Genetic algorithm benefits the same logic to generate fit solutions. Species correspond to solutions, fertilization of species corresponds to cross-over, and selection/elimination of individuals corresponds to replacement.

Evolution starts with a set of feasible solutions that are represented as chromosomes. Each solution has a fitness value, which evaluates the goodness of the solution. Fitness of solution determines the probability of the solution to be

mated. Fitter solutions are selected for cross-over. Mating fit chromosomes is thought to result with generation of fitter offspring. Mutation takes place randomly, as in nature. The ending population is selected according to fitness values. Fitter chromosomes continue to next iterations whereas non-fit chromosomes are eliminated.

The generic GA is summarized in Figure 4.1.

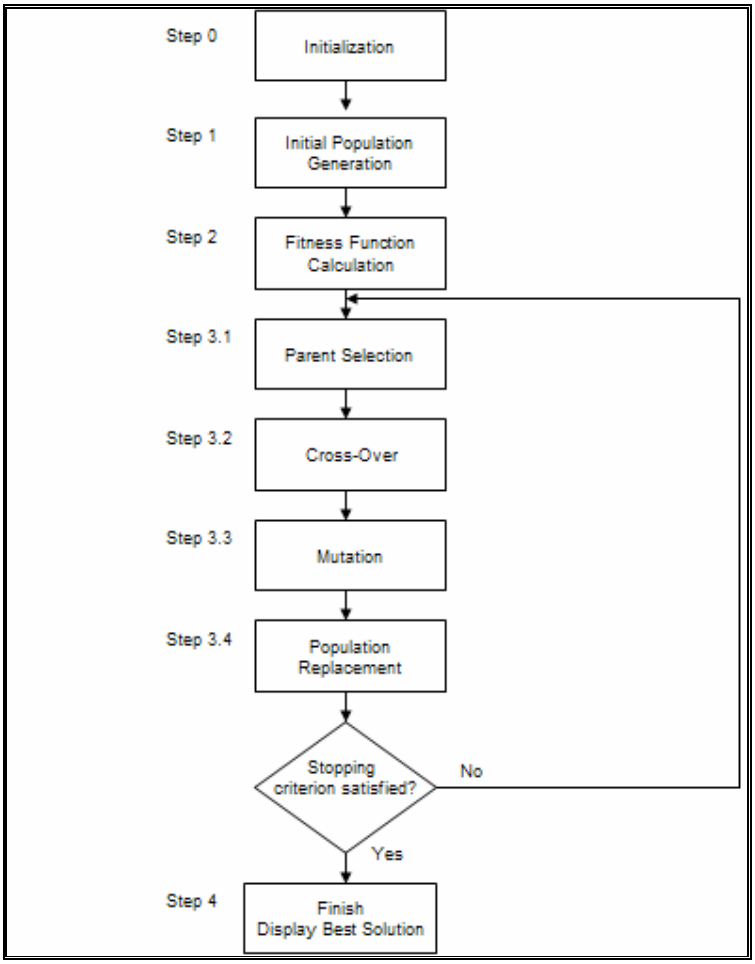


Figure 4.1 – Flowchart of GA

Step 1. Initial Population Generation

The algorithm starts with an initial set of solutions which is called population. The individual solutions are called chromosomes, and the parts of chromosomes are called genes. Initial set of chromosomes resemble Figure 4.2.

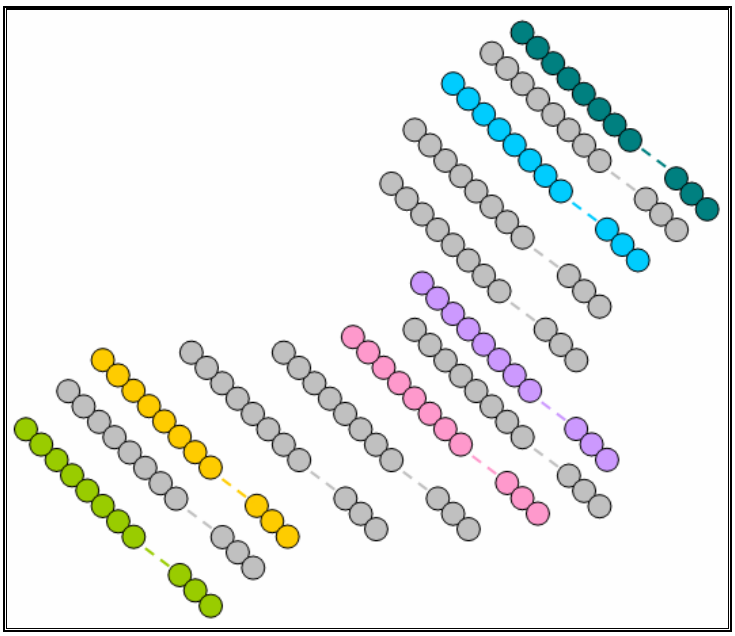


Figure 4.2 – Representation of initial set of chromosomes

Step 2. Fitness Function Computation

The chromosomes are evaluated according to their fitness values. Fitness values represent the goodness of the solution. Fitness function usually is the objective function. Slacks and surpluses of

unsatisfied constraints can be included as penalties.

Goodness of the solution specifies the probability of that solution to persist in next generations.

Step 3. Evolution

The aim of the algorithm is converging the population average to optimal solution of the search space. While a certain stopping condition is not verified, the population evolves with the following operations.

Step 3.1 Parent Selection

A mating pool is formed by selecting chromosomes of the population according to their fitness values. Mating pool is used to mate chromosomes which are called parent chromosomes to generate child chromosomes which are called offspring.

Selected parents are represented in Figure 4.3.

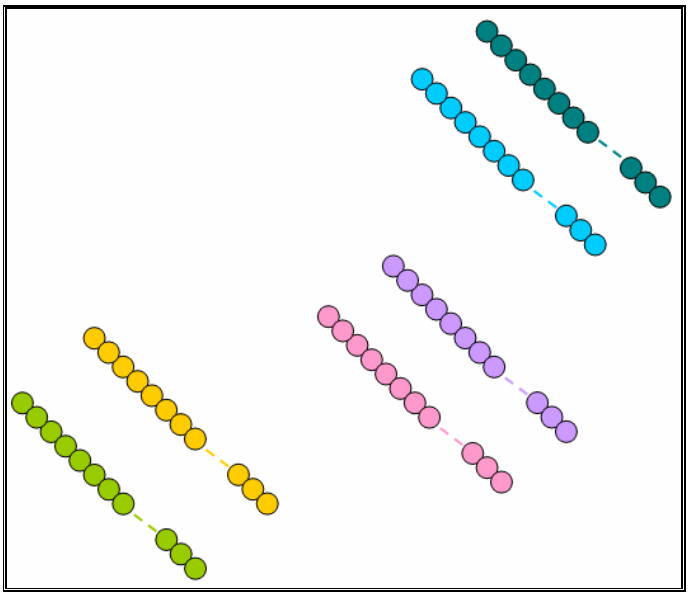


Figure 4.3 – Mating pool

Step 3.2 Cross-Over

Parent chromosome pairs merge by exchanging some of their genes and generate offspring. The way of exchange is determined by the cross-over strategy. Cross-over is effective in exploring the search space.

Cross-overed chromosomes are shown in Figure 4.4.

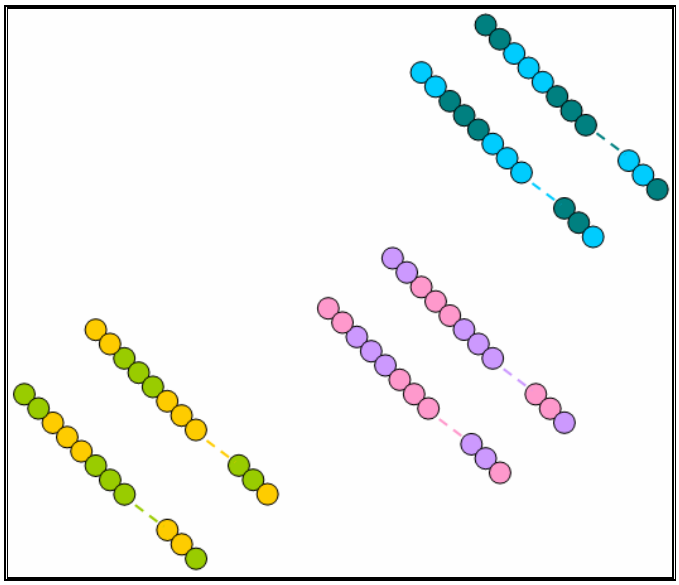


Figure 4.4 – Chromosomes after cross-over

Step 3.3 Mutation

The chromosomes are subjected to mutation by either modifying the chromosome completely or by modifying some of the genes. The way of mutation is determined by the mutation strategy. Mutation is effective in exploiting the search space.

Mutated chromosomes are shown in Figure 4.5.

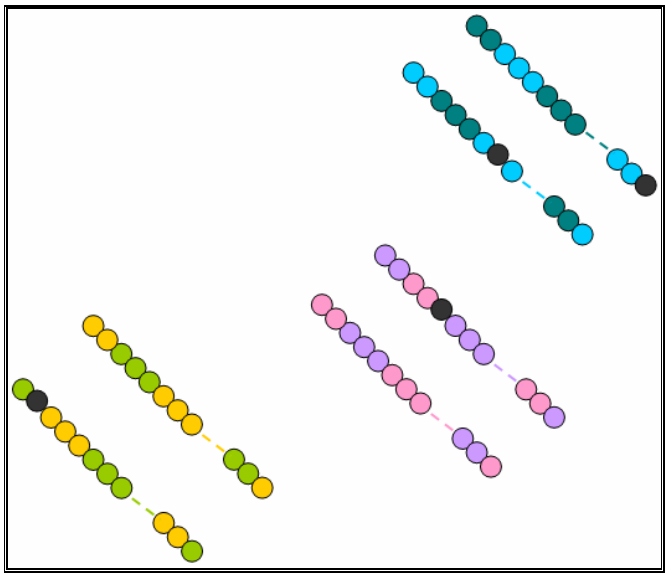


Figure 4.5 – Chromosomes after mutation

Step 3.4 Population Replacement

The offspring are replaced with the original population according to a replacement strategy according to fitness function values of the chromosomes. Resulting population looks like Figure 4.6.

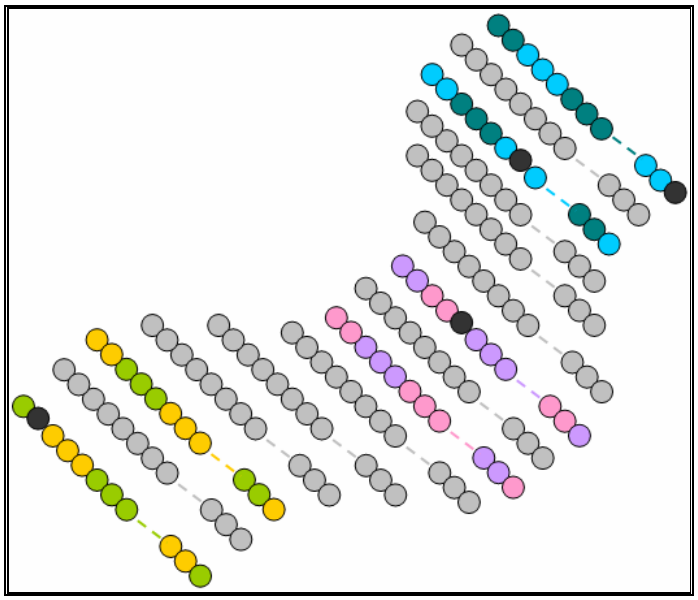


Figure 4.6 – Population after replacement

Step 4. Track of Best Solution

When the evolution procedure is finished, the best solution found so far is displayed.

4.2 ALGORITHM DEVELOPMENT

4.2.1 CONSTRUCTION OF THE ALGORITHM

Each step of generic GA should be tuned in order to obtain a problem-specific solver. As a starting point, representation of solutions carries a critical importance.

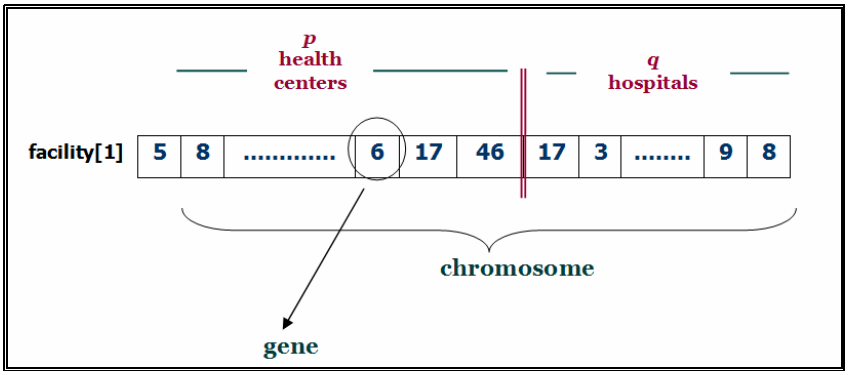


Figure 4.7 – Encoding of solutions

In Figure 4.7, the chromosomes are represented as union of two separate gene sets. The beginning gene set describes the nodes the health centers are opened whereas the ending gene set describes the nodes the hospitals are opened. The sizes of the gene sets are limited with the number of health centers-p and the number of hospitals-q, sequentially. Thus, the size of the chromosome is $p+q$.

Since there is no restriction to open health centers and hospitals in the same node, health center-gene set and hospital-gene set may contain same nodes. However,

opening more than one health centers/hospitals in the same node is prohibited. This is ensured by repairs taking place in relevant steps of the algorithm.

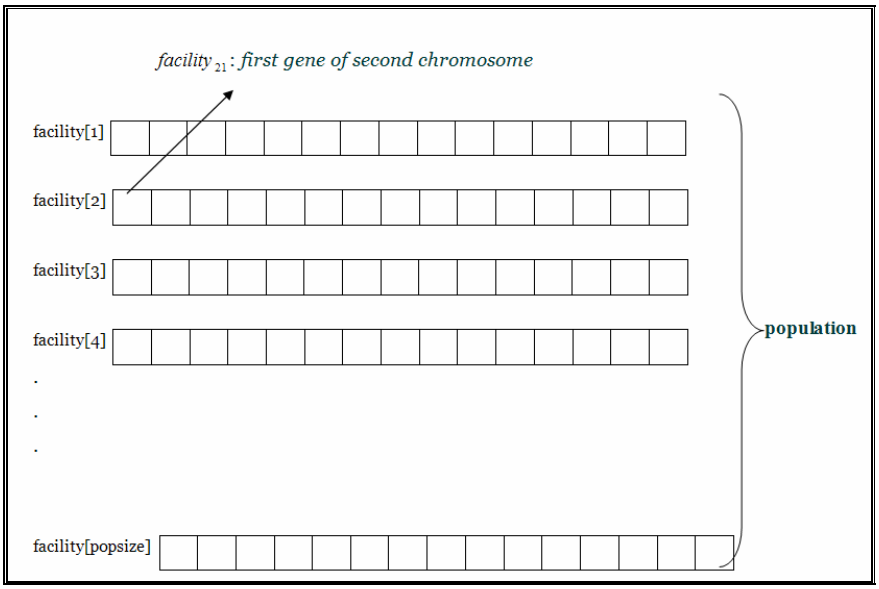


Figure 4.8 – Representation of population

Numerous chromosomes form the population, as in Figure 4.8, which evolves with cross-over, mutation and replacement throughout numerous iterations, as in Figure 4.9. The numbers such as population size, cross-over rate, number of iterations are left parametric during algorithm development. They attained their final values after experiments.

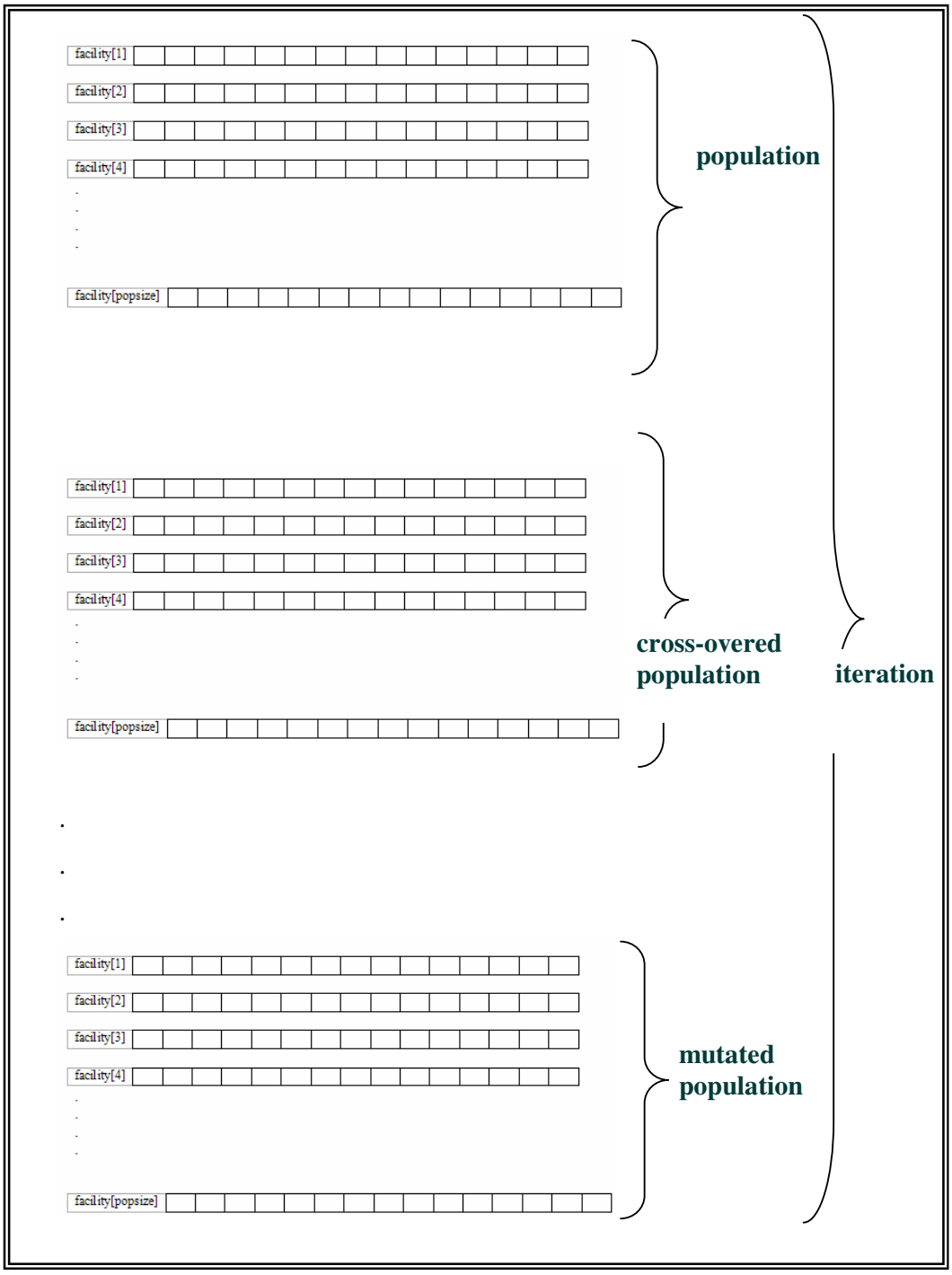


Figure 4.9 – Evolution of population

4.2.2 STEPS OF THE ALGORITHM

The steps of the algorithm are summarized below.

Step 0. Initialization

Coverage matrices are calculated and time is started.

Coverage of demand at node $i \in I$ by health center at node $j \in J$,

$$\text{cov}_{ij}^{1} : \begin{cases} 1 & if \quad dist_{ij} \le S^1 \\ \dfrac{T^1 - dist_{ij}}{T^1 - S^1} & if \quad S^1 \le dist_{ij} \le T^1 \\ 0 & if \quad dist_{ij} \ge T^1 \end{cases}$$

Coverage of demand at node $i \in I$ by hospital at node $j \in J$,

$$\text{cov}_{ij}^{2} : \begin{cases} 1 & if \quad dist_{ij} \le S^2 \\ \dfrac{T^2 - dist_{ij}}{T^2 - S^2} & if \quad S^2 \le dist_{ij} \le T^2 \\ 0 & if \quad dist_{ij} \ge T^2 \end{cases}$$

Coverage of health center at node $i \in J$ by hospital at node $j \in J$,

$$\text{cov}_{ij}^{3} : \begin{cases} 1 & if \quad dist_{ij} \le S^3 \\ \dfrac{T^3 - dist_{ij}}{T^3 - S^3} & if \quad S^3 \le dist_{ij} \le T^3 \\ 0 & if \quad dist_{ij} \ge T^3 \end{cases}$$

Coverage of demand at node $i \in J$ by health center at node $j \in J$,

$$\text{cov}_{ij}^{4}: \begin{cases} 1 & if \quad dist_{ij} \le S^1 \\ \dfrac{T^1 - dist_{ij}}{T^1 - S^1} & if \quad S^1 \le dist_{ij} \le T^1 \\ 0 & if \quad dist_{ij} \ge T^1 \end{cases}$$

Coverage of demand at node $i \in J$ by hospital at node $j \in J$,

$$\text{cov}_{ij}^{5}: \begin{cases} 1 & if \quad dist_{ij} \le S^2 \\ \dfrac{T^2 - dist_{ij}}{T^2 - S^2} & if \quad S^2 \le dist_{ij} \le T^2 \\ 0 & if \quad dist_{ij} \ge T^2 \end{cases}$$

where

I denotes the set of demand points, J denotes the set of potential facility sites; S^1 denotes minimum critical distance of demand-by-health center coverage, S^2 denotes minimum critical distance of demand-by-hospital coverage, S^3 denotes minimum critical distance of health center-by-hospital coverage; and T^1 denotes maximum critical distance of demand-by-health center coverage, T^2 denotes maximum critical distance of demand-by-hospital coverage, T^3 denotes maximum critical distance of health center-by-hospital coverage.

Step 1. Generate initial population

Initial population is formed of two groups – initial population that is generated totally randomly with ratio r_1 and initial population that is generated according to a heuristic or LP relaxation with ratio r_2, that is 1-r_1.

Randomly generated initial population uses a random number generator function to generate genes. Within p genes there is a control to prevent repetition of opened health centers. In case of repetition, the repeated gene is generated once more and control

starts from the beginning. The same control is performed within next q genes. Since there is no restriction in opening a health center and a hospital at the same place, controls are done separately.

Heuristically generated population uses column sum of coverages of all points having demand (demand points and potential facility sites). Column sums are calculated as if points are within critical distances of health centers, considering partial coverage. The calculation is presented in Figure 4.10.

	facility 1	facility 2	..	facility n
facility 1	..	coverage of demand at node 1 by health center at node 2	..	..
facility 2	..	coverage of demand at node 2 by health center at node 2	..	..
..	..	..	..	..
facility n	..	coverage of demand at node n by health center at node 2	..	..
demand 1	..	coverage of demand at node n+1 by health center at node 2	..	..
demand 2	..	coverage of demand at node n+2 by health center at node 2	..	..
...	..	..	..	..
demand m	..	coverage of demand at node n+m by health center at node 2	..	..
		column sum of facility 2		

Figure 4.10 – Calculation of column sums

Column sum uses health center coverages only. There is no need to include hospital coverages also, since health center coverage is the strictest coverage. The column sums represent total closeness of facilities to all nodes.

The facilities are column-sorted, the first p and q genes that give the highest column-sums can be taken to form a chromosome. Since the heuristic is deterministic, only one chromosome can be generated this way. However, a number of chromosomes are required to be generated. A probability factor is added as a control in order to generate required number of chromosomes.

With %70 probability, the facility that has the highest column sum is taken as the next gene. A random number is generated in every iteration, if number is greater than 0.3, the next facility is taken. If it is less than 0.3, the next facility is skipped. The total number of genes allowed to be skipped is controlled by a counter, since it is not preferable to skip more than possible genes then start taking the same facilities from the beginning. After the allowable limit, all facilities are sequentially included in the chromosome. Same procedure is repeated for q genes.

There is another way to generate the non-random proportion; by a heuristic that transfers the LP-relaxed solution to a feasible integral solution set. The optimal LP-relaxed solution that is obtained by GAMS, gives assignment of demand-health center, demand-hospital, health center-hospital values and opened health center values as non-integers between 0 and 1. The heuristic forms sets for opened health centers and hospitals by taking the non-zero valued health centers and hospitals to the sets and neglecting others.

If the number of potential facility sites is 12, the number of allowable hospitals is 4 and the corresponding GAMS output for opened hospitals is as follows for instance;

$z_1 = 0.5$
$z_2 = 0.33$
$z_3 = 0.33$
$z_4 = 0.33$
$z_5 = 0.5$
$z_6 = 0.4$
$z_7 = 0$
$z_8 = 0.4$
$z_9 = 0.4$
$z_{10} = 0.4$
$z_{11} = 0$
$z_{12} = 0.4$

Total opened hospitals = 4

where z_j denotes whether it hosts a hospital or not at site *j*; then, the relaxed hospital set is formed as {1, 2, 3, 4, 5, 6, 8, 9, 10, 12} since the GAMS values for these potential sites are non-zero. GAMS output is interpreted as the non-zero valued facilities make a contribution to the coverage, but the zero-valued facilities do not have any contribution. Therefore, the zero-valued facilities are neglected in generating initial population.

The chromosomes are formed by selecting the genes from the elements of the obtained relaxed health center and hospital sets by a heuristic and this approach, in a way, lessens the feasible region. In fact, our formulation does not include a variable set that denote opened health centers. However, the opened health centers can be found using demand-health center or health center-hospital assignment values. The assignment values are then transformed to opened health center and hospital values and the relaxed health center set is obtained.

A probabilistic parameter controls the selection of the p genes of chromosomes, from elements of the relaxed health center set. The controlling parameter is

$(1 - p / number\ of\ health\ centers\ in\ relaxed\ health\ center\ set)$.

If the size of relaxed health center set is denoted by $|RHC|$, this enables selection of p genes from $|RHC|$ genes; where p is always less than $|RHC|$ by the constraints. The probability is obliged to be greater than $|RHC| - p / |RHC|$; that is

$number\ of\ allowable\ genes\ to\ be\ skipped / total\ number\ of\ genes$

For instance, p is 10 and $|RHC|$ is 50. Then the corresponding controlling parameter is 0.8. If the generated random number is greater than 0.8, the element of relaxed health center set is included in the p genes and otherwise it is skipped.

The controlling parameter is selected so, in order to maintain a balance for every condition of p and $|RHC|$. If the controlling parameter was selected a fixed value at 0.5 for instance when p is 10 and $|RHC|$ is 50, the number of skipped elements would be small, and therefore the p genes of all chromosomes would always be the beginning elements of relaxed health center set. The ending elements would rarely be encountered to be included in the take/skip decisions. By increasing number of skipped elements, whole relaxed health center set is obliged to be spanned and included in chromosomes.

If the number of skipped elements exceeds the number of allowable elements to be skipped, all the next elements are included in the chromosome. This also is controlled in every skip.

The q genes are selected in the same way as the p genes. The controlling parameter is $1 - q/size\ \ of\ \ relaxed\ \ hospital\ \ set$.

Step 2. Calculate fitness functions

For all chromosomes, health centers and hospitals are represented to be opened or unopened. In chromosome l, variable x_{lj}^1 is fixed at 1 if node j takes place in first p genes, and 0 if not. Variable x_{lj}^2 is fixed at 1 if node j takes place in next q genes, and 0 otherwise. Variable x^1 defines opened/unopened situation of a health center, and x^2 defines opened/unopened situation of a hospital.

Demand $i \in I$ is tried to be assigned to health center-hospital pairs first, in sequence. If health center $j \in J$ covers demand $i \in I$ –if demand at $i \in I$ is within T^1 distance of health center at $j \in J$ – and hospital $k \in J$ covers health center $j \in J$ –if health center at node $j \in J$ is within T^3 distance of hospital at node $k \in J$ –, demand is tried to be assigned to health center $j \in J$ and then referred to hospital $k \in J$. The fitness value is calculated as

$$demand_i^1 * \mathrm{cov}_{ij}^1 * x_{lj}^1 + demand_i^1 * \mathrm{cov}_{ij}^1 * x_{lj}^1 * \mathrm{cov}_{jk}^3 * x_{lk}^2$$

where I denotes the set of demand points, J denotes the set of potential facility sites; demand of node $i \in I$ is represented as $demand_i^1$, coverage of demand $i \in I$ by health center $j \in J$ is represented as cov_{ij}^1, openness of health center $j \in J$ in chromosome l is represented as x_{lj}^1, coverage of health center $j \in J$ by hospital $k \in J$ is represented as cov_{jk}^3 and openness of hospital $k \in J$ in population l is represented as x_{lk}^2.

If health center $j \in J$ can not cover demand $i \in I$ or hospital $k \in J$ can not cover health center $j \in J$, demand $i \in I$ is not tried to be assigned to $j \in J$.

After trying all feasible combinations of health center-hospital pairs, demand is tried to be directly assigned to hospitals sequentially, only if hospital $k \in J$ can cover demand $i \in I$ – demand at node $i \in I$ is within T^2 distance of hospital $k \in J$ –. The fitness function is calculated as

$$demand_i^1 * \mathrm{cov}_{ij}^2 * x_{lj}^2$$

where I denotes the set of demand points, J denotes the set of potential facility sites; demand of node $i \in I$ is represented as $demand_i^1$, coverage of demand $i \in I$ by hospital $j \in J$ is represented as cov_{ij}^2, openness of hospital $j \in J$ in chromosome l is represented as x_{lj}^2.

From all the trials, the one with maximum fitness function is selected for demand $i \in I$.

Since the potential facility sites also possess demand, this calculation is repeated for potential facility sites. Potential facility site $i \in J$ is tried to be assigned to hospitals via health centers first, with fitness value calculation of

$$demand_i^2 * \mathrm{cov}_{ij}^4 * x_{lj}^1 + demand_i^2 * \mathrm{cov}_{ij}^4 * x_{lj}^1 * \mathrm{cov}_{jk}^3 * x_{lk}^2$$

where I denotes the set of demand points, J denotes the set of potential facility sites; demand of node $i \in J$ is represented as $demand_i^2$, coverage of demand $i \in J$ by health center $j \in J$ is represented as cov_{ij}^4, openness of health center $j \in J$ in chromosome l is represented as x_{lj}^1, coverage of health center $j \in J$ by hospital $k \in J$ is represented as cov_{jk}^3 and openness of hospital $k \in J$ in population l is represented as x_{lk}^2.

Then direct hospital assignments are considered with fitness value calculation of

$$demand_i^2 * \mathrm{cov}_{ij}^5 * x_{lj}^2$$

where I denotes the set of demand points, J denotes the set of potential facility sites; demand of node $i \in J$ is represented as $demand_i^2$, coverage of demand $i \in J$ by hospital $j \in J$ is represented as cov_{ij}^5, openness of hospital $j \in J$ in chromosome l is represented as x_{lj}^2.

From all the trials, the one with maximum fitness function is selected for demand at $i \in J$. This is repeated for all nodes. Sum of the fitness functions make up fitness function of chromosome *l*. This is repeated for all chromosomes.

Step 3.1. Parent Selection

First the probabilities of selection for the mating pool are calculated. Then parents are selected according to the probabilities. Fitness ranking is a choice in order to prevent domination of some particular chromosomes in the population. If fitness ranking is applied probabilities are updated.

The probability of selecting chromosome *k* into the mating pool is calculated by the following expression

$$prob_k = \frac{fitness_k - fitness_{\min}}{fitness_{\max} - fitness_{\min}}$$

where probability of selecting k^{th} chromosome into the mating pool is denoted by $prob_k$, fitness value of chromosome *k* is denoted by $fitness_k$, minimum fitness value is denoted by $fitness_{\min}$ and maximum fitness value is denoted by $fitness_{\max}$.

If fitness ranking is applied, fitness function values of chromosomes are ranked. The rank of the chromosome with the lowest fitness function value is assigned to 1. And as fitness value is increased, rank is increased. Chromosomes with same fitness value have same rank.

The probability of selecting chromosome *k* into the mating pool is updated as follows

$$prob_k = \frac{rankedfitness_k - rankedfitness_{\min}}{rankedfitness_{\max} - rankedfitness_{\min}}$$

where probability of selecting k^{th} chromosome into the mating pool is denoted by $prob_k$, rank of chromosome *k* is denoted by $rankedfitness_k$, minimum rank is denoted by $rankedfitness_{\min}$ and maximum rank is denoted by $rankedfitness_{\max}$.

Parents are selected according to the calculated $prob_k$ values, a chromosome with a higher probability has more chance to be selected as a parent. For chromosome *k*, a random probability is generated. If $prob_k$ is greater than random variable, chromosome *k* is included in the mating pool. Else, chromosome *k* is skipped. This is repeated until mating pool is filled. In case of skipping chromosomes such that chromosomes are finished but mating pool is unfilled, the procedure continues with turning back to the beginning chromosome. This allows including a chromosome more than once in the mating pool. The mating pool is kept.

Step 3.2. Cross-over

The consecutive chromosomes in the mating pool can be cross-overed according to 4 strategies; 1-point cross-over, 2-point cross-over, uniform mask cross-over and hybrid cross-over.

1-point cross-over is performed by changing middle genes of consecutive chromosomes. Cutting points are selected as $p/2$ and $p + q/2$ in first p genes and next q genes, as presented şn Figure 4.11.

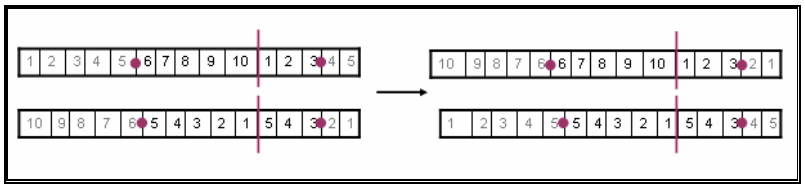


Figure 4.11 – 1-point cross-over

2-point cross-over is performed by changing middle genes in health center-hospital section of consecutive chromosomes. Cutting points are selected as $p/3$, $2p/3$, $p + q/3$ and $p + 2q/3$. 2-point cross-over is presented n Figure 4.12.

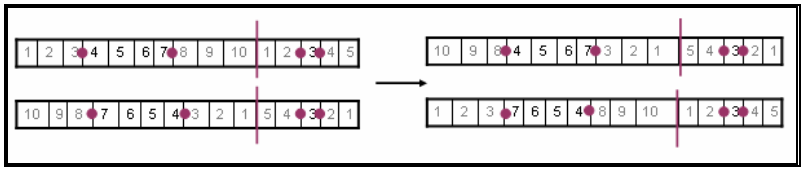


Figure 4.12 – 2-point cross-over

Uniform mask cross-over is performed according to a binary scheme, where 0's represent change-over in genes and 1's represent staying at place. A uniform mask is generated for each pair of chromosomes. Uniform mask, parent chromosomes and offspring are presented in Figure 4.13.

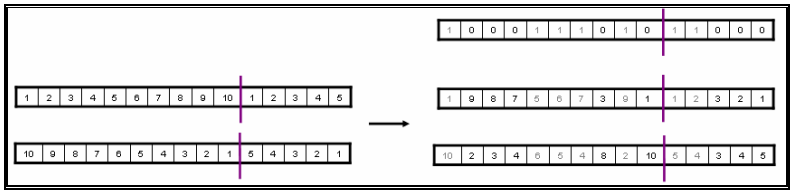


Figure 4.13 – Uniform mask cross-over

Hybrid cross-over is the random sequence of 1-point, 2-point and uniform mask cross-over operations. One of 0, 1 or 2 is generated randomly in each iteration to select cross-over strategy of the current iteration.

After cross-over, repair can be performed within p genes and q genes separately. If there is a recurrence amongst p genes, a random facility is generated. This is repeated until all p genes are different. Same procedure is performed also within q genes.

Step 3.3. Mutation

For each gene, a random probability is generated. If mutation rate is greater than the generated random probability, then mutation is

performed on the gene. If not, the gene is kept as it is. Mutation is performed by generating a random facility.

After mutation, repair can be performed within p genes and q genes separately. If there is a recurrence amongst p genes, a random facility is generated. This is repeated until all p genes are different. Same procedure is performed also within q genes.

Step 3.4. Population replacement

There are 4 alternatives for population replacement; unconditional replacement, unconditional replacement with transfer of best solution, selection of best solutions amongst original and offspring populations and conditional replacement.

Unconditional replacement is applied as below, Figure 4.14 represents it:

Replacement takes place before all operations. Chromosomes in the mating pool take place of original chromosomes. If the size of mating pool is less than the population size, last chromosomes are remained as they are.

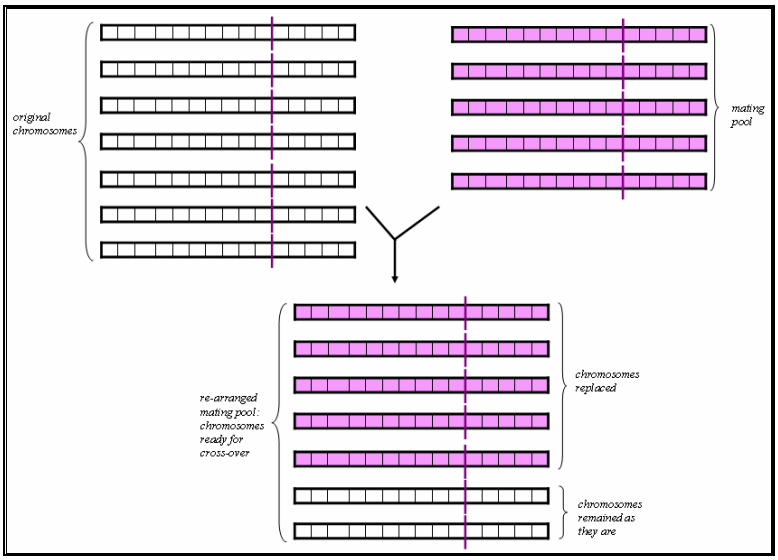


Figure 4.14 – Unconditional replacement

Unconditional replacement with transfer of best chromosome is applied as below, Figure 4.15 represents it:

Replacement explained in Step 7a is performed. The difference of transfer is adding the best chromosome of the last iteration to the parent chromosomes of the current iteration. Best chromosome is the chromosome with highest fitness function value, that is caught anywhere of the iteration; it might be an original chromosome, a chromosome with only cross-over or a chromosome with both cross-over and mutation.

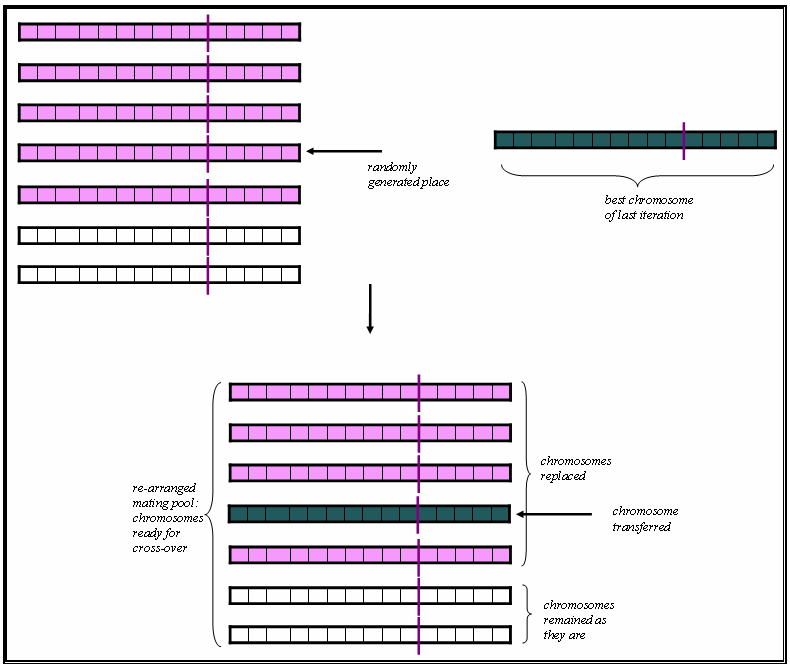


Figure 4.15 – Unconditional replacement with transfer

Best chromosome of the last iteration is inserted in a randomly generated place of the population formed by unconditional replacement explained above.

Selecting best of chromosomes in replacement

Offspring chromosomes are added to the original chromosomes as in Figure 4.16.

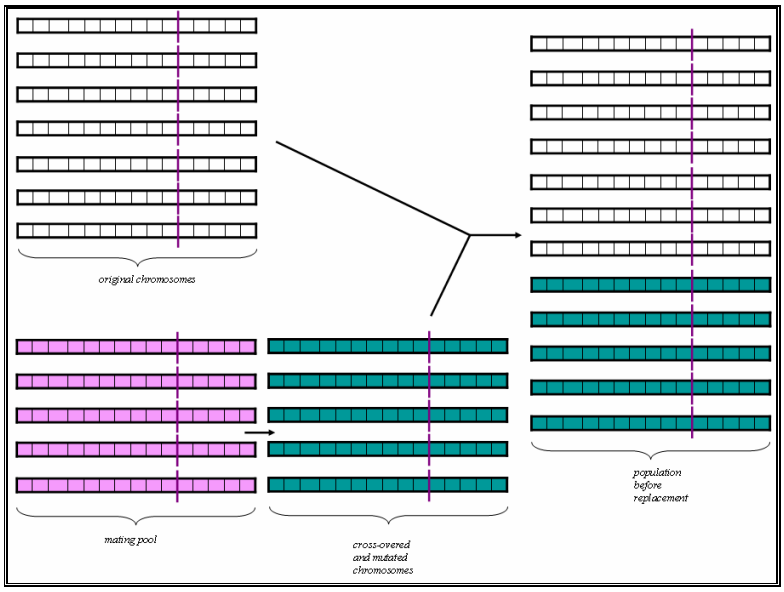


Figure 4.16 – Addition of offspring chromosomes to parent chromosomes

The formed enlarged population is sorted according to fitness function values, as in Figure 4.17. The best population size of the chromosomes are then selected and carried to the next iteration as the original population, as in Figure 4.18.

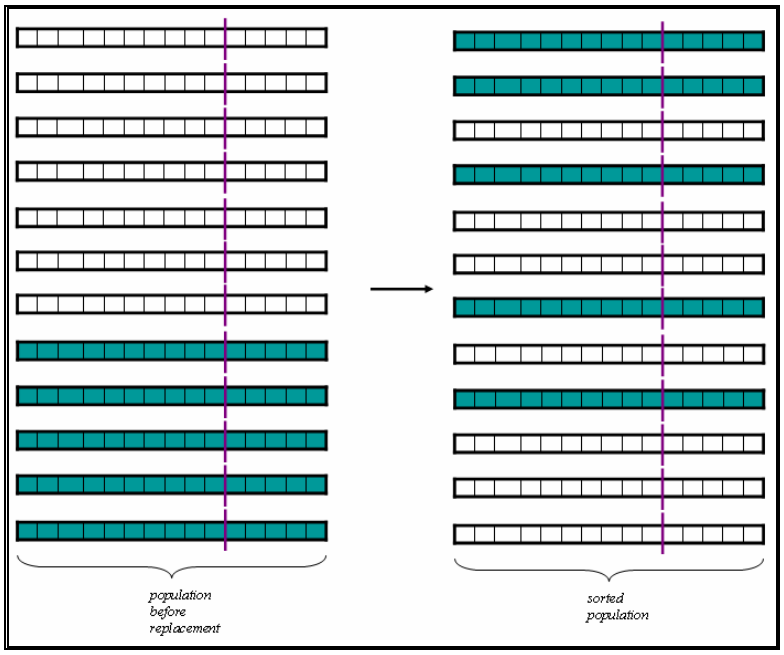


Figure 4.17 – Sorting of enlarged population

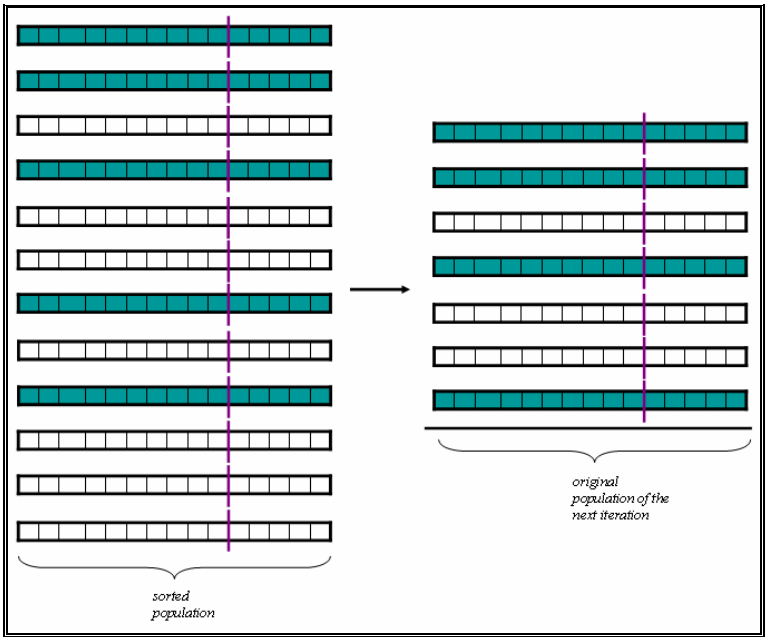


Figure 4.18 – Selection of best of chromosomes amongst sorted enlarged population

Replace cross-overed chromosomes with their parents if they are fitter.

For each chromosome of the mating pool kept in Step 3.1, fitness function values are calculated. Replacement of evolved population with mating pool takes place. If fitness function of evolved chromosome l is higher than its parent which is chromosome l in the mating pool, evolved chromosome l is replaced with chromosome l of mating pool. Otherwise, chromosome l of mating pool endures to next generation.

After replacement, procedure starting with Step 3.1 is repeated for number of iterations.

Step 4. Stop and display statistics.

Maximum fitness value, minimum fitness value, average fitness value and the best gene of the ending population are kept. The best fitness value of the population and solution time are also kept.

4.3 STRATEGY SELECTION

GA, like other meta-heuristic algorithms, is a generic algorithm which has to be pruned according to the specific characteristics of the problem. The methods and rates for generation of new solutions have to be analyzed thoroughly to obtain a good specific-to-problem algorithm.

The possible choices to prune are summarized in Table 4.1.

Table 4.1 – Possible choices for pruning the algorithm

Parameters	**Choices**			
Generation of Population				
Population Size	50	100	200	
Initial Population Generation Ratios (Random - Non-Random)	0.8 - 0.2	0.2 - 0.8		
Non-Random Initial Population Generation Technique	heuristic	LP-relaxation		
Parent Selection				
Mating Pool Selection	with mating pool selection	without mating pool selection		
Fitness Ranking	with ranking	without ranking		
Evolution				
Cross-Over Operator	1-point cross-over	2-point cross-over	uniform mask cross-over	random hybrid of cross-over types
Cross-Over Rate	0.8	1.0		
Mutation Rate	0.01	0.05	0.1	
Repair	with repair	without repair		
Number of Iterations	500	2000		
Replacement				
Replacement Method	unconditional replacement	unconditional replacement with transfer of best solution of the current generation to next generation	select best of sorted parent and offspring chromosomes	replace offspring with their parents if they are fitter
Replacement Sequence	before mutation	after mutation		

5 problems, whose caharacteristics are detailed in Table 4.2, are determined randomly to compare the choices of the parameters. Preliminary experiments and analyses are conducted to select the problem specific set of parameter values of Table 4.1. These experiments and analyses are explained through steps i-vii.

Table 4.2 – Problems selected for preliminary analysis of strategy selection for genetic algorithm

	$\|I\|$	$\|J\|$	q	p	S^1	S^2	S^3	T^1	T^2	T^3	w^1	w^2	w^3	δ
1	20	20	2	4	50	100	120	75	150	180	1	1	1	1
2	20	20	4	6	50	90	90	80	120	120	1	1	1	1
3	30	30	4	6	50	90	90	80	120	120	1	1	1	1
4	30	30	5	7	50	90	90	80	120	120	1	1	1	1
5	30	30	6	8	30	60	80	50	80	100	1	1	1	1

i) The first requirement that should be verified is thought to be the evolution pattern of the GA. Evolution pattern suggests a course of action on how well algorithm performs. Best solution of the algorithm should draw an increasing pattern. The maximum fitness value should also draw an increasing pattern while allowing deteriorations. Since deteriorations help escaping from sub-optimals. The average fitness of the population should converge to best fitness found so far to end iterations.

The important parameters that affect the evolution pattern are the method and sequence of replacement, the rate of mutation and the decision of selection of mating pool. The patterns corresponding to different combinations of these parameters are analyzed in Table 4.3.

5 problems indicated in Table 4.2 are solved with the different combinations of parameters for each trial. The graphs drawn for the problems of the same trial have different scales but similar patterns. Thus, the graphs inserted below are representative of the patterns of the statistical variables for the trials.

Table 4.3 – Analyses of GA patterns with respect to method and sequence of replacement, selection of mating pool and rate of mutation

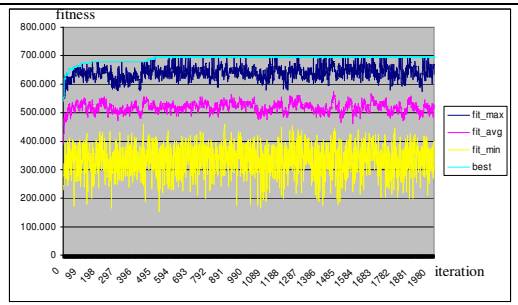
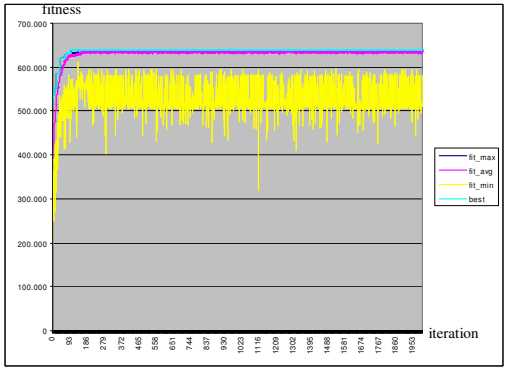
Trial	Method of Replacement	Sequence of Replacement	Selection of Mating Pool	Rate of Mutation	Corresponding Pattern*
I	Unconditional Replacement	sequence does not affect	selected	0.01	
II				0.05	
III				0.1	
IV			not selected	0.01	
V				0.05	
VI				0.1	
VII	Unconditional Replacement with Transfer	sequence does not affect	selected	0.01	
VIII				0.05	
IX				0.1	
X			not selected	0.01	
XI				0.05	
XII				0.1	
XIII	Select Best Solutions	sequence does not affect	selected	0.01	
XIV				0.05	
XV				0.1	
XVI			not selected	0.01	
XVII				0.05	
XVIII				0.1	

Table 4.3 (continued) – Analyses of GA patterns with respect to method and sequence of replacement, selection of mating pool and rate of mutation

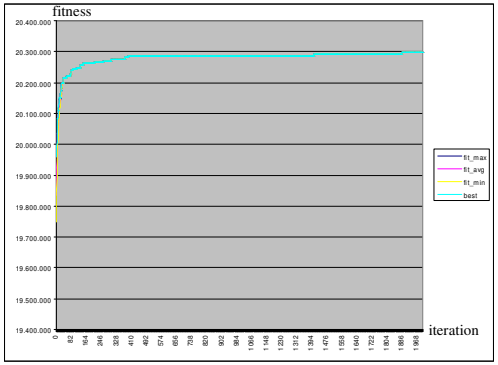
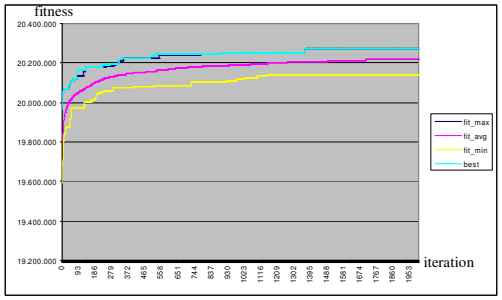
Trial	Method of Replacement	Sequence of Replacement	Selection of Mating Pool	Rate of Mutation	Corresponding Pattern*
XIX	Replace if Offspring Are Fitter	after mutation	selected	0.01	
XX				0.05	
XXI				0.1	
XXII			not selected	0.01	
XXIII				0.05	
XXIV				0.1	

Table 4.3 (continued) – Analyses of GA patterns with respect to method and sequence of replacement, selection of mating pool and rate of mutation

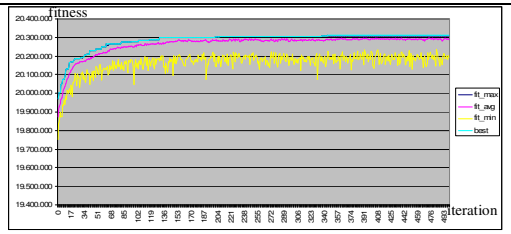
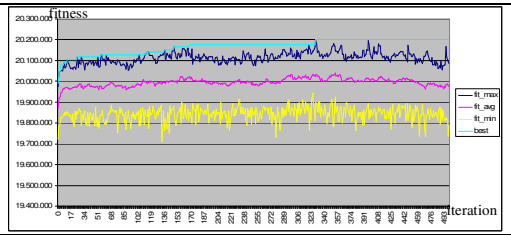
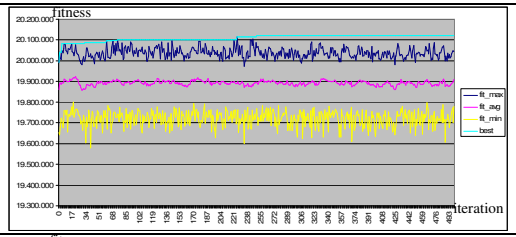
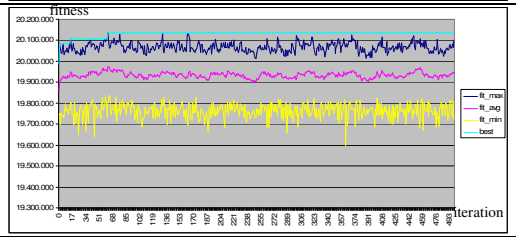
Trial	Method of Replacement	Sequence of Replacement	Selection of Mating Pool	Rate of Mutation	Corresponding Pattern*
XXV	Replace if Offspring Are Fitter	before mutation	selected	0.01	
XXVI				0.05	

Table 4.3 (continued) – Analyses of GA patterns with respect to method and sequence of replacement, selection of mating pool and rate of mutation

Trial	Method of Replacement	Sequence of Replacement	Selection of Mating Pool	Rate of Mutation	Corresponding Pattern*
XXVII	Replace if Offspring Are Fitter	before mutation	selected	0.1	
XXVIII			not selected	0.01	
XXIX				0.05	
XXX				0.1	

** Amongst the graphs that are drawn fitness versus iteration, the curves drawn with light blue indicate the best solution found so far, curves drawn with dark blue indicate the best fitness of the iterations, curves drawn with pink indicate the average fitness value of the iterations and the yellow curves indicate the minimum fitness of the iterations. Graphs are representative of 5 problems solved for each trial.*

Other parameters are kept constant as shown in Table 4.4 during the trials.

Table 4.4 – Parameters kept constant during pattern selection runs

Parameters	Choices
Generation of Population	
Population Size	100
Initial Population Generation Ratios (Random - Non-Random)	0.8 - 0.2
Non-Random Initial Population Generation Technique	heuristic
Parent Selection	
Fitness Ranking	with ranking
Evolution	
Cross-Over Operator	1-point cross-over
Cross-Over Rate	0.8
Repair	with repair
Number of Iterations	500

Amongst the trials I-XVIII, the method of replacement is the determining factor. When the replacement method is unconditional replacement with and without transfer of best gene to next iteration, population average has an unstable evolution. It indicates no net progress after some initial iterations since there exists no convergence. The problem of non-developing population average is solved when the replacement method is the selection of best solutions. However, the desired graph is still not obtained. Population average progresses but the progress is in company with progress of maximum fitness of the current iteration and best fitness found so far. Population average takes values a small amount less than the maximum fitness

values. This shows that most of the chromosomes resemble each other in a short time. This brings premature convergence, which is defined in literature as too early convergence of the population that they could not evolve.

For the trials XIX-XXIV, replacing offspring with their parents conditionally at the end is in question. If the mating pool is selected, the evolution of population matches with the logic of GA, but the entire statistical variables draw completely the same pattern a small time after start; that is the diversity of the population vanishes. If the mating pool is not selected, diversity is maintained, however population average does not converge to best fitness. The lack of natural selection takes these trials to non-convergence.

For the trials XXV-XXX that test replacing offspring conditionally between cross-over and mutation, when mating pool is not selected; the improvement in population average resembles the unconditional replacement trials. The improvement is unstable. When mating pool is selected, the mutation rate begins to be the determining factor. For the rates 0.05 and 0.1 which would be categorized as large rates according to literature, the population average indicates no net improvement with unstable pattern.

Amongst all the trials, trial XXV satisfies all requirements; the population average progresses and converges to best solution found so far. On the other hand, the population maintains its diversity since minimum fitness does not converge to best fitness and also alters frequently.

The results indicate that ‘without mating pool selection’ choice of mating pool selection parameter and ‘unconditional replacement,

'unconditional replacement with transfer' and 'select best population' choices of replacement scheme are eliminated.

ii) The second important factor that affects accuracy and rapidity of progress, or in other words the gradient of the evolution curve is the cross-over. Cross-over rate and method should be determined next.

With the replacement methods other than replace conditionally, the cross-over rate would be considerably effective. However when the replacement method is replace conditionally, in fact, the cross-over rate becomes variable. If none of the offspring has better fitness values than their parents, none will take place of their parents; thus it is identical to having a cross-over rate of 0.0. If all individuals are cross-overed and all offspring take place of their parents, then cross-over rate is identical to 1.0. For the non-extreme cases, it always varies. Therefore, keeping cross-over rate at 1.0 would provide maximum opportunity.

Also, there is no loss by making more than required number of cross-overs; since if the resulting offspring is not fit, it would not take place of its parent. Therefore, cross-over rate is selected as 1.0.

Cross-over method is selected by experiments; that is the net effect of change of cross-over operator is analyzed, other parameters being constant as in Table 4.5. Each operator is tried on 5 problems of Table 4.2. Operators are compared in table 4.6.

Table 4.5 – Parameters kept constant to compare cross-over operators

Parameters	Choices
Generation of Population	
Population Size	100
Initial Population Generation Ratios (Random - Non-Random)	0.8 - 0.2
Non-Random Initial Population Generation Technique	heuristic
Parent Selection	
Mating Pool Selection	with mating pool selection
Fitness Ranking	with ranking
Evolution	
Cross-Over Rate	1.0
Mutation Rate	0.01
Repair	with repair
Number of Iterations	500
Replacement	
Replacement Method	replace offspring with their parents if they are fitter
Replacement Sequence	before mutation

Table 4.6 – Comparison of cross-over operators

Cross-Over Operator	Statistics			
	Average of Deviations from Optimal	Maximum of Deviations from Optimal	Variance of Deviations From Optimal	Average Time (seconds)
1-point cross-over	2.07%	3.92%	1.14%	7.2
2-point cross-over	0.34%	1.54%	0.67%	7.3
uniform mask cross-over	2.09%	4.58%	1.47%	6.9
hybrid cross-over	3.72%	5.20%	1.60%	7.4

2-point cross-over operator is more successful than other cross-over operators. Thus, 1-point, uniform-mask and hybrid operators can be eliminated.

iii) The next important determinant is the quality of starting generation. The methods and ratios for generation of initial population are tested.

The quality and the diversity of the starting solution affect the resulting solutions. For diversity, two trials are made. Problems of Table 4.2 are solved with both combinations. The statistics of the deviations of starting and ending solutions from optimal are demonstrated in Table 4.8 while parameters kept constant are demonstrated in Table 4.7.

Table 4.7 – Parameters kept constant to analyze effect of initial population generation ratios

Parameters	Choices
Generation of Population	
Population Size	100
Initial Population Generation Ratios (Random - Non-Random)	0.8 - 0.2
Non-Random Initial Population Generation Technique	heuristic
Parent Selection	
Mating Pool Selection	with mating pool selection
Fitness Ranking	with ranking
Evolution	
Cross-Over Operator	2-point cross-over
Cross-Over Rate	1.0
Mutation Rate	0.01
Repair	with repair
Number of Iterations	500
Replacement	
Replacement Method	replace offspring with their parents if they are fitter
Replacement Sequence	before mutation

Table 4.8 – Comparison of initial population generation ratios

Initial Population Generation Ratios	Statistics	
	Deviation of Starting Solution From Optimal	Deviation of Ending Solution From Optimal
Random: 0.2 – Non-Random: 0.8	35.58%	0.24%
Random: 0.8 – Non-Random: 0.2	48.95%	5.43%

Results indicate that when the heuristically generated portion of initial population is increased, the quality of starting population is increased. Unless the randomly generated portion is decreased to 0.0, starting with more qualified starting solutions result with lower deviations from optimal.

If randomly generated proportion of the starting population vanishes, the logic of GA that necessitates randomness to explore the search space is violated. Thus, a random proportion is always required; however starting with more qualified solutions is preferable. The ratios are selected as 0.2-0.8 for random and non-random generation, sequentially.

For comparing the method of generation of non-random starting solutions, experiments are conducted on 5 problems of Table 4.2 for both trials. Table 4.10 and 4.11 compare the results while Table 4.9 demonstrate the constatnt parameters during experiments .

Table 4.9 - Parameters kept constant to analyze method of generation of non-random portion of initial solution

Parameters	Choices
Generation of Population	
Population Size	100
Initial Population Generation Ratios (Random - Non-Random)	0.2 - 0.8
Parent Selection	
Mating Pool Selection	with mating pool selection
Fitness Ranking	with ranking
Evolution	
Cross-Over Operator	2-point cross-over
Cross-Over Rate	1.0
Mutation Rate	0.01
Repair	with repair
Number of Iterations	500
Replacement	
Replacement Method	replace offspring with their parents if they are fitter
Replacement Sequence	before mutation

Table 4.10 – Comparison of non-random starting solution generation ratios according to deviations of starting and ending solutions from optimal

Method of Generation for Non-Random Portion of Starting Solution	Statistics	
	Deviation of Starting Solution From Optimal	Deviation of Ending Solution From Optimal
LP-Relaxation	26.16%	0.22%
Heuristic	35.58%	0.24%

Table 4.11 – Comparison of methods of non-random initial population generation according to statistical values

Method of Generation for Non-Random Portion of Starting Solution	Statistics			
	Average of Deviations From Optimal	Maximum of Deviations From Optimal	Variance of Deviations From Optimal	Average Time to Generate Initial Solution Set (seconds)
LP-Relaxation	0.22%	3.42%	1.42%	3
Heuristic	0.24%	3.27%	1.86%	1

Both heuristics obtain similar and near-optimal results even though LP-relaxation starts with about 10% better solutions. However, LP-relaxation heuristic takes a larger time since the relaxed model is sent to GAMS and the obtained optimal solution is taken back. Since, there does not exist considerable difference in the quality, generation of initial solution set with LP-relaxation heuristic is eliminated.

iv) It can be thought that repair is unnecessary, that GA would naturally eliminate the chromosomes that include recurring genes in selection phase; however when experiments are conducted, it is seen in Table 4.13 that repair makes a considerable effect. Table 4.12 presents the parameters kept constant during experiments.

Table 4.12 – Parameters kept constant during analyses on effect of repair

Parameters	Choices
Generation of Population	
Population Size	100
Initial Population Generation Ratios (Random - Non-Random)	0.2 - 0.8
Non-Random Initial Population Generation Technique	heuristic
Parent Selection	
Mating Pool Selection	with mating pool selection
Fitness Ranking	with ranking
Evolution	
Cross-Over Operator	2-point cross-over
Cross-Over Rate	1.0
Mutation Rate	0.01
Number of Iterations	500
Replacement	
Replacement Method	replace offspring with their parents if they are fitter
Replacement Sequence	before mutation

Table 4.13 – Analyses on effects of repair

	Statistics			
Repair of Chromosomes	Average of Deviations From Optimal	Maximum of Deviations From Optimal	Variance of Deviations From Optimal	Average Time (seconds)
with repair	0.24%	0.84%	0.36%	7.3
without repair	6.42%	8.74%	1.72%	5.6

5 problems presented in Table 4.2 are solved with and without repair. The statistical values demonstrate the average deviation, the

maximum deviation, the deviation variance and the average time for the 5 problems. The additional time required after generation of initial population, cross-over and mutation steps is inconsiderable when the improvement repair performs is regarded. Thus, 'without repair' option is eliminated.

v) For fine tuning, the option of fitness ranking is evaluated. When parents are not ranked, the differences in fitness values create noteworthy differences in probabilities of selection for mating pool. The effect of rank is analyzed through experiments on 5 problems presented in Table 4.2. Table 4.15 summarizes the results where Table 4.14 demonstrates the paramtere kept constant during experiments.

Table 4.14 – Parameters kept constant during analyses on effect of fitness ranking

Parameters	**Choices**
Generation of Population	
Population Size	100
Initial Population Generation Ratios (Random - Non-Random)	0.2 - 0.8
Non-Random Initial Population Generation Technique	heuristic
Parent Selection	
Mating Pool Selection	with mating pool selection
Evolution	
Cross-Over Operator	2-point cross-over
Cross-Over Rate	1.0
Mutation Rate	0.01
Repair	with repair
Number of Iterations	500
Replacement	
Replacement Method	replace offspring with their parents if they are fitter
Replacement Sequence	before mutation

Table 4.15 – Analyses on effects of fitness ranking

Fitness Ranking	Statistics			
	Average of Deviations From Optimal	Maximum of Deviations From Optimal	Variance of Deviations From Optimal	Average Time (seconds)
with ranking	0.24%	1.87%	0.89%	7.2
without ranking	5.79%	8.65%	2.79%	7.0

The effect of ranking worth the supplementary time required. The patterns in Figure 4.19 indicate that not ranking lessens the population diversity and brings premature convergence.

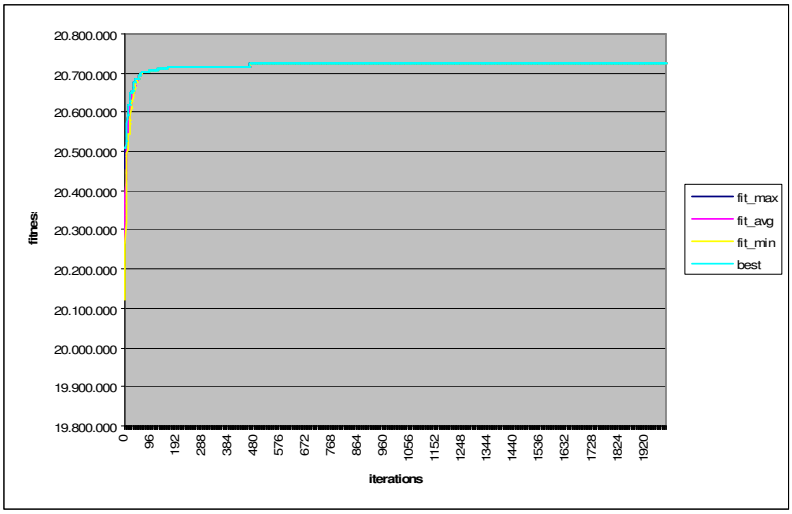


Figure 4.19 – GA pattern when fitness ranking is skipped

Thus, ranking is preferred and not ranking option is eliminated.

vi) Population size is another parameter that has an effect on population diversity. If population size is selected small, resemblance would appear in most of the steps. In generation of initial population, small population size would result with few randomly generated chromosomes. This would reduce the power of randomness of GA. In subsequent steps, since random chromosomes remain insufficient to influence others, population would loose its diversity. On the other hand, a two-fold large population size would take two-fold much time computationally.

The trials for population sizes are evaluated in accordance with their computational time requirements. Problems of Table 4.2 are solved with each population size, results of which are tabulated in Table 4.17. Table 4.16 shows parameters kept constant.

Table 4.16 – Parameters kept constant while analyzing the effect of population sizes

Parameters	Choices
Generation of Population	
Initial Population Generation Ratios (Random - Non-Random)	0.2 - 0.8
Non-Random Initial Population Generation Technique	heuristic
Parent Selection	
Mating Pool Selection	with mating pool selection
Fitness Ranking	with ranking
Evolution	
Cross-Over Operator	2-point cross-over
Cross-Over Rate	1.0
Mutation Rate	0.01
Repair	with repair
Number of Iterations	2000
Replacement	
Replacement Method	replace offspring with their parents if they are fitter
Replacement Sequence	before mutation

Table 4.17 – Comparison of population sizes

	Statistics			
Population Size	Average of Deviations From Optimal	Maximum of Deviations From Optimal	Variance of Deviations From Optimal	Average Time (seconds)
50	3.00%	4.65%	1.32%	3.5
100	0.30%	0.88%	0.35%	7.2
200	0.25%	0.88%	0.39%	14.1

Population size of 100 is considerably better than population size of 50, whereas the difference between the averages of deviations from optimal can be neglected when the population sizes of 100 and 200 are compared. On the other hand, solution times of population sizes of 100 and 200 are incomparable. Time difference can not be compensated with the small improvement in average deviations and no improvement in maximum deviations. Therefore, population size of 100 is selected.

vii) The last parameter that has to be taken into account with time considerations is the iteration number. Initial runs have been made using iteration number of 2000, however the graphs indicate that very minor improvements take place after the iteration limit of 500. Figure 4.20 is presented below as a representative of all problems.

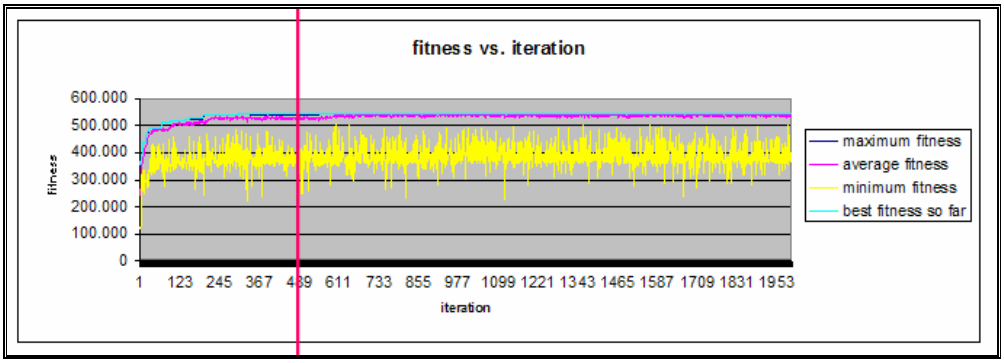


Figure 4.20 – Fitness vs. iteration graph to compare solution quality in 500 and 2000 iterations

The resulting problem-specific GA is then constituted from the parameter choices summarized in Table 4.18.

Table 4.18 – Resulting GA strategy

Parameter	Choice	Selected in Step
Generation of Population		
Population Size	100	vi
Initial Population Generation Ratios (Random - Non-Random)	0.2 - 0.8	iii
Non-Random Initial Population Generation Technique	heuristic	iii
Parent Selection		
Mating Pool Selection	with mating pool selection	i
Fitness Ranking	with ranking	v
Evolution		
Cross-Over Operator	2-point cross-over	ii
Cross-Over Rate	1.0	ii
Mutation Rate	0.01	i
Repair	with repair	iv
Number of Iterations	500	vii
Replacement		
Replacement Method	replace offspring with their parents if they are fitter	i
Replacement Sequence	before mutation	i

4.4 ALGORITHM ON AN EXAMPLE PROBLEM

The steps of the pruned algorithm are illustrated on the example problem of Section 3.6. Note that the sequence of steps 3.3 and 3.4 are exchanged and replacement is performed before mutation in order to allow deterioration in the population and prevent being stuck in sub-optimal solutions.

Parameters of the problem are re-represented in Table 4.19.

Table 4.19 – Example problem parameters for illustration of pruned GA

# of nodes	# of demand nodes	# of potential facility sites	# of hospitals	# of health centers	S^1	S^2	S^3	T^1	T^2	T^3	w^1	w^2	w^3	δ
50	-	50	6	14	30	60	80	50	80	100	1	1	1	1

Some chromosomes of the population are represented in Figures 4.21-4.32 to illustrate the procedure in each step, for whole chromosomes Appendix D can be seen.

Step 0. Initialize. Calculate coverage matrices and start clock.

Step 1. Generate initial population.

Step 1.1. Generate initial 20 chromosomes randomly. Repair chromosomes.

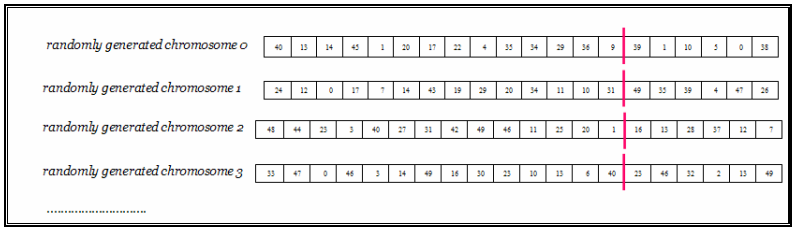


Figure 4.21 – Repaired randomly generated initial chromomes

Step 1.2. Generate initial 80 chromosomes using heuristic. Repair chromosomes.

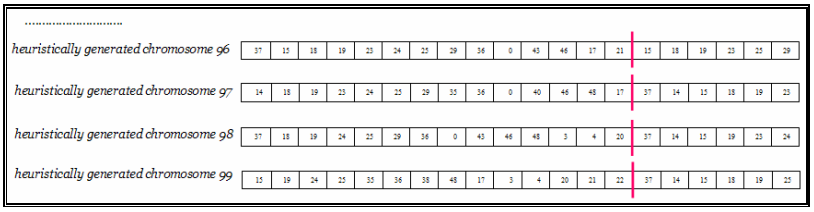


Figure 4.22 – Repaired heuristically generated initial chromosomes

Step 2. Calculate fitness function values. Keep statistics.

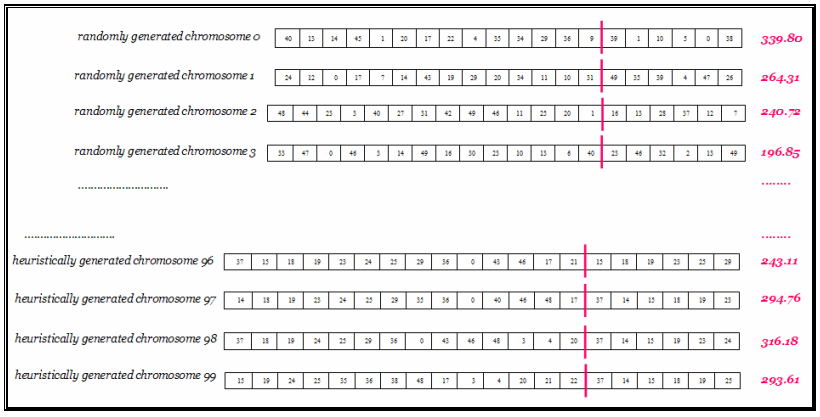


Figure 4.23 – Fitness functions of initial population

Step 3. For 500 iterations, repeat.

Step 3.1. Select parents.

Step 3.1.1. Calculate probabilities to be selected for mating pool in the presence of fitness ranking.

Step 3.1.2. Select parents.

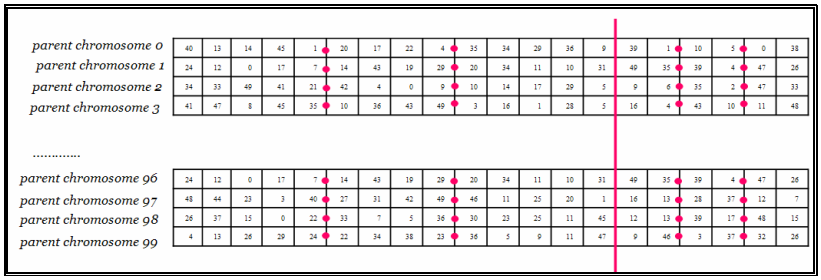


Figure 4.24 – Parent chromosomes

Step 3.2. Cross-over.

Step 3.2.1. Perform 2-point cross-over.

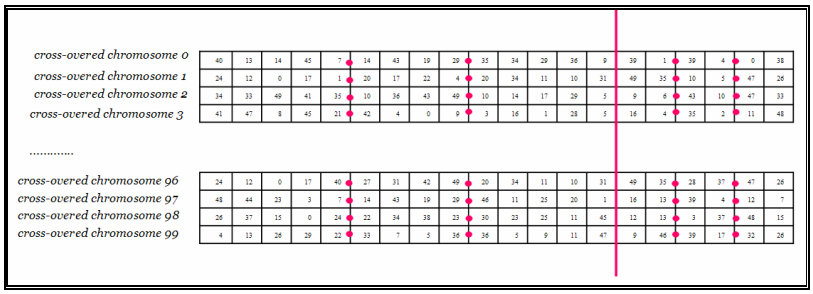


Figure 4.25 – Cross-overed chromosomes (offspring)

Cross-over is performed between two consecutive parents by

exchange of genes between first and second and third and fourth cutting points.

Step 3.2.2. Repair chromosomes.

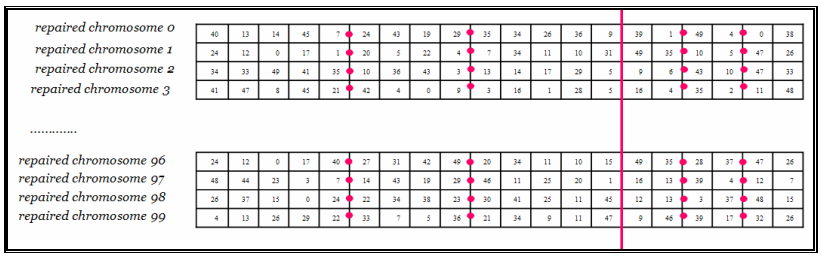


Figure 4.26 – Repaired offspring

Step 3.2.3. Calculate fitness function values.

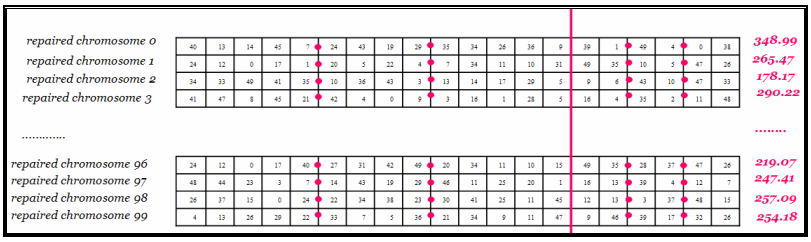


Figure 4.27 – Fitness function values of offspring population

Step 3.2.4. Keep statistics.

Step 3.3. Replace population.

Step 3.3.1. Calculate fitness function values of mating pool.

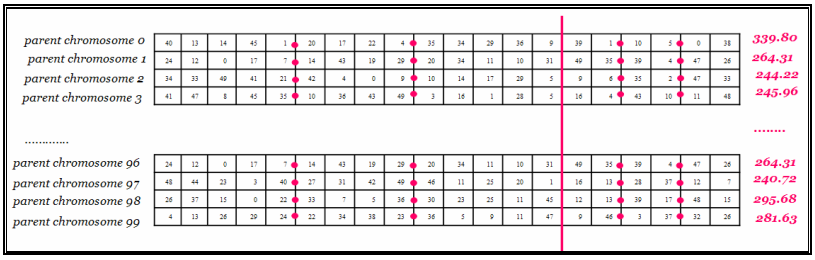


Figure 4.28 – Fitness function values of mating pool

Step 3.3.2. Replace offspring with parents if offspring are fitter.

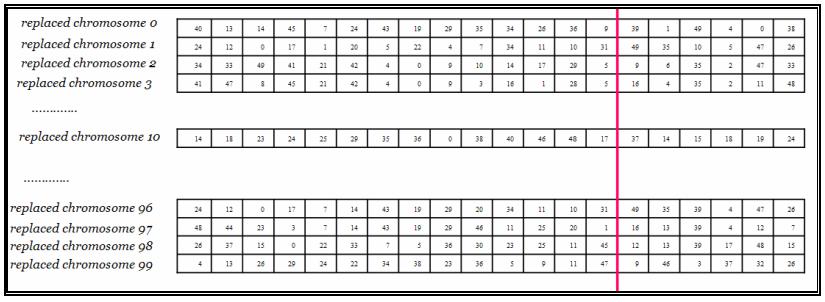


Figure 4.29 – Resulting population after conditional replacement of offspring with their parents

In Figure 4.29, the resulting population is presented. Offspring chromosome 0 with fitness value of 348.99 is replaced with its parent chromosome 0 which has a fitness value of 339.80. Offspring

chromosome 2 with fitness value of 178.17 does not take place of its parent however, since parent chromosome 2 has a fitness value of 244.22. Parent 0 is eliminated and offspring 0 is remained to next generations whereas offspring 2 is eliminated and parent 2 is remained to next generations.

Step 3.3.3. Keep statistics.

Step 3.4. Mutate.

Step 3.4.1. Perform mutation.

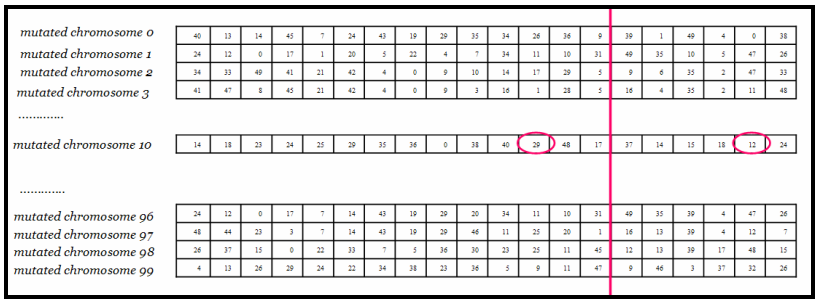


Figure 4.30 – Mutated population

Since mutation rate is small, it is encountered rarely. In chromosomes 0-3, no mutation takes place whereas in chromosome 10, two mutations take place.

Step 3.4.2. Repair chromosomes.

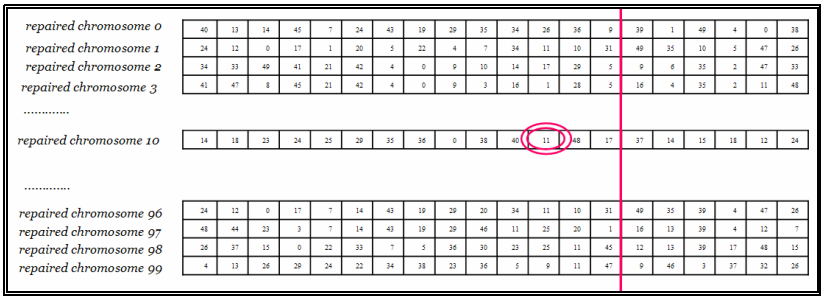


Figure 4.31 – Repaired mutated population

During mutation twelfth gene of chromosome 10 takes a recurring value with sixth gene. It is repaired by generating a random facility.

Step 3.4.3. Calculate fitness function values.

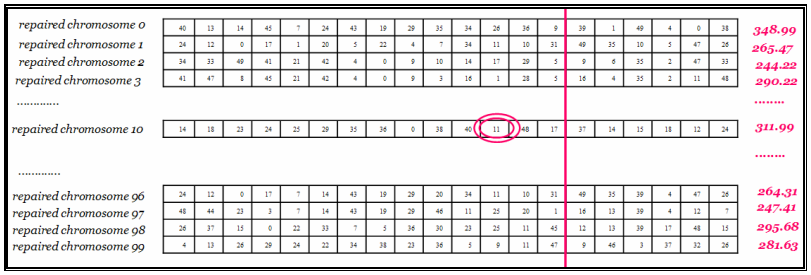


Figure 4.32 – Fitness function values of ending population of current iteration that will start to a new iteration

Step 3.4.4. Keep statistics.

Step 4. End. Stop clock. Display results.

Statistics obtained from the first iteration are presented in Table 4.20. Statistics of all iterations are presented in Appendix D.

Table 4.20 – Results of first iteration

iteration	maximum fitness	average fitness	minimum fitness	best fitness found so far
0	392.480	305.659	212.093	392.480

CHAPTER 5

COMPUTATIONAL EXPERIMENTS

A mixed-integer programming (MIP) model is constructed and a problem-specific Genetic Algorithm (GA) is developed for the Hierarchical Maximum Covering Location Problem (MCLP) with referral in presence of partial coverage (HMCLP(R)-P). Since the problem has not been studied in literature before, it is not possible to compare the results of the proposed GA with results of other studies. For small problems, results are compared with optimal results and for large problems, results are compared with the results of random heuristic that chooses the best solution amongst a randomly generated solution set.

5.1 EXPERIMENTAL SETTINGS

The initial phase is the generation of problem instances. Different node sizes, number of health centers, number of hospitals and different critical distances are tried in each problem instance and 5 problems with different seeds are generated for each instance. Problems are generated by generating x-coordinates uniformly in the range 0 and 1000, y-coordinates uniformly in the range 0 and 500, and demand weights for nodes uniformly in the range 1 and 20, in Visual C. Euclidean distance metrics are utilized for calculation of intra-nodal distances.

Weights of objective function terms are taken as 1 to give equal importance to all objectives and the rate of referral is taken as 1.

Table 5.1 – Tested problem instances

# of nodes	# of demand nodes	# of potential facility sites	# of hospitals	# of health centers	S^1	S^2	S^3	T^1	T^2	T^3
			2	4	50	100	120	75	150	180
			3	5	50	90	90	80	120	120
20	-	20	4	6	50	90	90	80	120	120
30	-	30	3	5	50	90	90	80	120	120
			4	6	50	90	90	80	120	120
			5	7	50	90	90	80	120	120
			6	8	30	60	80	50	80	100
40	-	40	4	8	50	90	90	80	120	120
			4	12	50	90	90	80	120	120
			6	12	30	60	80	50	80	100
			6	14	30	60	80	50	80	100
50	-	50	4	12	50	90	90	80	120	120
			6	12	30	60	80	50	80	100
			6	14	30	60	80	50	80	100
			8	16	30	60	80	50	80	100
60	-	60	6	12	50	90	90	80	120	120
			6	14	50	90	90	80	120	120
			8	16	50	90	90	80	120	120
			10	20	30	50	80	80	75	120
250	200	50	5	10	50	90	90	80	120	120
			10	15	30	60	80	50	80	100
500	450	50	5	10	50	90	90	80	120	120
			10	15	30	60	80	50	80	100
	400	100	5	10	50	90	90	80	120	120
			10	15	20	60	60	30	90	90
			20	30	10	50	50	15	75	75
1000	950	50	5	10	30	50	80	50	75	120
			10	15	20	60	60	30	90	90
	900	100	5	10	30	50	80	50	75	120
			10	15	30	60	80	50	80	100
			20	30	10	50	50	15	75	75
	850	150	5	10	30	50	80	50	75	120
			10	15	30	60	80	50	80	100
			20	30	10	50	50	15	75	75
			30	45	10	40	40	15	60	60

The critical distances are determined randomly but according to some basic rules of thumb and utilizing the results of Section 3.6. These rules are given below.

- Minimum critical distance for coverage of demand by hospital (S^2) is larger than minimum critical distance for coverage of demand by health center (S^1),
- Minimum referral critical distance (S^3) is larger than or equal to minimum critical distance for coverage of demand by hospital (S^2),
- Maximum critical distances are at least about 150% of minimum critical distances

The problem instances are summarized in Table 5.1, while $w^1 = w^2 = w^3 = \delta = 1$. The parameters such as the radii of critical distances, the number of health centers and the number of hospitals determine the problem hardness when problems are tried to be solved optimally. If the proportion of the total coverage area to the total area is large, then the optimal configuration of facilities contains more overlaps and this hardens and extends the Branch-and-Bound (B&B) procedure.

MIP models, presented in Appendices A and B, are solved using GAMS 19.6 with CPLEX solver. GA, pseudocode of which is presented in Appendix C, is coded in Visual C. For comparisons, a random solver is also coded in Visual C. The runs are conducted in a Pentium M Laptop with 1.86 GHz processor and 1 GB RAM.

5.2 RANDOM HEURISTIC

Random heuristic that generates a set of random solutions and takes the best solution amongst all is developed. The same procedure that is used for generation of random proportion of initial population of GA is applied without repair phase.

For determination of number of random solutions to be generated, experiments are conducted. Table 5.3 compares the changes in solution quality and required time for different number of solutions, which are tested on the problem set presented in Table 5.2.

Table 5.2 – Test problems for random heuristic

	$\|I\|$	$\|J\|$	q	p	S^1	S^2	S^3	T^1	T^2	T^3	w^1	w^2	w^3	δ
1	20	20	3	5	50	90	90	80	120	120	1	1	1	1
2	20	20	4	6	50	90	90	80	120	120	1	1	1	1
3	30	30	3	5	50	90	90	80	120	120	1	1	1	1
4	30	30	4	6	50	90	90	80	120	120	1	1	1	1
5	30	30	5	7	50	90	90	80	120	120	1	1	1	1

Table 5.3 – Changes in solution quality and time with increasing iterations

5000 iterations vs. 10000 iterations	10000 iterations vs. 20000 iterations	20000 iterations vs. 25000 iterations	25000 iterations vs. 30000 iterations	30000 iterations vs. 40000 iterations	40000 iterations vs. 50000 iterations	50000 iterations vs. 100000 iterations
Average of Improvements						
0,72%	0,67%	0,54%	0,00%	0,06%	0,06%	0,09%
Average Difference in Runtimes (sec.)						
0,11	0,15	0,11	0,10	0,15	0,17	0,86

The number of solutions to be generated is selected as 25000, considering solution quality and time requirement trade-off.

5.3 RESULTS

For problem sizes up to 50 nodes, optimal results could be obtained by GAMS and GA results are compared with GAMS results. For problem sizes of more than 50 nodes, GAMS could not find solution in 3600 seconds although depth-first search and putting bounds on variable strategies are tried. Large problems are compared with random heuristic results.

The results in Table 5.4 indicate that the GA finds solutions with maximum of 5% deviation from optimal results on the average. The amounts of deviations seem to follow a generally increasing pattern with increase of problem size which is expected, however the increase is very small. There is a higher increase in maximum deviations which indicate that increase in problem size brings increase in variance.

When compared with random heuristic, GA creates difference about 20% in average, especially when the problem sizes increase.

When time requirements are considered as in Table 5.5, GAMS requires highly varying times according to the complexity of the problem. For problems of size 60 nodes and larger, it was not possible to find solutions in 3600 seconds. GA, however, is not affected from the problem complexity since the logic is the exploration – exploitation of the search space which takes constant computation time for the same problem sizes. Also, the time requirements are certainly acceptable when quality of solutions is regarded. The time requirement to solve a problem of size 1000 nodes is at most 7 minutes.

Table 5.4 – Results of GA compared with optimal and random solutions

# of Nodes	# of Demand Nodes	# of Potential Facility Sites	# of Hospitals	# of Health Centers		(Optimal-GA Result)/Optimal					(GA Result-Random)/Random			
						Average of Deviations	Minimum of Deviations	Maximum of Deviations	Variance of Deviations	# of Optimals Found by GA	Average of Deviations	Minimum of Deviations	Maximum of Deviations	Variance of Deviations
20	-	20	2	4		0.00%	0.00%	0.01%	0.00%	4	4.38%	0.00%	9.49%	3.58%
			3	5		1.45%	0.00%	6.04%	2.61%	1	4.74%	1.83%	8.96%	2.86%
			4	6		0.19%	0.00%	0.89%	0.39%	3	9.54%	4.08%	13.63%	3.52%
30	-	30	3	5		2.99%	0.00%	10.17%	4.22%	2	10.66%	1.55%	17.42%	6.07%
			4	6		1.60%	0.00%	4.33%	1.78%	1	12.00%	7.51%	15.98%	3.71%
			5	7		0.08%	0.00%	0.38%	0.17%	3	14.29%	10.34%	16.40%	2.42%
			6	8		0.87%	0.00%	1.87%	0.87%	2	18.83%	12.61%	25.38%	4.71%
40	-	40	4	8		1.65%	0.00%	3.74%	1.68%	1	19.50%	14.60%	23.80%	3.37%
			4	12		3.45%	0.31%	4.89%	1.85%	0	17.30%	8.85%	23.64%	6.08%
			6	12		1.91%	0.00%	6.39%	2.56%	0	23.04%	19.31%	25.06%	2.22%
			6	14		1.90%	0.00%	4.73%	2.29%	1	21.59%	17.99%	24.08%	2.29%
50	-	50	4	12	*	4.19%	1.47%	7.42%	2.50%	0	21.36%	17.90%	25.59%	3.17%
			6	12		1.77%	0.53%	4.17%	1.50%	0	27.02%	23.50%	31.96%	3.37%
			6	14		4.49%	2.08%	8.74%	2.62%	0	24.38%	20.55%	28.00%	2.67%
			8	16		3.23%	0.04%	6.71%	2.37%	0	25.11%	22.06%	27.50%	2.26%
60	-	60	6	12	**	5.70%	5.70%	5.70%	5.70%	0	22.80%	21.76%	23.90%	0.94%
			6	14	***	-	-	-	-	-	23.31%	20.90%	27.03%	2.27%
			8	16	***	-	-	-	-	-	22.09%	18.11%	24.12%	2.37%
			10	20	***	-	-	-	-	-	24.67%	23.10%	28.74%	2.33%

Table 5.4 (continued) – Results of GA compared with optimal and random solutions

# of Nodes	# of Demand Nodes	# of Potential Facility Sites	# of Hospitals	# of Health Centers		(Optimal-GA Result)/Optimal					(GA Result-Random)/Random			
						Average of Deviations	Minimum of Deviations	Maximum of Deviations	Variance of Deviations	# of Optimals Found by GA	Average of Deviations	Minimum of Deviations	Maximum of Deviations	Variance of Deviations
250	200	50	5	10	***	-	-	-	-	-	21.81%	19.33%	24.75%	2.22%
			10	15	***	-	-	-	-	-	23.08%	18.19%	25.40%	2.88%
500	450	50	5	10	***	-	-	-	-	-	21.57%	15.29%	25.71%	3.84%
			10	15	***	-	-	-	-	-	22.05%	19.92%	24.41%	1.70%
	400	100	5	10	***	-	-	-	-	-	24.41%	20.56%	27.33%	2.52%
			10	15	***	-	-	-	-	-	23.78%	21.20%	26.47%	2.06%
			20	30	***	-	-	-	-	-	22.81%	20.85%	24.84%	1.48%
1000	950	50	5	10	***	-	-	-	-	-	20.92%	18.25%	24.06%	2.31%
			10	15	***	-	-	-	-	-	15.95%	14.83%	19.05%	1.75%
	900	100	5	10	***	-	-	-	-	-	22.36%	19.38%	25.43%	2.90%
			10	15	***	-	-	-	-	-	25.49%	22.41%	28.80%	2.37%
			20	30	***	-	-	-	-	-	20.48%	19.24%	21.92%	1.30%
	850	150	5	10	***	-	-	-	-	-	27.50%	21.95%	33.25%	4.87%
			10	15	***	-	-	-	-	-	25.82%	22.94%	27.51%	1.87%
			20	30	***	-	-	-	-	-	22.06%	20.56%	23.96%	1.34%
			30	45	***	-	-	-	-	-	25.18%	23.03%	27.23%	1.99%

** 1 of 5 problems could not be solved in 3600 sec. The statistics are calculated amongst 4 problems.*
*** Only 1 of 5 problems could be solved in 3600 seconds by introducing lower bound on the objective function variable.*
**** None of the problems could be solved optimally in 3600 seconds.*

Table 5.5 – Computational time requirements of GA compared with GAMS CPLEX and random heuristic

						GAMS Time (seconds)				**GA Time (seconds)**				**Random Time (seconds)**			
# of Nodes	# of Demand Nodes	# of Potential Facility Sites	# of Hospitals	# of Health Centers		Avg Time	Min Time	Max Time	Variance in Time	Avg Time	Min Time	Max Time	Variance in Time	Avg Time	Min Time	Max Time	Variance in Time
			2	4		0.08	0.06	0.09	0.01	1.76	1.67	1.88	0.08	0.36	0.33	0.42	0.04
			3	5		0.56	0.05	1.55	0.70	1.79	1.65	1.88	0.09	0.35	0.27	0.42	0.06
20	-	20	4	6		0.22	0.06	0.80	0.32	2.01	1.91	2.14	0.10	0.43	0.38	0.50	0.05
30	-	30	3	5		1.80	0.03	5.10	2.43	3.41	3.27	3.59	0.13	0.61	0.55	0.66	0.04
			4	6		7.27	0.08	21.63	8.72	3.54	3.27	3.88	0.23	0.64	0.59	0.67	0.03
			5	7		5.68	0.13	19.06	7.69	3.81	3.69	4.05	0.15	0.68	0.61	0.75	0.05
			6	8		0.08	0.08	0.11	0.01	3.63	3.47	3.75	0.11	0.67	0.64	0.69	0.02
40	-	40	4	8		41.59	13.89	109.47	39.28	6.17	6.06	6.36	0.11	1.00	0.92	1.05	0.05
			4	12		354.03	5.41	1615.20	706.87	7.00	6.69	7.34	0.27	1.09	1.08	1.11	0.02
			6	12		0.39	0.09	1.58	0.66	6.29	6.06	6.39	0.13	1.04	1.00	1.08	0.03
			6	14		33.74	1.00	115.42	47.70	6.80	6.41	6.97	0.23	1.11	1.08	1.13	0.02
50	-	50	4	12	*	1377.53	212.97	2936.53	1240.05	10.02	9.61	10.36	0.27	1.50	1.42	1.55	0.05
			6	12		8.12	2.11	28.23	11.26	9.06	8.84	9.52	0.27	1.44	1.41	1.45	0.02
			6	14		30.59	1.00	146.55	64.83	9.34	9.14	9.55	0.20	1.47	1.39	1.50	0.05
			8	16		266.67	1.00	1087.72	466.43	9.86	9.58	10.20	0.29	1.54	1.52	1.56	0.02
60	-	60	6	12	**	1837.44	1837.44	1837.44	1837.44	13.83	13.53	14.16	0.25	2.07	2.00	2.24	0.10
			6	14	***	-	-	-	-	14.34	14.03	14.53	0.21	2.21	2.13	2.27	0.06
			8	16	***	-	-	-	-	14.85	14.50	15.27	0.35	2.29	2.16	2.36	0.08
			10	20	***	-	-	-	-	16.12	15.56	16.70	0.44	2.52	2.44	2.61	0.06

Table 5.5 (continued) – Computational time requirements of GA compared with GAMS CPLEX and random heuristic

					GAMS Time (seconds)					GA Time (seconds)				Random Time (seconds)			
# of Nodes	# of Demand Nodes	# of Potential Facility Sites	# of Hospitals	# of Health Centers		Avg Time	Min Time	Max Time	Variance in Time	Avg Time	Min Time	Max Time	Variance in Time	Avg Time	Min Time	Max Time	Variance in Time
250	200	50	5	10	***	-	-	-	-	41.10	40.31	41.77	0.59	5.96	5.88	6.11	0.10
			10	15	***	-	-	-	-	38.49	37.89	38.94	0.38	5.69	5.66	5.77	0.05
500	450	50	5	10	***	-	-	-	-	79.65	79.16	79.98	0.36	11.54	11.25	11.80	0.23
			10	15	***	-	-	-	-	73.61	72.75	74.45	0.67	10.90	10.72	11.09	0.15
	400	100	5	10	***	-	-	-	-	153.18	151.28	154.94	1.67	22.54	22.41	22.78	0.15
			10	15	***	-	-	-	-	133.17	131.92	135.16	1.28	20.38	20.02	20.72	0.29
			20	30	***	-	-	-	-	134.74	132.53	139.75	2.91	20.42	20.31	20.53	0.09
1000	950	50	5	10	***	-	-	-	-	136.23	135.25	137.17	0.80	20.81	20.56	21.44	0.37
			10	15	***	-	-	-	-	135.13	133.03	136.47	1.27	20.52	20.25	20.77	0.20
	900	100	5	10	***	-	-	-	-	297.84	296.28	298.94	1.04	47.44	46.94	47.92	0.41
			10	15	***	-	-	-	-	312.67	311.22	314.11	1.08	49.13	48.75	49.47	0.32
			20	30	***	-	-	-	-	305.55	295.36	311.91	7.31	46.89	46.58	47.06	0.23
	850	150	5	10	***	-	-	-	-	411.20	408.69	416.44	3.15	63.29	62.58	64.23	0.63
			10	15	***	-	-	-	-	444.98	438.17	453.72	6.45	66.17	65.78	66.89	0.43
			20	30	***	-	-	-	-	415.45	412.72	423.14	4.32	62.92	62.33	64.80	1.06
			30	45	***	-	-	-	-	409.96	408.76	411.12	0.90	63.46	62.89	64.13	0.59

** 1 of 5 problems could not be solved in 3600 sec. The statistics are calculated amongst 4 problems.*
*** Only 1 of 5 problems could be solved in 3600 seconds by introducing lower bound on the objective function variable.*
**** None of the problems could be solved optimally in 3600 seconds.*

CHAPTER 6

CONCLUSION AND FUTURE RESEARCH

We combined HCMLP, referral and MCLP-P, and proposed a HMCLP(R)-P formulation to model the requirements of health systems more realistically. Proposed formulation has several extensions to classical HMCLP with different combination of characteristics: (i) 3 types of demand –demand requiring low-level service, demand requiring high-level service and demand requiring both levels of service at the same time- is considered but all demand of a demand point is covered as a whole. (ii) We considered a successively inclusive hierarchy and referral to meet the 3 types of demand requirement at once. (iii) We integrated partial coverage to HMCLP.

Integration of partial coverage increases the complexity of the problem. In classical MCLP's and HMCLP's, the information of which facility covers which demand is not important. The important notion is the coverage and whether a demand point can be covered or not. However, integration of partial coverage brings assignment to HMCLP(R)-P, since calculation of partial coverage requires information of distance between nodes. Thus, the NP-hard HMCLP becomes even harder to solve.

We proposed a MIP formulation and tried to find optimal results using GAMS 19.6 with CPLEX solver. GAMS was able to solve problems up to size of 50 nodes within a time limit of 3600 seconds. For the problems of larger scale, frequently used time-reducing methods such as modifying the B&B strategy to

depth-first search or putting bounds on variables to accelerate fathoming of B&B procedure were even not of use.

We proposed a problem-specific GA that is fast and produces near-optimal results for large-size problems. The algorithm has pruned its final state after initial experiments for eah strategy. It is tested on problems of sizes 20 to 1000 nodes and compared with optimal solutions for small-sized and with random solutions for large-sized problems. The deviations and time requirements are reasonable.

Even though MCLP has been studied widely, it can be extended on several directions. HMCLP is one of those extensions. We developed and proposed a solution procedure. A future research direction would be developing heuristics or applying other meta-heuristics to HMCLP(R)-P, such as Simulated Annealing and Tabu Search.

Another future research might be studying the capacitated version of HMCLP(R)-P. Since we already included assignments, introduction of capacity would not require additional variables but only additional constraints.

REFERENCES

Beasley, J. E., Bull, D. R. & Martin, R. R. (1993). An Overview of Genetic Algorithms: Part I Fundamentals. *University Comp*, 15, 170-181.

Beasley, J. E. & Chu, P. C. (1996). A Genetic Algorithm for the Set Covering Problem. *European Journal of Operational Research*, 94, 392-404.

Berman, O. & Krass, D. (2002). The Generalized Maximal Covering Location Problem. *Computers & Operations Research*, 29, 563-581.

Berman, O., Krass, D. & Drezner, Z. (2003). The Gradual Covering Decay Location Problem On A Network. *European Journal of Operational Research*, 151, 474-480.

Charnes, A. & Storbeck, J. (1980). A Goal Programming Model for the Siting of Multilevel EMS Systems. *Socio-Econ. Plan. Sci.*, 14, 155-161.

Chung, C-H. (1986). Recent Applications of the Maximal Covering Location Planning (M.C.L.P.) Model. *J. Opl. Res. Soc.*, 37(8), 735-746.

Church, R. & ReVelle, C. (1974). The Maximal Covering Location Problem. *Papers of the Regional Science Association*, 32, 101-118.

Drezner, Z., Wesolowsky, G. O., & Drezner, T. (2004). The Gradual Covering Problem. *Naval Research Logistics*, 51, 841-855.

Eitan, Y., Narula, S.C. & Tien, J. M. (1991). A Generalized Approach to Modeling the Hierarchical Location-Allocation Problem. *IEEE Transactions on Systems, Man and Cybernetics*, 21(1), 39-46.

Espejo, L. G. A., Galvão, R. D. & Boffey, B. (2003). Dual-Based Heuristics for a Hierarchical Covering Location Problem. *Computers & Operations Research*, 30, 165-180.

Goldberg, D. E. (1989). Genetic Algorithms in Search, Optimization and Machine Learning. *Reading, MA: Addison-Wesley.*

Holland, J. (1975). Adaptation in Natural and Artificial Systems. *Univ. of Michigan Press, Ann Arbor, MI.*

Karasakal, O. & Karasakal, E. (2004). A Maximal Covering Location Model in The Presence of Partial Coverage. *Computers & Operations Research*, 31, 1515-1526.

Li, X. & Yeh, A. G. (2004). Integration of Genetic Algorithms and GIS for Optimal Location Search. *International Journal of Geographical Information Science*. 19(5), 581-601.

Marianov, V. & Serra, D. (2001). Hierarchical Location-Allocation Models for Congested Systems. *European Journal of Operational Research*, 135, 195-208.

Moore, G. C. & ReVelle, C. (1982). The Hierarchical Service Location Problem. *Management Science*, 28(7), 775-780.

Narula, S. C. & Ogbu, U. I. (1978). An Hierarchical Location-Allocation Problem. *OMEGA. The Int. Jl of Mgmt. Sci.*, 7(2), 137-143.

Narula, S. C. & Ogbu, U. I. (1984). Lagrangean Relaxation and Decomposition in an Uncapacitated 2-Hierarchical Location-Allocation Problem. *Computers & Operations Research*, 12(2), 169-180.

Şahin, G. & Süral, H. (2007). A Review of Hierarchical Facility Location Models. *Computers & Operations Research*, 34, 2310-2331.

Toregas, C., Swain, R., ReVelle, C. & Bergman, L. (1971). The Location of Emergency Service Facilities. *Operations Research*, 19, 1363-1373.

Töreyen, Ö., Karasakal, E. & Karasakal, O. (2006). Hierarchical Maximal Covering Location Problem with Referral in Presence of Partial Coverage. Presented at the *26th National Operations Research and Industrial Engineering Congress 2006,* Kocaeli, Turkey.

APPENDIX A

GAMS FORMULATION 1

```
sets
        i nodes /1*50/;


alias (i,j);
alias (i,k);

parameters d(i) demand matrix
$include "C:\Documents and
Settings\oz_tez\gams_bastan\book41.txt";

table dist(i,j) distance between nodes i and j
$include "C:\Documents and
Settings\oz_tez\gams_bastan\book40.txt";

parameter s1 critical distance1;
s1 = 30;
parameter t1 critical distance2;
t1 = 50;
parameter s2 critical distance3;
s2 = 60;
parameter t2 critical distance4;
t2 = 80;
parameter s3 critical distance5;
s3 = 80;
parameter t3 critical distance6;
t3 = 100;


parameter    a1(i,j) binary coverage (T1) of demand i by
health center at j;
a1(i,j) = 0;
a1(i,j)$(dist(i,j) ne t1) = (1 + (1- (dist(i,j) / t1)) /
abs(1 - (dist(i,j) /t1))) / 2;

parameter    a2(i,j) binary coverage (T2) of demand at i
hospital at j;
```

```
a2(i,j) = 0;
a2(i,j)$(dist(i,j) ne t2) = (1 + (1- (dist(i,j) / t2)) /
abs(1 - (dist(i,j) /t2))) / 2;

parameter    a3(i,j) binary coverage (T3) of health center
at i by hospital at j;
a3(i,j) = 0;
a3(i,j)$(dist(i,j) ne t3) = (1 + (1- (dist(i,j) / t3)) /
abs(1 - (dist(i,j) /t3))) / 2;

parameter    c1(i,j) partial coverage of demand i by health
center at j;
c1(i,j) = min(1 , max(0 , (t1 - dist(i,j)) / (t1-s1)));

parameter    c2(i,j) partial coverage of demand at i
hospital at j;
c2(i,j) = min(1 , max(0 , (t2 - dist(i,j)) / (t2-s2)));

parameter    c3(i,j) partial coverage of health center at i
by hospital at j;
c3(i,j) = min(1 , max(0 , (t3 - dist(i,j)) / (t3-s3)));

sets
         m1(i,j)         first coverage
         m2(i,j)         second coverage
         m3(i,j)         hospital coverage;

         m1(i,j)=no;
         m2(i,j)=no;
         m3(i,j)=no;

         m1(i,j)$(a1(i,j) eq 1)=yes;
         m2(i,j)$(a2(i,j) eq 1)=yes;
         m3(i,j)$(a3(i,j) eq 1)=yes;

binary variables
         x1(i,j)  if demand at i is assigned to health
center at j
         x2(i,j)  if demand at i is assigned to hospital at
j
         y(i,j)   if health center at i is opened and
assigned to hospital at j
         z(j)     if hospital is opened at j ;

positive variables
         u(j,k)   demand in health center j that is covered
by hospital k ;

variable t   objective function value ;

equations
```

```
         obj             objective function
         numfac1         number of hospitals limited to q
         numfac2         number of  health centers limited
to p
         cov1(i,j)       demand-health center coverage
         cov2(i,j)       demand-hospital coverage
         cov3(i,j)       health center-hospital coverage
         ass1(i)         demand-health center and hospital
assignment
         ass2(i)         health center-hospital assignment
         lin1(j,k)       linearization1
         lin2(j,k)       linearization2;



obj..                    t =e= sum((i,j)$m1(i,j),
d(i)*c1(i,j)*x1(i,j))+sum((i,j)$m2(i,j)
,d(i)*c2(i,j)*x2(i,j))+sum((j,k)$m3(j,k), u(j,k));
numfac1..                sum(j,z(j)) =e= 6;
numfac2..                sum((i,j)$m3(i,j),y(i,j)) =l= 14;
cov1(i,j)$m1(i,j)..      x1(i,j) =l= sum(k$(a3(j,k) eq
1),y(j,k));
cov2(i,j)$m2(i,j)..      x2(i,j) =l= z(j);
cov3(i,j)$m3(i,j)..      y(i,j) =l= z(j);
ass1(i)..                sum(j$(a1(i,j) eq
1),x1(i,j))+sum(j$(a2(i,j) eq 1),x2(i,j)) =l= 1;
ass2(i)..                sum(j$(a3(i,j) eq 1),y(i,j)) =l=
1;
lin1(j,k)$m3(j,k)..      u(j,k) =l= sum(i$(a1(i,j) eq
1),d(i)*c1(i,j)*x1(i,j))*c3(j,k);
lin2(j,k)$m3(j,k)..      u(j,k) =l= 1000*y(j,k);



model oz /all/;

OPTIONS LIMROW=200, LIMCOL=200, SYSOUT=OFF, SOLPRINT=ON,
ITERLIM=2000000, RESLIM=40800, optcr=0.0, BRATIO=0,
MIP=cplex;


solve oz using mip maximizing t;
display x1.l, x1.m, x2.l, x2.m, y.l, y.m, z.l, z.m, u.l,
u.m;
```

APPENDIX B

GAMS FORMULATION 2

```
sets
        i nodes /1*20/;



alias (i,j);
alias (i,k);

parameters d(i) demand matrix
$include "C:\Documents and
Settings\oz_tez\gams_bastan\book41.txt";

table dist(i,j) distance between nodes i and j
$include "C:\Documents and
Settings\oz_tez\gams_bastan\book40.txt";

parameter s1 critical distance1;
s1 = 10;
parameter t1 critical distance2;
t1 = 20;
parameter s2 critical distance3;
s2 = 20;
parameter t2 critical distance4;
t2 = 40;
parameter s3 critical distance5;
s3 = 25;
parameter t3 critical distance6;
t3 = 50;


parameter    a1(i,j) binary coverage (T1) of demand i by
health center at j;
a1(i,j) = 0;
a1(i,j)$(dist(i,j) ne t1) = (1 + (1- (dist(i,j) / t1)) /
abs(1 - (dist(i,j) /t1))) / 2;

parameter    a2(i,j) binary coverage (T2) of demand at i
hospital at j;
a2(i,j) = 0;
a2(i,j)$(dist(i,j) ne t2) = (1 + (1- (dist(i,j) / t2)) /
abs(1 - (dist(i,j) /t2))) / 2;
```

```
parameter    a3(i,j) binary coverage (T3) of health center
at i by hospital at j;
a3(i,j) = 0;
a3(i,j)$(dist(i,j) ne t3) = (1 + (1- (dist(i,j) / t3)) /
abs(1 - (dist(i,j) /t3))) / 2;

parameter    c1(i,j) partial coverage of demand i by health
center at j;
c1(i,j) = min(1 , max(0 , (t1 - dist(i,j)) / (t1-s1)));

parameter    c2(i,j) partial coverage of demand at i
hospital at j;
c2(i,j) = min(1 , max(0 , (t2 - dist(i,j)) / (t2-s2)));

parameter    c3(i,j) partial coverage of health center at i
by hospital at j;
c3(i,j) = min(1 , max(0 , (t3 - dist(i,j)) / (t3-s3)));

sets
         m1(i,j)         first coverage
         m2(i,j)         second coverage
         m3(i,j)         hospital coverage;

         m1(i,j)=no;
         m2(i,j)=no;
         m3(i,j)=no;

         m1(i,j)$(a1(i,j) eq 1)=yes;
         m2(i,j)$(a2(i,j) eq 1)=yes;
         m3(i,j)$(a3(i,j) eq 1)=yes;

binary variables
         x1(i,j)  if demand at i is assigned to health
center at j
         x2(i,j)  if demand at i is assigned to hospital at
j
         y(i,j)   if health center at i is opened and
assigned to hospital at j
         z(j)     if hospital is opened at j
         u(i,j,k) if demand i is assigned to health center
j and health center j is assigned to hospital k ;

variable t   objective function value;

equations

         obj             objective function
         numfac1         number of hospitals limited to p
         numfac2         number of  health centers limited
to q
         cov1(i,j)       demand-health center coverage
```

```
         cov2(i,j)       demand-hospital coverage
         cov3(i,j)       health center-hospital coverage
         ass1(i)         demand-health center and hospital
assignment
         ass2(i)         health center-hospital assignment
         lin(i,j,k)      linearization;



obj..                                        t =e=
sum((i,j)$m1(i,j),d(i)*c1(i,j)*x1(i,j))+sum((i,j)$m2(i,j),d
(i)*c2(i,j)*x2(i,j))+sum((i,j,k)$(m1(i,j) and
m3(j,k)),d(i)*c1(i,j)*c3(j,k)*u(i,j,k));
numfac1..                                    sum(j,z(j)) =e= 4;
numfac2..
sum((i,j)$m3(i,j),y(i,j)) =l= 6;
cov1(i,j)$m1(i,j)..                          x1(i,j) =l=
sum(k$(a3(j,k) eq 1),y(j,k));
cov2(i,j)$m2(i,j)..                          x2(i,j) =l= z(j);
cov3(i,j)$m3(i,j)..                          y(i,j) =l= z(j);
ass1(i)..                                    sum(j$(a1(i,j) eq
1),x1(i,j))+sum(j$(a2(i,j) eq 1),x2(i,j)) =l= 1;
ass2(i)..                                    sum(j$(a3(i,j) eq
1),y(i,j)) =l= 1;
lin(i,j,k)$(m1(i,j) and m3(j,k))..           u(i,j,k) =l=
0.5*x1(i,j)+0.5*y(j,k);




model oz /all/;

OPTIONS LIMROW=0, LIMCOL=0, SYSOUT=OFF, SOLPRINT=ON,
ITERLIM=2000000, RESLIM=40800, optcr=0.0, BRATIO=0,
MIP=cplex;

solve oz using mip maximizing t;
  display x1.l, x1.m, x2.l, x2.m, y.l, y.m, z.l, z.m, u.l,
                            u.m;
```

APPENDIX C

GA PSEUDOCODE

```
0       generate problem
  0.1       distance1 (from demand nodes to potential facility nodes) matrix
            generation
  0.2           for i=1 to num_dem,  repeat
  0.3               for j=1 to num_fac, repeat
  0.4                   generate distance1[i,j] ← random
                        distances~Uniform[1,200] using
                        lcgrand function
  0.5       distance2 (between potential facility nodes) matrix generation
  0.6           for i=1 to num_fac,  repeat
  0.7               diagonal is 0
  0.8               for j=1 to num_fac (upper tringle), repeat
  0.9                   generate distance2[i,j] ← random
                        distances~Uniform[1,200] using
                        lcgrand function
  0.10                  take lower triangle symmetric with
                        upper triangle
  0.11      demand1 (demand nodes) matrix generation
            for i=1 to num_dem, repeat
                generate demand1[i] ← random
                demand~Uniform[1,20] using lcgrand function
  0.11      demand2 (potencial facility nodes) matrix generation
  0.12          for i=1 to num_fac, repeat
  0.13              generate demand2[i] ← random
                    demand~Uniform[1,20] using lcgrand function
  0.14      write distance and demand matrices
  0.15      for ℓ =1,2
  0.16          for i=1 to num_dem, repeat
  0.17              for  j=1 to num_fac, repeat
  0.18                  calculate cov[ℓ][i,j] ←
  0.19                  cov[ℓ][i,j] = 1,              if
                        distance1[i,j] < S^ℓ
  0.20                  cov[ℓ][i,j] = (T^ℓ - distance)/(T^ℓ - S^ℓ),
                                                  if S^ℓ
                                                  <distance1[i,j]
                                                  < T^ℓ
  0.21                  cov [ℓ][i,j] = 0,             if
```

```
                                        distance1[i,j] > T^ℓ
0.22            for ℓ =3
0.23                for i=1 to num_fac, repeat
0.24                    for  j=1 to num_fac, repeat
0.25                        calculate cov [ℓ][i,j] ←
0.26                        cov [ℓ][i,j] = 1,           if
                            distance2[i,j] < S^ℓ
0.27                        cov [ℓ][i,j] = (T^ℓ - distance)/(T^ℓ - S^ℓ),
                                                        if S^ℓ
                                                        <distance2[i,j]
                                                        < T^ℓ
0.28                        cov [ℓ][i,j] = 0,           if
                            distance2[i,j] > T^ℓ
0.29            for ℓ =1,2
0.30                for i=1 to num_fac, repeat
0.31                    for  j=1 to num_fac, repeat
0.32                        calculate cov[ℓ+3][i,j] ←
0.33                        cov [ℓ+3][i,j] = 1,         if
                            distance2[i,j] < S^ℓ
0.34                        cov [ℓ+3][i,j] = (T^ℓ - distance)/(T^ℓ - S^ℓ),
                                                        if S^ℓ
                                                        <distance2[i,j]
                                                        < T^ℓ
0.35                        cov [ℓ+3][i,j] = 0,         if
                            distance2[i,j] > T^ℓ
1               for rep= 1 to rep_num, repeat
                start clock
                generate initial population
1.1             generate initial population – randomly
1.2                 for i=1 to r1*popsize, repeat
1.3                     for j=1 to p, repeat
1.4                         generate facility[i,j] ← random numbers
                            (mode num_fac)
1.5                         for k=1 to j, repeat
1.6                             if facility[i,j]=facility[i,k], go to
                                Step 1.4
1.7                             else continue
1.8                     for j=p+1 to p+q, repeat
1.9                         generate random numbers (mode
                            num_fac)
1.10                        for k=p+1 to j, repeat
1.11                            if facility[i,j]=facility[i,k], go to
                                Step 1.9
1.12                            else continue
1.13            generate initial population – heuristic
1.14                for j=1 to num_fac, repeat
```

```
1.15                    for i=1 to num_dem, repeat
1.16                        sum[j] ← sum cov [1][i,j]
1.15                    for k=1 to num_fac, repeat
1.16                        sum[j] ← sum cov [4][k,j]
1.17                for j=1 to num_fac, repeat
                        for k=1,2, repeat
1.18                        form sorted_fac[k,j] ← first rows
                            indicate j's and second rows indicate
                            column sum of j's(sum[j]'s)
1.19                for j=1 to num_fac, repeat
1.20                    for k=j+1 to num_fac, repeat
1.21                        if sum[k] > sum[j], swap columns
1.22                        else continue
1.23                for i=r1*popsize+1 to popsize, repeat
1.24                    for j=1 to p, repeat
1.25                        start with the first element of sorted_fac
                            matrix
1.26                        if the number of untaken facilities <
                            num_fac – p, generate a random number
1.27                            if random number is greater
                                than 0.3, take next sorted_fac
                                element as the next chromosome
1.28                            else skip that sorted_fac element
1.29                        else take all remaining elements
                            sequentially
1.30                    for j=p+1 to p+q, repeat
1.31                        start with the first element of sorted_fac
                            matrix
1.32                        if the number of untaken facilities <
                            num_fac – q, generate a random number
1.33                            if random number is greater
                                than 0.3, take next sorted_fac as
                                the next gene
1.34                            else skip that sorted_fac element
1.35                        else take all remaining elements
                            sequentially
2           find fitness functions
2.1             calculate x1[i,j] and x2[i,j]
2.2                 for i=1 to popsize, repeat
2.3                     for j=1 to num_fac, repeat
2.4                         for k=1 to p, repeat
2.5                             if facility[i,k]=j, count
2.6                             else continue
2.7                         if count >= 1, x1[i,j]=1
2.8                         else x1[i,j] = 0
2.9                     for j=1 to num_fac, repeat
2.10                        for k=p+1 to p+q, repeat
2.11                            if facility[i,k]=j, count
2.12                            else continue
2.13                        if count >= 1, x2[i,j]=1
2.14                        else x2[i,j] = 0
```

```
2.15    calculate fitness functions
2.16        for l=1 to popsize, repeat
2.17            for i=1 to num_dem, repeat
2.18                for j=1 to num_fac, repeat
2.19                    if either cov[1][i,j] is 0 or
                        clinique j is unopened in the
                        population, increment j by 1 and
                        go to Step 2.18
2.20                    else for k=1 to num_fac, repeat
2.21                        if either cov[3][j,k] is 0
                            or hospital k is
                            unopened in the
                            population, increment k
                            by 1 and go to Step 2.20
2.22                        else calculate temp5 ←
                            coverage of demand i by
                            clinique j and then
                            hospital k
2.23                for j=1 to num_fac, repeat
2.24                    if either cov[2][i,j] is 0 or
                        hospital j is unopened in the
                        population, increment j by 1 and
                        go to Step 2.23
2.25                    else calculate temp5 ←
                        coverage of demand i by
                        hospital j
2.26                find coverage[l,i] ← take  the highest
                    temp5
2.27            find fitness value of the gene fitness[l] ← sum
                coverage[l,i]'s
2.28            for i=1 to num_fac, repeat
2.29                for j=1 to num_fac, repeat
2.30                    if either cov[4][i,j] is 0 or
                        clinique j is unopened in the
                        population, increment j by 1 and
                        go to Step 2.29
2.31                    else for k=1 to num_fac, repeat
2.32                        if either cov[3][j,k] is 0
                            or hospital k is
                            unopened in the
                            population, increment k
                            by 1 and go to Step 2.31
2.33                        else calculate temp5 ←
                            coverage of demand i by
                            clinique j and then
                            hospital k
2.34                for j=1 to num_fac, repeat
2.35                    if either cov[5][i,j] is 0 or
                        hospital j is unopened in the
                        population, increment j by 1 and
                        go to Step 2.34
```

2.36 *else calculate temp5 ← coverage of demand i by hospital j*

2.37 *find coverage[l,i] ← take the highest temp5*

2.38 *update fitness value of the gene fitness[l] ← fitness[l] + sum coverage[l,i]'s*

2.39 *keep population statistics*

2.40 *sort the population according to fitness function values*

2.41 *for k=1 to popsize, repeat*

2.42 *for l=1,2, repeat*

2.43 *form sorted_fit[l,k] ← first rows indicate population k's and the second rows indicate fitness values of k's*

2.44 *for k=1 to popsize, repeat*

2.45 *for l=k+1 to popsize, repeat*

2.46 *if fitness[l] > fitness[k], swap columns*

2.47 *else continue*

2.48 *fit_max ← first element of sorted_fit*

2.49 *fit_min ← last element of sorted_fit*

2.50 *for k=1 to popsize, repeat*

2.51 *fit_avg ← find average fitness value*

2.52 *for i=1 to p+q, repeat*

2.53 *keep best_gene[i] ← chromosome[i] of maximum fit gene*

2.54 *best solution track*

2.55 *if fit_max > best_soln[rep], update best_sol[rep]*

2.56 *for j=1 to p+q, repeat*

2.57 *form best_gene_rep[rep,j] ← genes of fit_max*

3 *stopping condition*

for iter=1 to iter_num, repeat

3.1 *fitness ranking*

3.2 *form ranked fitness[k] r_fitness ← 1 for the first element of sorted_fit*

3.3 *for k=1 to popsize, repeat*

3.4 *if k^{th} fitness of sorted_fit = $k+1^{th}$ element of sorted_fit, r_fitness[k+1]= r_fitness[k]*

3.5 *else r_fitness[k+1]= r_fitness[k]+1*

3.6 *for k=1 to popsize, repeat*

3.7 *revert the order such that the fittest chromosome has the highest rank*

3.8 *r_fit_max = highest rank*

3.9 *r_fit_min = 1*

3.10 *parent selection – according to replacement scheme go to 3.10a, 3.10b, 3.10c or 3.10d*

```
3.10a   parent selection – unconditional replacement
3.11        for k=1 to popsize, repeat
3.12            calculate probability of selecting population k to
                mating pool prob[k] ← (r_fitness[k]-
                r_fit_min)/(r_fit_max-r_fit_min)
3.13        for k=1 to popsize, repeat
3.14            for j=1 to p+q, repeat
3.15                define offspring[k,j] ← facility[k,j]
                    where offspring[k,j] is the transition
                    matrix, it is used only for selection
3.16            for l=1 to pc*popsize, repeat
3.17                for k=count (count indicates the
                    chromosome we will decide to take or
                    not) to popsize, repeat
3.18                    if prob[k] > a random number
                        generated with lcgrand function,
                        for j=1 to p+q, repeat
3.19                        set facility[l,j] ←
                            offspring[k,j]
3.20                        if count=popsize,
                            count=0; so one
                            chromosome may be
                            selected more than once
3.21                    else, pass to the next
                        chromosome by incrementing
                        count and decide whether to
                        take it or not using prob[k]
3.22                        if count=popsize,
                            count=0; so one
                            chromosome may be
                            selected more than once
3.23    crossover type selection
3.24        generate a ← a random number using lcgrand function
            (mode 3), this allows hybrid crossover
3.25    if a = 1, crossover 1-point
3.26        for l=1 to pc*popsize, repeat for every pair of
            chromosomes
3.27            for j=p/2 to p+q/2, repeat
3.28                change gene j's of sequential
                    chromosomes
3.29    if a = 2, crossover – 2-point
3.30        for l=1 to pc*popsize, repeat for every pair of
            chromosomes
3.31            for j=p/3 to 2p/3, repeat
3.32                change gene j's of sequential
                    chromosomes
3.33        for l=1 to pc*popsize, repeat for every pair of
```

chromosomes

3.34 *for j=p+q/3 to p+2q/3, repeat*

3.35 *change gene j's of sequential chromosomes*

3.36 *if a = 0, input mask crossover*

3.37 *generate mask[j] ← a random number using lcgrand function (mode 2)*

3.38 *for l=1 to pc*popsize, repeat for every pair of chromosomes*

3.39 *if mask[j]=1, do not swap*

3.40 *else swap gene j's*

3.41 *repair*

3.42 *for l=1 to pc*popsize, repeat*

3.43 *for j=2 to p, repeat*

3.44 *for k=1 to j, repeat*

3.45 *if facility[l,j]=facility[l,k], generate facility[l,j] ← a random number using lcgrand function (mode num_fac) and decrement j to check from beginning*

3.46 *for j=p+2 to p+q, repeat*

3.47 *for k=p+1 to j, repeat*

3.48 *if facility[l,j]=facility[l,k], generate facility[l,j] ← a random number using lcgrand function (mode num_fac) and decrement j to check from beginning*

3.49 *fitness function calculation with crossover*

3.50 *repeat steps 2.1- 2.57*

3.51 *mutation*

3.52 *for k=1 to popsize, repeat*

3.53 *for j=1 to p+q, repeat*

3.54 *if pm > a random generated number, facility[k,j] ← random number*

3.55 *repair*

3.56 *repeat steps 3.42-3.48*

3.57 *fitness function calculation with crossover and mutation*

3.58 *repeat steps 2.1- 2.57*

3.59 *stop clock*

end of iterations

go to Step 4.

```
3.10b   parent selection – transfer replacement
3.11        for k=1 to popsize, repeat
3.12            calculate probability of selecting population k to
                mating pool prob[k] ← (r_fitness[k]-
                r_fit_min)/(r_fit_max-r_fit_min)
3.13        for k=1 to popsize, repeat
3.14            for j=1 to p+q, repeat
3.15                define offspring[k,j] ← facility[k,j]
                    where offspring[k,j] is the transition
                    matrix, it is used only for selection
3.16            for l=1 to pc*popsize, repeat
3.17                for k=count (count indicates the
                    chromosome we will decide to take or
                    not) to popsize, repeat
3.18                    if prob[k] > a random number
                        generated with lcgrand function,
                        for j=1 to p+q, repeat
3.19                        set facility[l,j] ←
                            offspring[k,j]
3.20                        if count=popsize,
                            count=0; so one
                            chromosome may be
                            selected more than once
3.21                    else, pass to the next
                        chromosome by incrementing
                        count and decide whether to
                        take it or not using prob[k]
3.22                        if count=popsize,
                            count=0; so one
                            chromosome may be
                            selected more than once
3.23    add best gene to a random place in the population
3.24        generate l ← a random place using lcgrand function
            (mode popsize)
3.25        for j=1 to p+q, repeat
3.26            facility[l][j] ← best_gene_rep[rep][j], best
                gene of current replication
3.27    crossover type selection
3.28        generate a ← a random number using lcgrand function
            (mode 3), this allows hybrid crossover
3.29    if a = 1, crossover 1-point
3.30        for l=1 to pc*popsize, repeat for every pair of
            chromosomes
3.31            for j=p/2 to p+q/2, repeat
3.32                change gene j's of sequential
                    chromosomes
3.33    if a = 2, crossover – 2-point
3.34        for l=1 to pc*popsize, repeat for every pair of
            chromosomes
3.35            for j=p/3 to 2p/3, repeat
3.36                change gene j's of sequential
```

```
                                    chromosomes
3.37                    for l=1 to pc*popsize, repeat for every pair of
                        chromosomes
3.38                            for j=p+q/3 to p+2q/3, repeat
3.39                                    change gene j's of sequential
                                        chromosomes
3.40            if a = 0, input mask crossover
3.41                    generate mask[j] ← a random number using lcgrand
                        function (mode 2)
3.42                    for l=1 to pc*popsize, repeat for every pair of
                        chromosomes
3.43                            if mask[j]=1, do not swap
3.44                            else swap gene j's
3.45            repair
3.46                    for l=1 to pc*popsize, repeat
3.47                            for j=2 to p, repeat
3.48                                    for k=1 to j, repeat
3.49                                            if facility[l,j]=facility[l,k],
                                                generate facility[l,j] ← a
                                                random number using lcgrand
                                                function (mode num_fac) and
                                                decrement j to check from
                                                beginning
3.50                            for j=p+2 to p+q, repeat
3.51                                    for k=p+1 to j, repeat
3.52                                            if facility[l,j]=facility[l,k],
                                                generate facility[l,j] ← a
                                                random number using lcgrand
                                                function (mode num_fac) and
                                                decrement j to check from
                                                beginning
3.53            fitness function calculation with crossover
3.54                    repeat steps 2.1- 2.57
3.55            mutation
3.56                    for k=1 to popsize, repeat
3.57                            for j=1 to p+q, repeat
3.58                                    if pm > a random generated number,
                                        facility[k,j] ← random number
3.59            repair
3.60                    repeat steps 3.46-3.52
3.61            fitness function calculation with crossover and mutation
3.62                    repeat steps 2.1- 2.57
3.63    stop clock
        end of iterations
        go to Step 4.
```

```
3.10c   parent selection – selection of best fitted population
3.11        for k=1 to popsize, repeat
3.12            calculate probability of selecting population k to
                mating pool prob[k] ← (r_fitness[k]-
                r_fit_min)/(r_fit_max-r_fit_min)
3.13        for l=1 to pc*popsize, repeat
3.14            for k=count (count indicates the chromosome we
                will decide to take or not) to popsize, repeat
3.15                if prob[k] > a random number
                    generated with lcgrand function, for j=1
                    to p+q, repeat
3.16                    set parent[l,j] ← facility[k,j]
3.17                    if count=popsize, count ← 0; so
                        one chromosome may be
                        selected more than once
3.18                    else, pass to the next
                        chromosome by incrementing
                        count and decide whether to
                        take it or not using prob[k]
3.19                        if count=popsize, count
                            ← 0; so one
                            chromosome may be
                            selected more than once
        crossover type selection
            generate a ← a random number using lcgrand function
            (mode 3), this allows hybrid crossover
3.20    if a = 1, crossover – 1-point
3.21        for l=1 to pc*popsize, repeat
3.22            for j=1 to p+q, repeat
3.23                define offspring[l,j] ← parent[l,j]
3.24        for l=1 to pc*popsize, repeat for every pair of
            chromosomes
3.25            for j=p/2 to p+q/2, repeat
3.26                change gene j's of sequential
                    chromosomes
3.27        for l=pc*popsize+1 to (1+pc)*popsize, repeat
3.28            for j=1 to p+q, repeat
3.29                while incrementing k, define
                    offspring[l,j] ← facility[k,j] whole
                    population is added to the mating pool
                    and the size of the population
                    isincreased to  (1+pc)*popsize
3.30    if a = 2, crossover – 2-point
3.31        for l=1 to pc*popsize, repeat
3.32            for j=1 to p+q, repeat
3.33                define offspring[l,j] ← parent[l,j]
3.34        for l=1 to pc*popsize, repeat for every pair of
            chromosomes
3.35            for j=p/3 to 2p/3, repeat
3.36                change gene j's of sequential
```

```
                                chromosomes
3.37            for l=1 to pc*popsize, repeat for every pair of
                chromosomes
3.38                    for j=p+q/3 to p+2q/3, repeat
3.39                            change gene j's of sequential
                                chromosomes
3.40            for l=pc*popsize+1 to (1+pc)*popsize, repeat
3.41                    for j=1 to p+q, repeat
3.42                            while incrementing k, define
                                offspring[l,j] ← facility[k,j] whole
                                population is added to the mating pool
                                and the size of the population
                                isincreased to  (1+pc)*popsize
3.43        if a = 0, crossover – uniform mask
3.44            generate mask[j] ← a random number using lcgrand
                function (mode 2)
3.45            for l=1 to pc*popsize, repeat
3.46                    for j=1 to p+q, repeat
3.47                            define offspring[l,j] ← parent[l,j]
3.48            for l=1 to pc*popsize, repeat for every pair of
                chromosomes
3.49                    if mask[j] =1, do not swap
3.50                    else swap gene j's of sequential chromosomes
3.51            for l=pc*popsize+1 to (1+pc)*popsize, repeat
3.52                    for j=1 to p+q, repeat
3.53                            while incrementing k, define
                                offspring[l,j] ← facility[k,j] whole
                                population is added to the mating pool
                                and the size of the population
                                isincreased to  (1+pc)*popsize
3.54        repair
3.55            for l=1 to pc*popsize, repeat
3.56                    for j=2 to p, repeat
3.57                            for k=1 to j, repeat
3.58                                    if offspring[l,j]=offspring[l,k],
                                        generate offspring[l,j] ← a
                                        random number using lcgrand
                                        function (mode num_fac) and
                                        decrement j to check from
                                        beginning
3.59                    for j=p+2 to p+q, repeat
3.60                            for k=p+1 to j, repeat
3.61                                    if offspring[l,j]=offspring[l,k],
                                        generate offspring[l,j] ← a
                                        random number using lcgrand
                                        function (mode num_fac) and
                                        decrement j to check from
                                        beginning
3.62        fitness function calculation with crossover
3.63        calculate off_x1[j] and off_x2[j]
3.64            for i=1 to (1+pc)*popsize, repeat
```

```
3.65                    for j=1 to num_fac, repeat
3.66                        for k=1 to p, repeat
3.67                            if offspring[i,k]=j, count
3.68                            else continue
3.69                        if count >= 1, off_x1[i,j]=1
3.70                        else off_x1[i,j] = 0
3.71                    for j=1 to num_fac, repeat
3.72                        for k=p+1 to p+q, repeat
3.73                            if offspring[i,k]=j, count
3.74                            else continue
3.75                        if count >= 1, off_x2[i,j]=1
3.76                        else off_x2[i,j] = 0
3.77            calculate fitness functions
3.78                for l=1 to (1+pc)*popsize, repeat
3.79                    for i=1 to num_dem, repeat
3.80                        for j=1 to num_fac, repeat
3.81                            if either cov[1][i,j] is 0 or
                                clinique j is unopened in the
                                population, increment j by 1 and
                                go to Step 3.80
3.82                            else for k=1 to num_fac, repeat
3.83                                if either cov[3][j,k] is 0
                                    or hospital k is
                                    unopened in the
                                    population, increment k
                                    by 1 and go to Step 3.82
3.84                                else calculate temp5 ←
                                    coverage of demand i by
                                    clinique j and then
                                    hospital k
3.85                        for j=1 to num_fac, repeat
3.86                            if either cov[2][i,j] is 0 or
                                hospital j is unopened in the
                                population, increment j by 1 and
                                go to Step 3.85
3.87                            else calculate temp5 ←
                                coverage of demand i by
                                hospital j
3.88                        find off_coverage [l,i] ← take  the
                            highest temp5
3.89                    find fitness value of the gene fitness_off[l] ←
                        sum off_coverage[l,i]'s
3.90                    for i=1 to num_fac, repeat
3.91                        for j=1 to num_fac, repeat
3.92                            if either cov[4][i,j] is 0 or
                                clinique j is unopened in the
                                population, increment j by 1 and
                                go to Step 2.29
3.93                            else for k=1 to num_fac, repeat
3.94                                if either cov[3][j,k] is 0
                                    or hospital k is
```

unopened in the population, increment k by 1 and go to Step 2.31

3.95 *else calculate temp5 ← coverage of demand i by clinique j and then hospital k*

3.96 *for j=1 to num_fac, repeat*

3.97 *if either cov[5][i,j] is 0 or hospital j is unopened in the population, increment j by 1 and go to Step 2.34*

3.98 *else calculate temp5 ← coverage of demand i by hospital j*

3.99 *find off_coverage[l,i] ← take the highest temp5*

3.100 *update fitness value of the gene fitness_off[l] ← fitness_off[l] + sum off_coverage[l,i]'s*

3.101 *keep population statistics*

3.102 *sort the population according to fitness function values*

3.103 *for k=1 to (1+pc)*popsize, repeat*

3.104 *for l=1,2, repeat*

3.105 *form sorted_fit_off[l,k] ← first rows indicate population k's and the second rows indicate fitness values of k's*

3.106 *for k=1 to (1+pc)*popsize, repeat*

3.107 *for l=k+1 to (1+pc)*popsize, repeat*

3.108 *if fitness[l] > fitness[k], swap both rows*

3.109 *else continue*

3.110 *fit_max ← first element of sorted_fit_off*

3.111 *fit_min ← last element of sorted_fit_off*

3.112 *for k=1 to popsize, repeat*

3.113 *fit_avg ← find average fitness value*

3.114 *for i=1 to p+q, repeat*

3.115 *keep best_gene[i] ← chromosome[i] of maximum fit gene*

3.116 *best solution track*

3.117 *if fit_max > best_soln[rep], update best_soln[rep]*

3.118 *for j=1 to p+q, repeat*

3.119 *form best_gene_rep[rep,j] ← genes of fit_max*

3.120 *mutation (note that although crossover is applied to the first pc*popsize number of chromosomes, mutation is applied to the joint population which has a size of (1+pc)*popsize)*

3.121 *for k=1 to (1+pc)*popsize, repeat*

3.122 *for j=1 to p+q, repeat*

3.123 *if pm > a random generated number, offspring[k,j] ← random number*

```
3.124       repair
3.125           for l=1 to (1+pc)*popsize, repeat
3.126           repeat steps 3.55-3.61
3.127       fitness function calculation with crossover and mutation
3.128           repeat steps 3.63-3.119
3.129       replacement: take the highest fitted popsize number of
            chromosomes, eliminate others
3.130           for k=1 to popsize, repeat
3.131               for j=1 to p+q, repeat
3.132                   facility[k,j] ← offspring[temp1,j] where
                        temp1 indicates the next sorted
                        chromosome
3.133   stop clock
        end of iterations
        go to Step 4.
```

```
3.10d       parent selection – conditional  replacement
3.11            for k=1 to popsize, repeat
3.12                calculate probability of selecting population k to
                    mating pool prob[k] ← (r_fitness[k]-
                    r_fit_min)/(r_fit_max-r_fit_min)
3.13            for k=1 to popsize, repeat
3.14                for j=1 to p+q, repeat
3.15                    define offspring[k,j] ← facility[k,j]
                        where offspring[k,j] is the transition
                        matrix, it is used only for selection
3.16                for l=1 to pc*popsize, repeat
3.17                    for k=count (count indicates the
                        chromosome we will decide to take or
                        not) to popsize, repeat
3.18                        if prob[k] > a random number
                            generated with lcgrand function,
                            for j=1 to p+q, repeat
3.19                            set facility[l,j] ←
                                offspring[k,j] where
                                facility[l,j] is used for
                                mating pool here
3.20                            if count=popsize,
                                count=0; so one
                                chromosome may be
                                selected more than once
3.21                        else, pass to the next
                            chromosome by incrementing
                            count and decide whether to
                            take it or not using prob[k]
3.22                            if count=popsize,
```

```
                                                    count=0; so one
                                                    chromosome may be
                                                    selected more than once
3.23            for k=1 to popsize, repeat
3.24                    for j=1 to p+q, repeat
3.25                            define offspring[k,j] ← facility[k,j] to
                                transmit mating pool to offspring[k,j]
                                because facility[k,j]  is the population
                                that will continue evolution and
                                offspring[k,j] is kept as the mating pool
                                matrix, in latter steps the evolved
                                facility[k,j] population  will be
                                compared with  the offspring[k,j]
                                population in conditional replacement
3.26            crossover type selection
3.27                    generate a ← a random number using lcgrand function
                        (mode 3), this allows hybrid crossover
3.28            if a = 1, crossover 1-point
3.29                    for l=1 to pc*popsize, repeat for every pair of
                        chromosomes of
3.30                            for j=p/2 to p+q/2, repeat
3.31                                    change gene j's of sequential facility[l,j]
                                        chromosomes
3.32            if a = 2, crossover – 2-point
3.33                    for l=1 to pc*popsize, repeat for every pair of
                        chromosomes
3.34                            for j=p/3 to 2p/3, repeat
3.35                                    change gene j's of sequential facility[l,j]
                                        chromosomes
3.36                    for l=1 to pc*popsize, repeat for every pair of
                        chromosomes
3.37                            for j=p+q/3 to p+2q/3, repeat
3.38                                    change gene j's of sequential facility[l,j]
                                        chromosomes
3.39            if a = 0, input mask crossover
3.40                    generate mask[j] ← a random number using lcgrand
                        function (mode 2)
3.41                    for l=1 to pc*popsize, repeat for every pair of
                        facility[l,j] chromosomes
3.42                            if mask[j]=1, do not swap
3.43                            else swap gene j's
3.44            repair
3.45                    for l=1 to pc*popsize, repeat
3.46                            for j=2 to p, repeat
3.47                                    for k=1 to j, repeat
3.48                                            if facility[l,j]=facility[l,k],
                                                generate facility[l,j] ← a
                                                random number using lcgrand
                                                function (mode num_fac) and
                                                decrement j to check from
                                                beginning
```

3.49 *for j=p+2 to p+q, repeat*
3.50 *for k=p+1 to j, repeat*
3.51 *if facility[l,j]=facility[l,k], generate facility[l,j] ← a random number using lcgrand function (mode num_fac) and decrement j to check from beginning*
3.52 *fitness function calculation with crossover*
3.53 *repeat steps 2.1- 2.57*
3.54 *calculate off_x1[j] and off_x2[j]*
3.55 *for i=1 to (1+pc)*popsize, repeat*
3.56 *for j=1 to num_fac, repeat*
3.57 *for k=1 to p, repeat*
3.58 *if offspring[i,k]=j, count*
3.59 *else continue*
3.60 *if count >= 1, off_x1[i,j]=1*
3.61 *else off_x1[i,j] = 0*
3.62 *for j=1 to num_fac, repeat*
3.63 *for k=p+1 to p+q, repeat*
3.64 *if offspring[i,k]=j, count*
3.65 *else continue*
3.66 *if count >= 1, off_x2[i,j]=1*
3.67 *else off_x2[i,j] = 0*
3.68 *calculate fitness functions of mating pool offspring[k,j] in order to compare with evolved population facility[k,j]*
3.69 *for l=1 to (1+pc)*popsize, repeat*
3.70 *for i=1 to num_dem, repeat*
3.71 *for j=1 to num_fac, repeat*
3.72 *if either cov[1][i,j] is 0 or clinique j is unopened in the population, increment j by 1 and go to Step 3.80*
3.73 *else for k=1 to num_fac, repeat*
3.74 *if either cov[3][j,k] is 0 or hospital k is unopened in the population, increment k by 1 and go to Step 3.82*
3.75 *else calculate temp5 ← coverage of demand i by clinique j and then hospital k*
3.76 *for j=1 to num_fac, repeat*
3.77 *if either cov[2][i,j] is 0 or hospital j is unopened in the population, increment j by 1 and go to Step 3.85*
3.78 *else calculate temp5 ← coverage of demand i by hospital j*

```
3.79                        find off_coverage [l,i] ← take  the
                            highest temp5
3.80                    find fitness value of the gene fitness_off[l] ←
                        sum off_coverage[l,i]'s
3.81                    for i=1 to num_fac, repeat
3.82                        for j=1 to num_fac, repeat
3.83                            if either cov[4][i,j] is 0 or
                                clinique j is unopened in the
                                population, increment j by 1 and
                                go to Step 2.29
3.84                            else for k=1 to num_fac, repeat
3.85                                if either cov[3][j,k] is 0
                                    or hospital k is
                                    unopened in the
                                    population, increment k
                                    by 1 and go to Step 2.31
3.86                                else calculate temp5 ←
                                    coverage of demand i by
                                    clinique j and then
                                    hospital k
3.87                        for j=1 to num_fac, repeat
3.88                            if either cov[5][i,j] is 0 or
                                hospital j is unopened in the
                                population, increment j by 1 and
                                go to Step 2.34
3.89                            else calculate temp5 ←
                                coverage of demand i by
                                hospital j
3.90                        find off_coverage[l,i] ← take  the
                            highest temp5
3.91                    update fitness value of the gene fitness_off[l] ←
                        fitness_off[l] + sum off_coverage[l,i]'s
3.92            conditional replacement
3.93                for k=1 to popsize, repeat
3.94                    if off_fitness[k]>fitness[k] for j=1 to p+q,
                        repeat
3.95                        facility[k,j] ← offspring[k,j], replace
                            evolved population with mating pool
3.96                    fitness[k] ← off_fitness[k], update fitness
                        function values of the replaced chromosomes
3.97                    else do nothing
3.98            keep population statistics
3.99                repeat steps 2.40-2.57
3.100           mutation
3.101               for k=1 to popsize, repeat
3.102                   for j=1 to p+q, repeat
3.103                       if pm > a random generated number,
                            facility[k,j] ← random number
3.104           repair
3.105               repeat steps 3.45-3.51
3.106           fitness function calculation with crossover and mutation
```

3.107 repeat steps 2.1- 2.57
3.108 stop clock
end of iterations
go to Step 4.

4 statistics
4.1 write fit_max
4.2 write fit_min
4.3 write fit_avg
4.4 write best_soln[rep]
4.5 for j=1 to p+q, repeat
4.6 write gene j of best_soln[rep]
4.7 write total time elapsed
4.8 for t=1 to 30, repeat
4.9 write time elapsed for each section
end of replications

APPENDIX D

GA EXAMPLE

Problem parameters of example in Section 4.4 are re-represented in Table D.1, and coordinates of the nodes are shown in Table D.2.

Table D.1 – Problem parameters

# of nodes	# of demand nodes	# of potential facility sites	# of hospitals	# of health centers	S^1	S^2	S^3	T^1	T^2	T^3	w^1	w^2	w^3	δ
50	-	50	6	14	30	60	80	50	80	100	1	1	1	1

Table D.2 – Coordinates of the nodes of the problem

node	x-coordinate	y-coordinate	node	x-coordinate	y-coordinate	node	x-coordinate	y-coordinate
			18	813	353	35	735	480
1	685	117	19	402	298	36	266	175
2	247	312	20	44	427	37	729	211
3	874	185	21	352	256	38	290	189
4	193	463	22	837	280	39	271	74
5	690	238	23	55	41	40	384	162
6	750	301	24	371	459	41	315	180
7	190	404	25	414	310	42	540	419
8	374	413	26	164	119	43	331	490
9	837	492	27	622	223	44	367	446
10	692	302	28	587	469	45	206	218
11	36	243	29	493	364	46	212	350
12	150	55	30	741	229	47	22	429
13	854	428				48	996	496
14	319	240	31	95	84	49	244	68
15	713	107	32	259	231	50	505	313
16	144	97	33	125	281			
17	18	84	34	441	211			

Intranodal distances are calculated according to Euclidean metrics. They are presented in Table D.3.

Table D.3 – Intranodal distances of the problem

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
1	0	479	201	601	121	195	572	429	405	185	661	539	354	386	30	541	668	268	336	712	361	223	635	464	333	521	123	365	313	125	591	441	584	261	366	423	104	402	416	304	375	335	514	458	490	527	733	490	444	266
2	479	0	640	160	449	503	108	162	617	445	222	275	618	102	509	238	323	567	156	233	119	591	332	192	167	210	385	375	251	501	274	82	126	219	516	138	492	130	239	203	148	312	197	180	103	52	254	771	244	258
3	201	640	0	736	191	170	718	550	309	216	840	736	244	558	179	735	862	179	485	865	527	102	832	573	477	713	255	404	421	140	786	617	755	434	326	608	147	584	613	491	559	408	623	570	669	682	886	334	641	391
4	601	160	736	0	546	580	59	188	645	524	270	410	662	256	630	369	417	630	266	153	261	670	444	178	269	345	492	394	316	596	391	241	194	354	542	297	592	291	397	356	308	350	141	175	245	115	174	804	398	346
5	121	449	191	546	0	87	527	361	293	64	654	570	251	371	133	564	689	168	294	673	338	153	665	388	285	539	70	253	234	52	615	431	567	250	246	429	47	403	450	315	379	235	439	384	484	491	695	400	477	200
6	195	503	170	580	87	0	569	392	210	58	716	648	164	435	198	639	763	82	348	717	401	90	742	411	336	614	150	234	265	73	690	496	625	322	180	500	92	473	530	392	452	241	460	410	550	540	739	314	557	245
7	572	108	718	59	527	569	0	184	653	512	223	351	664	209	601	310	363	625	237	148	219	659	387	189	243	286	468	402	306	578	334	186	139	317	550	241	573	237	340	310	257	350	165	182	187	58	170	811	340	328
8	429	162	550	188	361	392	184	0	470	337	378	422	480	182	457	391	485	443	118	330	159	482	490	46	110	361	312	220	129	411	431	215	282	213	367	261	408	239	354	251	240	166	88	34	257	174	352	628	369	165
9	405	617	309	645	293	210	653	470	0	239	839	814	66	576	404	798	915	141	476	796	539	212	903	467	460	769	344	251	367	280	847	634	743	486	103	653	301	625	704	560	608	306	506	472	688	641	817	159	729	377
10	185	445	216	524	64	58	512	337	239	0	659	596	205	378	196	585	708	131	290	660	343	147	688	357	278	559	106	197	208	88	636	439	567	267	183	445	98	418	479	338	396	192	407	355	493	482	682	361	505	187
11	661	222	840	270	654	716	223	378	839	659	0	220	839	283	691	182	160	785	370	184	316	802	203	399	384	178	586	596	473	705	170	223	97	406	738	240	694	260	289	357	286	534	385	388	172	206	187	993	272	474
12	539	275	736	410	570	648	351	422	814	596	220	0	797	251	565	42	135	727	350	387	285	723	96	461	367	66	501	602	462	616	62	207	227	330	723	167	600	194	122	257	207	533	471	447	172	301	395	954	95	439
13	354	618	244	662	251	164	664	480	66	205	839	797	0	567	351	783	904	85	470	810	531	149	888	484	456	756	310	270	367	229	833	627	744	467	130	640	250	613	682	540	593	314	527	487	681	647	832	157	708	367
14	386	102	558	256	371	435	209	182	576	378	283	251	567	0	416	226	339	507	101	333	37	520	331	225	118	197	303	353	214	422	273	61	198	125	480	84	411	59	173	102	60	284	250	212	115	153	352	724	188	200
15	30	509	179	630	133	198	601	457	404	196	691	565	351	416	0	569	695	266	365	742	391	213	661	491	361	549	147	383	338	125	618	471	613	291	374	452	105	431	443	334	405	357	541	484	519	557	762	481	471	293
16	541	238	735	369	564	639	310	391	798	585	182	42	783	226	569	0	127	716	327	345	262	717	105	427	344	30	494	578	439	611	51	177	185	318	704	145	596	173	129	249	190	510	435	414	136	262	354	941	104	421
17	668	323	862	417	689	763	363	485	915	708	160	135	904	339	695	127	0	839	440	344	376	842	57	515	456	150	620	687	551	737	77	282	224	442	819	264	722	292	253	374	312	620	513	503	231	329	345	1061	227	538
18	268	567	179	630	168	82	625	443	141	131	785	727	85	507	266	716	839	0	415	773	471	77	820	455	401	690	231	254	320	143	767	567	692	398	149	575	165	548	610	470	527	281	501	456	622	601	795	232	636	311
19	336	156	485	266	294	348	237	118	476	290	370	350	470	101	365	327	440	415	0	381	65	435	432	164	17	298	232	252	112	346	374	158	278	95	379	183	338	156	259	137	147	184	205	152	212	197	402	626	279	104
20	712	233	865	153	673	717	148	330	796	660	184	387	810	333	742	345	344	773	381	0	352	807	386	329	388	331	613	545	453	725	347	291	167	452	693	336	718	342	420	431	367	496	294	324	264	185	393	955	411	475
21	361	119	527	261	338	401	219	159	539	343	316	285	531	37	391	262	376	471	65	352	0	486	367	204	82	233	272	317	178	390	309	96	228	100	444	118	380	91	199	99	85	249	235	191	151	169	373	687	217	163
22	223	591	102	670	153	90	659	482	212	147	802	723	149	520	213	717	842	77	435	807	486	0	818	499	424	692	222	313	354	109	767	580	712	402	225	581	128	555	602	468	531	328	548	498	634	629	829	268	630	334
23	635	332	832	444	665	742	387	490	903	688	203	96	888	331	661	105	57	820	432	386	367	818	0	524	449	134	595	683	544	711	59	279	250	422	809	250	695	278	219	351	295	615	527	511	233	347	389	1045	191	526
24	464	192	573	178	388	411	189	46	467	357	399	461	484	225	491	427	515	455	164	329	204	499	524	0	155	398	345	216	155	436	466	254	304	258	365	303	436	282	398	297	285	174	51	14	292	193	350	626	411	198
25	333	167	477	269	285	336	243	110	460	278	384	367	456	118	361	344	456	401	17	388	82	424	449	155	0	315	225	235	96	337	391	174	290	103	363	200	330	173	276	151	163	167	198	144	227	206	410	611	296	91
26	521	210	713	345	539	614	286	361	769	559	178	66	756	197	549	30	150	690	298	331	233	692	134	398	315	0	470	549	410	587	77	147	167	292	676	116	572	144	116	224	163	481	407	385	108	236	341	913	95	392
27	123	385	255	492	70	150	468	312	344	106	586	501	310	303	147	494	620	231	232	613	272	222	595	345	225	470	0	248	191	119	545	363	500	181	281	359	108	334	381	246	310	212	395	339	416	429	634	463	409	148
28	365	375	404	394	253	234	402	220	251	197	596	602	270	353	383	578	687	254	252	545	317	313	683	216	235	549	248	0	141	285	625	405	499	296	148	435	295	408	506	368	397	69	257	221	456	393	566	410	528	176
29	313	251	421	316	234	265	306	129	367	208	473	462	367	214	338	439	551	320	112	453	178	354	544	155	96	410	191	141	0	282	487	269	377	162	268	295	281	268	365	230	256	72	205	150	322	281	475	520	387	52
30	125	501	140	596	52	73	578	411	280	88	705	616	229	422	125	611	737	143	346	725	390	109	711	436	337	587	119	285	282	0	662	482	618	301	251	478	22	453	495	363	429	277	486	432	535	543	746	369	522	251
31	591	274	786	391	615	690	334	431	847	636	170	62	833	273	618	51	77	767	374	347	309	767	59	466	391	77	545	625	487	662	0	220	199	369	753	194	647	221	176	299	240	557	470	453	174	291	353	991	150	470
32	441	82	617	241	431	496	186	215	634	439	223	207	627	61	471	177	282	567	158	291	96	580	279	254	174	147	363	405	269	482	220	0	143	183	537	56	470	52	157	143	76	338	269	241	55	128	309	783	164	259
33	584	126	755	194	567	625	139	282	743	567	97	227	744	198	613	185	224	692	278	167	228	712	250	304	290	167	500	499	377	618	199	143	0	324	642	176	608	189	253	285	215	437	293	293	103	111	180	897	244	381

Table D.3 (continued) – Intranodal distances of the problem

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
34	261	219	434	354	250	322	317	213	486	267	406	330	467	125	291	318	442	398	95	452	100	402	422	258	103	292	181	296	162	301	369	183	324	0	398	179	288	153	218	75	130	230	300	246	235	268	472	624	243	120
35	366	516	326	542	246	180	550	367	103	183	738	723	130	480	374	704	819	149	379	693	444	225	809	365	363	676	281	148	268	251	753	537	642	398	0	559	269	532	617	474	516	204	404	370	590	539	715	261	641	284
36	423	138	608	297	429	500	241	261	653	445	240	167	640	84	452	145	264	575	183	336	118	581	250	303	200	116	359	435	295	478	194	56	176	179	559	0	464	28	101	119	49	367	322	289	74	183	352	797	109	276
37	104	492	147	592	47	92	573	408	301	98	694	600	250	411	105	596	722	165	338	718	380	128	695	436	330	572	108	295	281	22	647	470	608	288	269	464	0	440	478	348	415	281	486	432	523	535	740	391	506	246
38	402	130	584	291	403	473	237	239	625	418	260	194	613	59	431	173	292	548	156	342	91	555	278	282	173	144	334	408	268	453	221	52	189	153	532	28	440	0	117	98	27	340	304	268	89	179	360	770	129	248
39	416	239	613	397	450	530	340	354	704	479	289	122	682	173	443	129	253	610	259	420	199	602	219	398	276	116	381	506	365	495	176	157	253	218	617	101	478	117	0	143	115	437	420	384	158	282	434	839	28	334
40	304	203	491	356	315	392	310	251	560	338	357	257	540	102	334	249	374	470	137	431	99	468	351	297	151	224	246	368	230	363	299	143	285	75	474	119	348	98	143	0	71	301	332	285	187	255	450	697	169	194
41	375	148	559	308	379	452	257	240	608	396	286	207	593	60	405	190	312	527	147	367	85	531	295	285	163	163	310	397	256	429	240	76	215	130	516	49	415	27	115	71	0	328	310	271	115	199	385	751	133	232
42	335	312	408	350	235	241	350	166	306	192	534	533	314	284	357	510	620	281	184	496	249	328	615	174	167	481	212	69	72	277	557	338	437	230	204	367	281	340	437	301	328	0	221	175	390	335	518	462	459	112
43	514	197	623	141	439	460	165	88	506	407	385	471	527	250	541	435	513	501	205	294	235	548	527	51	198	407	395	257	205	486	470	269	293	300	404	322	486	304	420	332	310	221	0	57	299	184	315	665	431	248
44	458	180	570	175	384	410	182	34	472	355	388	447	487	212	484	414	503	456	152	324	191	498	511	14	144	385	339	221	150	432	453	241	293	246	370	289	432	268	384	285	271	175	57	0	279	182	345	631	398	192
45	490	103	669	245	484	550	187	257	688	493	172	172	681	115	519	136	231	622	212	264	151	634	233	292	227	108	416	456	322	535	174	55	103	235	590	74	523	89	158	187	115	390	299	279	0	132	280	837	155	314
46	527	52	682	115	491	540	58	174	641	482	206	301	647	153	557	262	329	601	197	185	169	629	347	193	206	236	429	393	281	543	291	128	111	268	539	183	535	179	282	255	199	335	184	182	132	0	206	797	284	295
47	733	254	886	174	695	739	170	352	817	682	187	395	832	352	762	354	345	795	402	393	373	829	389	350	410	341	634	566	475	746	353	309	180	472	715	352	740	360	434	450	385	518	315	345	280	206	0	976	424	497
48	490	771	334	804	400	314	811	628	159	361	993	954	157	724	481	941	1061	232	626	955	687	268	1045	626	611	913	463	410	520	369	991	783	897	624	261	797	391	770	839	697	751	462	665	631	837	797	976	0	865	524
49	444	244	641	398	477	557	340	369	729	505	272	95	708	188	471	104	227	636	279	411	217	630	191	411	296	95	409	528	387	522	150	164	244	243	641	109	506	129	28	169	133	459	431	398	155	284	424	865	0	358
50	266	258	391	346	200	245	328	165	377	187	474	439	367	200	293	421	538	311	104	475	163	334	526	198	91	392	148	176	52	251	470	259	381	120	284	276	246	248	334	194	232	112	248	192	314	295	497	524	358	0

Demand weights of nodes are presented in Table D.4.

Table D.4 – Demand weights of nodes of the problem

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