

# Allocation Model of Health Care Facilities with Genetic Algorithm

遺伝的アルゴリズムを用いた医療施設の配置モデル

Fauzy Ammari\* Suzuki Takaji\*\* Miyagi Toshihiko\*\*\*

## 1. Introduction

In many countries efficiently and loss costly provision of health care facilities is an important public policy. A common planning problem is to locate the facilities to maximize services to an existing population. These services are offered in a hierarchical way in order to satisfy different level of demands as an example describe in figure 1.

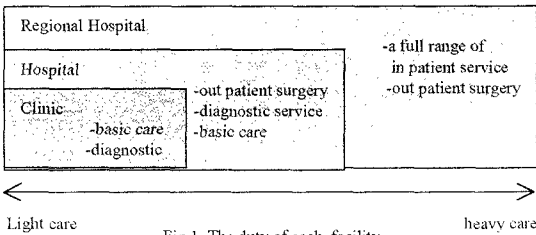


Fig 1. The duty of each facility

In the hierarchical health care facilities, cover associated with a certain distance in which have strong relation to the save of patients, as an illustration in figure 2. Good planning of these facilities allow the covering of maximum area.

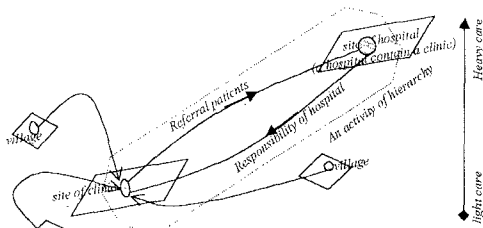


Fig 2 Model patient flows

This study aims at proposing a solution method to the allocation of hierarchy systems of health care facilities. The problem could be formulate in term of integer linear programming. Motivated by Genetic Algorithm (GA), based on computation time and larger scale problem.

Keywords: Hierarchical Facility Location, Genetic Algorithm.

\*\*\*Member of JSCE, Faculty of Regional Studies.

\*\* Member of JSCE, Research Associate, Faculty of Engineering.

\* Student, Graduate School of Engineering Gifu University.

## 2. An Allocation Model of Health Care Facilities

A model to minimize total patients weighted distance between a demand node (village etc.) and a nearest health care facility could be described as follows: suppose we want to locate  $H$  hospitals and  $C$  clinics in any area. Because of the death risk of patients, each clinic must be located within a distance  $D_{hc}$  of the hospital. The model as follows;

$H$  = maximum number of hospitals to be located  
 $C$  = maximum number of clinics to be located  
 $d_{ij}$  = distance between node  $i$  and candidate hospital  $j$   
 $d_{ik}$  = distance between node  $i$  and candidate clinic  $k$   
 $l_{jk}$  = distance between candidate hospital  $j$  and candidate clinic  $k$   
 $h_i$  = population (proportional to patient) in node  $i$   
 $D_{hc}$  = critical coverage distance between hospitals and clinics

### Input Variables

$a_{jk} = \begin{cases} 1: & \text{if candidate site clinic } k \text{ is within } D_{hc} \text{ distance} \\ & \text{unit of candidate hospital } j \\ 0: & \text{if not} \end{cases}$

### Decision Variables

$X_j = \begin{cases} 1: & \text{if candidate hospital site } j \text{ is selected} \\ 0: & \text{if not} \end{cases}$        $W_j = \begin{cases} 1: & \text{if demands at node } i \text{ are satisfies} \\ & \text{by a hospital at candidate site } j \\ 0: & \text{if not} \end{cases}$   
 $Y_k = \begin{cases} 1: & \text{if candidate clinic site } k \text{ is selected} \\ 0: & \text{if not} \end{cases}$        $V_k = \begin{cases} 1: & \text{if demands at node } i \text{ are satisfies} \\ & \text{by a clinic at candidate site } k \\ 0: & \text{if not} \end{cases}$

$$\text{minimize } \sum_i \sum_k h_i d_{ik} V_{ik} + \sum_i \sum_j h_i d_{ij} W_{ij} \quad (1.a)$$

$$\text{s.t. } \sum_j X_j \leq H \quad (1.b)$$

$$\sum_k Y_k \leq C \quad (1.c)$$

$$\sum_j W_{ij} + \sum_k V_{ik} = 1 \quad \forall i \quad (1.d)$$

$$l_{jk} a_{jk} \leq D_{hc} \quad \forall j, k \quad (1.e)$$

$$X_j \leq \sum_k a_{jk} Y_k \quad \forall k \quad (1.f)$$

$$W_{ij} - X_j \leq 0 \quad \forall i, j \quad (1.g)$$

$$V_{ik} - Y_k \leq 0 \quad \forall i, k \quad (1.h)$$

$$X_j, Y_k, W_{ij}, V_{ik} = 0, 1 \quad \forall i, j, k \quad (1.i)$$

Constraints (1.e) and constraints (1.f) state the guarantee of coverage distance between clinic and hospital to which the hierarchical system can be applied. Constraints(1.g) and (1.h) link the location variables and allocation variables.

## 3. Genetic Algorithm (GA) Approach

Based on constraints, genes are established as 0 and 1, where "1" means locate and "0" otherwise.

Generate gene at random, sum of "1" are checked in each chromosome. we only use chromosome with sum equal to number of facility. In our approach, a pair chromosomes contains an information where to locate hospitals and clinics. Each individual has two chromosome, the first for site of hospitals and second for site of clinics. Chromosome of clinic will be use if it's candidate sites are satisfies a coverage distance but not in same site with hospital. Then, under minimum path, each node  $i$  to be assigned to one facility (constraints (1.d),(1.g). and(1.h)). The objective function can be calculated by a given data and a

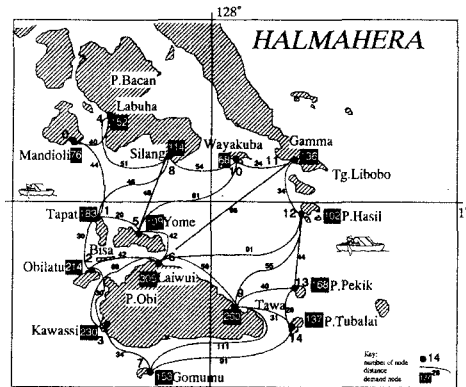


fig.4. Network with demand node and distance unit in km

original map of Halmahera Island Indonesia. fig.4. Two hospitals and six clinics will be located, with coverage distance equal 155. Length of chromosome equal to total number of nodes.

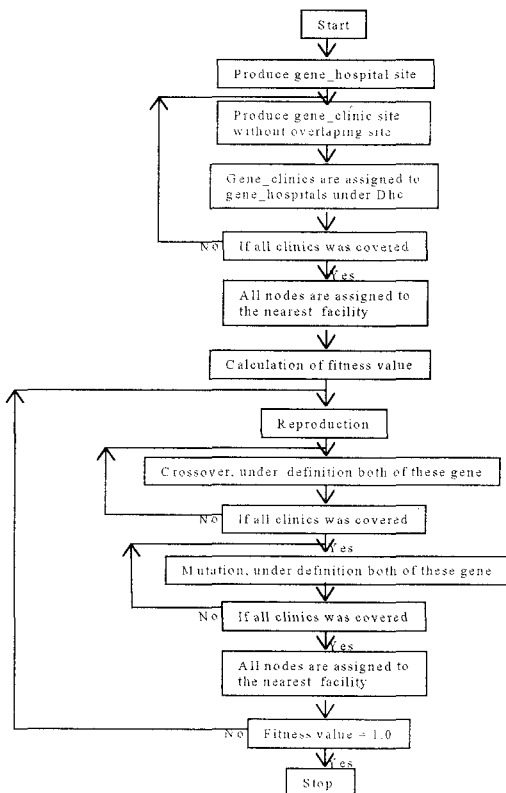
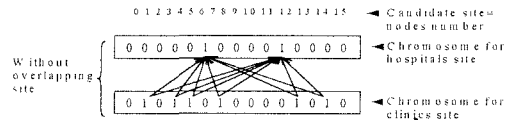


Fig. 3. Flowchart of GA approach

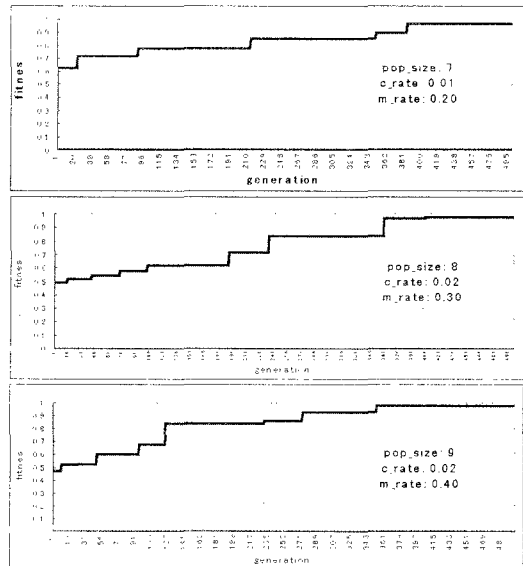


Fig. 5. GA Performance

result of each node  $i$  are satisfies by a facility as an allocation variables. GA operations still kept in the constraints as described in flowchart, fig. 3.

#### 4. An Application of GA Approach

We attempt to show the GA performance in a network with 15 nodes. area without hospital in

Hospitals will be located at node 5 and 10, clinics at node 2,3,4,6,9, and 11. Objective equal 35279.

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