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GENROUTE: A genetic algorithm printed wire board (printed wire board (PWB) Router)

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GENROUTE:
A Genetic Algorithm Printed Wire Board (Printed Wire Board (PWB) Router)

By

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A thesis, submitted to
The Faculty of the Department of Computer Science,
in partial fulfillment of the requirements for the degree of
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To Rochester Institute of Technology

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Dedication

This is not a memorial therefore I will not actually dedicate this to anyone.

However, I do want anyone who accesses this information to know that I am sincerely grateful to my wife, Caroline, for working with me to complete this degree. If it were not for her help and support I would never have completed this work and you would never have the opportunity to utilize this research; her unselfishness has enabled both of us. During my pursuit of the degree she was extremely patient and supportive of my personal and singular need to acquire this degree. She carried my responsibilities to our family for the several years it took to complete this.

I owe her and our two children, Sean and Robert, a lot more than I care to describe here. For what it is worth I am publishing this acknowledgement just as

"Foot prints in the sand ..."

leaves an impression and a change.

Thank you

Statistical Genetic Algorithms Applied to NP-Hard Search Problems

An investigation of genetic algorithms applied to solving NP-Hard combinatorial optimization problems. The problem cases investigated here are, in least to most significant order, *N Queens,and PWB Routing*. Included in the discussions are algorithm implementations and optimization techniques based upon problem schema and characteristics. Solution algorithm efficiency will be recorded and quantified by testing solution algorithm variations upon a chosen controlled set of problems.

Preface

The major effort of this thesis was to develop an electronic circuit routing system that utilizes genetic algorithms to perform Printed Wire Board (PWB) routing rather than brute force exhaustive searching methods. This problem can be classified as an NP-Hard optimization problem searching a large solution space. Some desirable characteristics of an electronic routing system are that it:

Minimize the number of potential solutions
Minimize the number of board layers and tap holes
Minimize trace lengths and the number of "jogs"
Minimize trace cross-talk and the board capacitance

My goal was to develop a system that will work for a reasonable but small number of components (connections) and then investigate and report upon how characteristics of my representation and my heuristics and decision rule functions affect the efficiency of solution generation. I measured efficiency by time required to converge upon a solution, simplicity of the solution, and the number of evolutions required to generate the solution.

This routing system is a simulation package developed to gain an understanding of how genetic algorithms can be applied to solving NP-Hard optimization problems. With this goal in sight, the system restricted the number of components it will allow within a design as well as what the components are. These restrictions imposed to make the task a tractable one. My intent was to supply the GA routing system with moderate size designs and be able to produce solutions to the PWB routing problem in a reasonable amount of time.

I iterated the simulation process many times for a few different electronic designs in order to learn and evaluate characteristics of genetic solution algorithms. This enabled me to observe the effects of the heuristic predictors of the decision algorithm. Features of interest here are annealing techniques and rules applied to the predictor functions. Additional factors in modifying and testing decision functions and annealing rules were distances between connections, number of trace lines in a bus path, the number of junctions / connections per trace, and neighboring components.

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Introduction

Emphasis of this thesis was the investigation of convergent classes of GENETIC ALGORITHMS with finite populations, N operators and M degrees of freedom applied to NP-Hard combinatorial search space problems. By finite population I am referring to the entire search space; the complete and exhaustive set of entries valid within the problem statements and conditions. The algorithms, during solution generation, may select any proper subset of the population (search space) to evaluate for convergence to a solution. This subset is sometimes called the working population. The term convergent, here, means that the algorithm will iterate through population subsets searching out a solution to a predetermined accuracy within a reasonable period of time based upon the problem. N operators refers to the number of functions / operations that an algorithm will apply to change the search space while converging upon the solution. M degrees of freedom refer to the number of possible states that each population entry and condition in the problem can change to. By identifying the algorithm operators and restricting the possible condition states, we are bounding the possible solution space to be finite.

Solution algorithms to NP-Hard optimization problems of this nature suffer from combinatorial explosion in their search space as well as many other problems, and are best solved with a strategy that can be referred to as constraint satisfaction, e.g., how do I identify a set of conditions that, when applied to the population, leads to a solution even though all conditions sometimes cannot be met. Generally, it is not easy to identify all of the necessary and sufficient constraints in order to define an exact solution, let alone test all population entries and

exhaustively search the solution space to converge on an answer. Testing the union and intersection of problem conditions to identify a solution are typically the best we can do, but this is usually inadequate to completely isolate a solution because of the number and complexity of the conditions of the problems.

Because of a problem's complexity and computational restrictions, there is the need to break down the problem and solution method into more, less complex components. The problem structure and statement components can be described as:

1) A crisp problem and problem statement
2) An appropriate problem and computational representation
3) A solution tolerance / accuracy range
4) A graceful failure or fall back scheme

No matter what the solution technique is, I believe all problems require a rigorous investigation and description of each of the four problem categories listed above. With the growing popularity of AI techniques being applied to problems, we are seeing a significant amount of investigation and effort being placed upon bullets number two and three. These four problem requirements will be referred to throughout subsequent discussions and example problems.

Adequately describing the four categories required in comprehending a typical NP-Hard problem is not trivial. Factors as simple as how do we model and represent 3D objects in 2D spaces may hinder the problem description. Other difficulties of a problem investigation relate to implementation techniques, which have constraints within themselves. For example, do you use matrices or vectors as a data representation model, and should the data be binary or multivalued. One must also beware of implementation accuracy (are you attempting to get

double precision accuracy out of single precision numbers), resource requirements and errors introduced by the algorithm itself (invalid population conditions). In this thesis I intend to investigate and discuss how the above four categories operate to properly specify a problem and its solution in terms of genetic algorithms.

In working to solve NP-Hard search space problems and recognizing the above four conditions, I believe that genetic algorithms are reasonable techniques and representation models. Inherent in genetic algorithms is the ability to describe and act upon vectors of complex relationships that allows for convergence upon a solution without having to represent or search an entire population space. This modeling and search characteristic of genetic algorithms is a significant asset to the resource requirement constraints and representation needs of solution algorithms to NP-Hard problems.

The class of genetic algorithms I intend to investigate here has a strong foundation based in Monte Carlo[1] and statistical methods[2]. These techniques lend themselves very nicely to modeling complex nondeterministic interactions. Other genetic algorithm modeling characteristics are similar to simulated annealing techniques described in current neural network research, where there is an ability to control the amount of "heat" / change that occurs over time, given certain conditions in the solution set. Another feature of the genetic algorithm representation is that the implementor can incorporate other problem solution techniques such as greedy algorithm techniques, hill climbing techniques, or pseudo random search techniques into the GA. The genetic algorithm's inherent ability to combine multiple problem solution techniques, allows for hybrid

1. SIAM Series #3, Symposium on applied probability and Monte Carlo Methods, 1967
2. Binder, Kurt, Monte Carlo methods in statistical physics, 1/1/79, QC 174 8S.m64 M66

approaches to problem solutions that can work over a wide range of problems classes.

Genetic Algorithms are well suited for solving NP-Hard optimization problems of Higher Order Dimensional Spaces (HODS) that can be represented by vectors and matrixes. An example of an HODS problem could be human interactions, specifically the complex relations and interactions that occur and regulate our daily activities. Characteristics such as weather, time of day, place and general mood have an effect on how individuals act and react to situations. Each characteristic has many possible conditions (e.g. weather: sunny, damp, ...) and each condition will act upon an individual differently at different times. All of these factors and conditions can be represented as a series of vectors and matrixes that, when combined, represent a multidimensional, highly complex set of relationships. If one were to picture / model these relationships, they would have to be represented in high order dimensions (e.g. contour plots, 3D plots, ...). In this thesis I intend to investigate and discuss the effects of problem representation/implementation on algorithm efficiency.

The types of problems that I will be investigating in this thesis are referred to as NP-Hard combinatorial search space problems. Examples of some are the Traveling Salesman Problem, Eight Queens problem, and even electronic design placement and routing algorithms for chip and board designs. Genetic algorithms also have been applied to applications that perform document storage and retrieval (Michael Gordon ACM 1988[3]), pattern and feature recognition (Lee 1984), as well as simulations and game treeing problems. These problems all have large search spaces from which an algorithm must find either a unique

3. Gorden, M., D., Adaptive subject indexing in document retrieval. (PHD dissertation at University of Michigan), Dissertation abstracts international, 45(2), 611B

solution or one of many possible solutions within an acceptable tolerance level. In order for an algorithm to solve these types of problems successfully, it must be able to search pieces of the solution space and converge upon an answer. A difficulty with many of these types of problems is the fact that an algorithm typically does not know the exact, correct answer until that answer is found. This is because the algorithm must iterate through the search space on a trial and error basis, applying constraint satisfaction and optimization methods to determine if a satisfactory solution has been reached. Figure 1.1 is an example of some simple multi-modal search spaces might look like.

Combinatorial search and optimization[5] problems have similar characteristics in that they combine multivariat conditions into complex relationships that generally need to be represented in higher ordered dimensional space by sequences of vectors and matrices. These matrices then can be manipulated by an algorithm that will cause them to change to different working sets of the population and converge upon a solution satisfying the set of solution constraints. Genetic algorithms are well suited for operating upon problems whose representation can be vectors and matrices.

The efficient convergence requirement upon optimization problems is the basis for most of the algorithm research on NP-Hard combinatorial problems . A successful algorithm must be able to converge to a solution set within the bounds of the population description, without causing the population to diverge and generate invalid entries, or to converge to a wrong/false solution. Given that we desire the algorithm to do something useful, like converge upon a solution, we utilize constraints by which we measure and rank potential solutions. For example, we

5. Booker, L., B., Improving search in genetic algorithms, L. Davis book on Genetic algorithms and simulated annealing, p 61-74, London Press.

fix the working population size to be finite and manageable, but we also must restrict the number and type of operators applied to the population. Constraints such as these help us to make the solution algorithm tractable and easier to manage. Other constraints are accuracy tolerance ranges for solutions or simple tests such as, does the solution work. Solution algorithms must incorporate an adequate balance of constraints and degrees of freedom (randomness) because, an improper amount of either can cause an algorithm never to converge upon a solution.

DeJong in 1975[6] published papers investigating the problem of premature convergence due to inadequate population modeling and prediction trends. In light of the convergence problem and its criticality to the solution, Holland in 1975[7] and later Goldberg & Lingle in 1985[8] published works identifying reordering procedures specifically for genetic algorithms. Their work attempted to address convergence problems of stochastic search space algorithms more adequately. This researches and includes aspects of these and other such studies in my development and characterization of genetic algorithms so that they operate effectively and efficiently.

Problems inherent in algorithms that search large spaces and implement stochastic, non-exhaustive solution methods are not limited to convergence or divergence problems, but also the effects of randomness on population testing and backtracking. What I am referring to here by randomness is the measure or rate of uncontrolled and nondeterministic change in the working population. If there is too much random change in the population entries, then the solution algorithm

6. DeJong, k., A., An analysis of the behavior of a class of genetic adaptive systems, Dissertation abstracts international 36(10), 51408.

7. Holland, J., H., Adaptation in natural and artificial systems, University of Michigan Press (1975)

8. Goldberg, D., E., & Lingle, R., Alleles, Loci and the traveling salesman problem, Proceedings of an international conference on genetic algorithms and their applications pps154-159

may exhibit a thrashing behavior and never converge. Conversely, if there is not enough randomness, then the algorithm may stagnate or converge on something other than the solution set. Another type of randomness is that encountered in the problem itself, not in the solution algorithm. For example, in the human interaction problem suggested earlier, how do we properly account for characteristics such as place and time. It is obvious that not all events can occur in all places or at any arbitrary time. A solution algorithm must successfully model the valid combinations and omit those that are not.

In NP-Hard problems with solutions containing conflicting requirements, there must be an acceptable solution accuracy or tolerance in order for algorithms to function successfully. As mentioned earlier, there are many factors and characteristics of NP-Hard problems that require careful control and balance in order for an algorithm to generate working populations that converge upon a solution. An example of how one might utilize these controls could be to strictly regulate the working population size and the accuracy required to describe a solution. Generally, the larger the population space, the greater amount of randomness that can be tolerated before thrashing occurs. Utilizing a larger working population also lowers the probability that it will stagnate or converge prematurely. Another degree of control typically used in NP-Hard optimization problems is to impose a tolerance range for acceptable solutions rather than accepting only one unique solution.

At this point, let me just hint at the extent and complexity of the relationships that need to be managed in order to achieve a good algorithm. One cannot just make the working population very large and assume that randomness and other regulation problems will be masked, because if the population is too large, then the algorithm execution becomes inefficient and may never converge. Here we see

the need to regulate a working populations size with the amount of randomness that can be tolerated; otherwise, the algorithm will suffer from premature convergence or, even worse, divergence. Another subtle problem is a solution's acceptable tolerance range. If the range is too large, then the solution is of no use; yet if the range is too small and restrictive, then the algorithm may never converge or require an inordinate amount of time and resources in order to converge. As part of the scope of this thesis, I investigated the effects that changes in population size and randomness have upon an algorithm's ability to converge upon a solution.

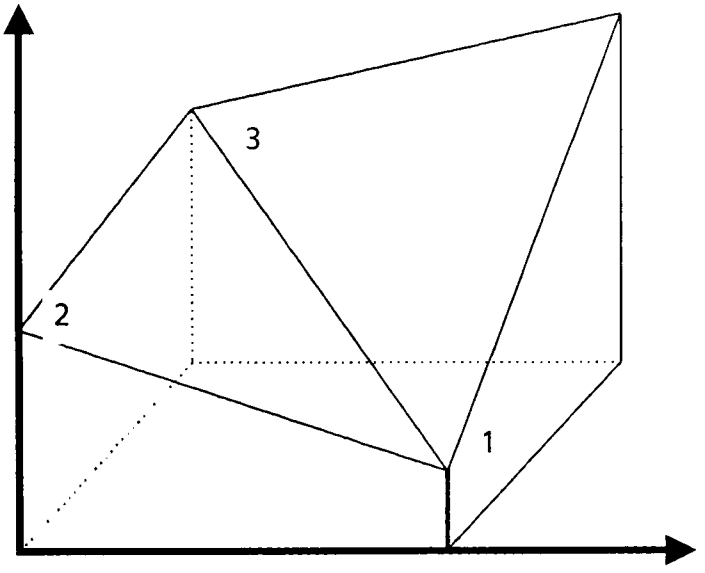
Goldberg & Thomas in 1986[9] published a work on search problems and machine learning that investigates solution algorithms accounting for randomness of population change and the effects of backtracking or thrashing in finite sized populations. Their research included investigating convergence of large solution space problems and how, by limiting the population space to be finite, the problems become tractable. The characteristics of random population changes (mutation in genetic algorithms), backtracking, and population size can be likened to techniques known as simulated annealing, feedback, or back propagation, in Neural Network research.

All of these prior topics were investigated and where appropriate, applied to my experimentation. The NP-Hard problems I investigated are:8 Queens
PWB routing

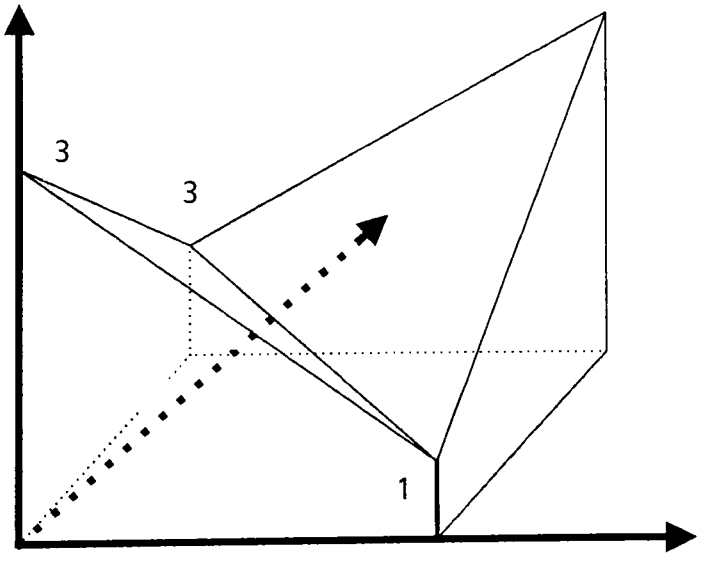
The first problem was simple and used as an initial development example in order to help me focus the development of programming techniques and utilities to conduct the primary experiment. I utilized the PWB routing task as the primary

9. Goldberg, D., E., & Thomas, A., L., Genetic Algorithms: a bibliography (1962-1986), TCGA report #86001, University of Alabama.

experiment. I view the effort exerted in applying some of the investigated and proven Genetic Algorithm techniques as a method of developing software tools and utilities that I can expect to complete and be able to demonstrate their correctness. This ability to prove the tools and effects of some of the algorithm techniques such as annealing strategies gave me testable / quantifiable positive feed back on some of the theories that I am investigating and intending to apply to the highly complex PWB routing problem.



Example of a complex 3D search space
where it is possible to arrive at 3 false minima
if the algorithm is incapable of properly traversing
the surface planes during its evaluation



Another example of a complex 3D search space
where it is possible to arrive at 3 false minima
if the algorithm is incapable of properly traversing
the surface planes during its evaluation

Figure 1.1

This section introduces characteristics of NP-Hard problems and genetic algorithm solution techniques utilizing statistical processes.

2.1 Monte Carlo Theories

Monte Carlo methods are typically utilized as a method of statistical integration. I intend to utilize this theory to aid in the development of the investigated genetic algorithms. Genetic search algorithms are fundamentally based in statistical optimization; therefore, I believe that proper application of Monte Carlo methods utilized in my genetic algorithms and annealing functions will aid the efficiency of my solution algorithms. The key function of the Monte Carlo theory is to apply statistical methods to improve optimization algorithms and feedback systems in order to improve the confidence levels of evolution, predictor functions, and estimator functions. (Hammersley & Handscomb '65[1] , SIAM 1969[2] , Binder et. al '79[3]).

2.2 How to Measure the Efficiency of an Algorithm.

Within manuscript I intend to treat Efficiency as a numerical value referred to as EFF.

$$EFF = \sum_{i=1}^{n} F_i(ES, CS) \quad EQN\ \#\ 1$$

Where F_i is a family of functions that consist of the characteristics of the EFF descriptor. For example

$$F_1 = SolutionStartTime - SolutionStopTime$$

1. Hammersley, J. m. & Handscomb, D. C. Monte Carlo Methods, 1965, QA.273.H224
2. Studies In Applied Mathematics, #3 Symposium on applied probability and Monte Carlo Methods, 1967, QA.1.S863
3. Binder, K. Et. Al, Monte Carlo methods in statistical physics, 1979, QC.174.85.M64

$$F_2 = Number\ of\ Genetic\ Evolutions / Generations$$

$$F_3 = Max\ Memory\ Required\ For\ Solution$$

There are factors such as resources and time required to arrive at the solution. Other factors such as does the addition or subtraction of resources scale the solution time and complexity; if so, is it linear, exponential, ...? Other aspects of measuring the efficiency may attempt to eliminate time as a factor and try to measure an algorithm based upon numbers of operations (compares, additions, multiplications, ...) required to achieve the solution. These types of factors can be considered almost unitless since they are values of the computer environment; whereas, time is not an independent measurement. Time as a measure of efficiency is very environment and problem specific. For example, solution time will vary depending upon the speed the computer and the type of resources available to it. Within this thesis, I intend to focus upon two primary measurement criteria, time and number of generations required to converge upon a solution.

As for the time criterion, I must point out that there are cases where it is not a valid unit of measurement. For example, if the time required to generate a solution for a computer board is a week, but you intend to manufacture and sell thousands of the boards, then the week investment is justified. The flavor of what I am implying here is that there are situations where time is not a critical measure; but since I will be investigating small examples and never using the solutions more than once, I believe time is an appropriate measure here. I will fully identify the hardware and its resources in order to give the reader a relative understanding of the relative compute power being applied to the problem.

In using the number of generations as an efficiency criterion, I am trying to use this as a criterion that has units only reflective or contingent on the problem. By measuring the algorithm based upon the number of generations, I can account for the factors such as search space size, population size, and number of genetic operators required to evolve a generation. These types of measurement units are time and resource independent, which is important since they allow us to measure an algorithm without physical resource implications (size and speed of computer, efficiency of simulation program, ...). I will attempt to provide the user with an idea of how many operations occur in a generation cycle.

2.3 Fuzzy Cognitive Machines

These are tools developed as extensions of signal flow graphs of electronic circuits. The Fuzzy Cognitive Machines FCMs will be used to identify trends of a hardware system and its components [4] [5]. The utility of these tools is to be able to imperially, with minimal overhead and effort, determine where critical and potentially active paths and devices are within an electronic system. This characteristic information about the circuit will be incorporated into the solution algorithm to help efficiently and more directly find solutions to the routing problems.

Part of the measurement criteria is the rate at which the algorithm converges upon an optimally acceptable solution. This rate (number of iterations / evolutions) can be reduced or minimized if we can identify a way in which to restrict the generation of less than optimal population entries.

4. Styblinski, M. A. & Meyer, B. D., Fuzzy Cognitive Maps, Signal Flow Graphs and Qualitative Circuit Analysis, Proc. IEEE Conf on Neural Networks, 6/87

5. Kosko, B., "Fuzzy Cognitive Maps", International Journal of Man-Machine Studies, Volume 24, pps 65-75, 1/1986.

I designed the genetic algorithm to utilize the information from signal flow graphs to order and rank the importance of possible population entries. This filtering of population entries can be likened to restricting the evolution process to only promoting and creating population entries that have or will yield to the highest possible utility values.

2.4 Annealing Techniques

This is a concept from neural network research and was adopted into the genetic algorithm fitness function as a feedback method for adjusting the amount of randomness / heat applied to the optimization algorithm (Davis '88 [6]). This parameter is a means of controlling the mutation rates and thrashing of the population entries. The genetic algorithm will monitor the rate of progress of the population (e.g., population fitness value, average population value and its change rate, ...). The character function discussed in Section 4 is the primary global status monitor. Population and evolution information will be utilized by the annealing function to regulate the amount of randomness / mutation that will occur during population evolution. The goal here is to be able to prevent the population from either stagnating or thrashing while maintaining enough randomness to be able to effectively explore the solution space.

Annealing techniques as implemented within this investigation can be thought of as a system G(h) with feedback A(G(h)) to help regulate both the evolving population and the evolution algorithms. The feedback A() is the annealing information that will regulate factors such as population size, mutation, randomness, etc. A generic diagram of the system could be represented as in figure 2.4.1.

6. Davis, L. & SteenStrup, M. (1987). Genetic Algorithms and simulated annealing: An overview in.

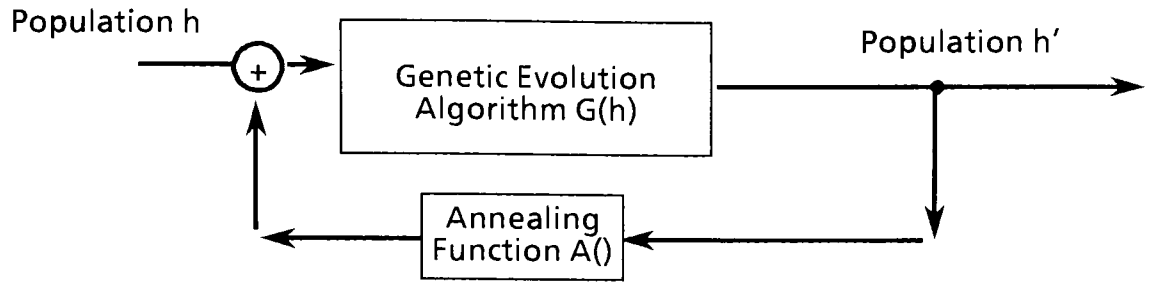


Figure 2.4.1

Top level view of genetic Algorithm flow

2.5 Probability and Statistical Theory of Optimization

Genetic algorithms all require a certain amount of randomness implemented as mutation and crossover. The probability or rate at which mutations occur should be relative to the rate at which the evolution process is evolving the population; cautions here are such that one does not want to induce thrashing into the population yet, there must be enough randomness to cause the population not to converge upon a false minima and stagnate.

Other degrees of freedom that were statistically regulated:

1) the selection of which population citizens are to be activated
2) Are all activated population entries entered into the bidding process
3) at what point in their bit string do they crossover.

In making these decisions, there is an amount of pure randomness as well as control. This control may take the form of selecting the entries of the highest utility to crossover. This is a form of assigning statistical merit to high utility values of population entries, and by operating upon them, the algorithm will yield

resultant population entries of equal or greater value. Hence, there should be efficient convergence onto a solution.

Some of the standard theorems of statistical measurement that will be utilized are[7]:

1) Standard Deviation for an Entire Population

$$\sigma = \left[\frac{(X - \mu)^2}{N} \right]^{-2} \quad EQN\#2$$

For these experiments the entire population is known, therefore, the mean for the population can be calculated and also the Standard Deviation.

2) Standard Deviation for a Sub-Sample of a Population

$$s = \left[\frac{n \sum_{i=1}^{i=n} X^2 - \left(\sum_{i=1}^{i=n} X \right)^2}{n(n-1)} \right]^{-2} \quad EQN\#3$$

3) Skewness of the population

$$g_1 = \left[\frac{n^2 \sum_{i=1}^{i=N} X^3 - 3N \sum_{i=1}^{i=N} X^2 \sum_{i=1}^{i=N} X + 2\left(\sum_{i=1}^{i=N} X \right)^3}{s^3} \right] \quad EQN\#4$$

This is a measure of symmetry of the population. If g_1 is < 0 then the population entries are skewed to the left tail and if g_1 is > 0 then the population entries are skewed to the right tail. If $g_1 = 0$ then we can assume a normal distribution.

4) Kurtosis of the population

$$g_2 = \left[\frac{\left(ABS(ABS(g_1^2 - s^{-2}) - ABS(Z^{-2} - \sigma))^2 \right)}{s^4} \right] \quad EQN\#5$$

This function is used to describe the shape of the distribution's tails / roll

7. Glossary and tables for statistical quality control. Published American society for quality control 1973

off. If g_2 is < 0, then the population distribution plot has shorter tails than a normal distribution. And if g_2 is > 0, then the population distribution plot has longer tails than a normal distribution. If $g_2 = 0$, then we can assume a normal distribution.

5) Test of the means of two different populations

$$z = t_{\infty} = \frac{\overline{(X_1 - X_2)} - \overline{(\mu_1 - \mu_2)}}{\left[\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}\right]^{-2}} \quad EQN\#6$$

This function will be utilized to compare the mean, of two populations (most likely successive populations).

The previous statistical information was used to determine if the evolution process was evolving the populations forward towards a solution, backwards away from a solution, or if the population has stagnated stagnated. I utilized this characteristic data to modify annealing algorithms, randomness factors, and general population management. For example the Kurtosis function gave me information that directly affected the randomness and mutation parameters of the genetic algorithms. If the population had a kurtosis of g_2 less than zero then the genetic algorithm would increase the randomness and mutation rates. The population having short tails for distributions means that there were fewer "outlyer" population entries that could be involved to cause the population to evolve in a productive positive manner oppositely it was more likely that the population would stagnate or evolve towards a less productive path. It was safe to up the mutation rates with out less concern about causing the population to thrash.

2.7 Genetic operators

In the development of my solution algorithms I started with the common basic genetic operators:

1) Replication: Is the operation of replicating population entries some number of times based upon their utility value
2) Crossover: The operation of selecting two entries from a replicated population and merging / crossing over parts of the two input population entries to generate a new third population entry.
3) Mutation: The operation of randomly changing one or more population entries simply by changing some value / characteristic of the entry.
4) Utility: A measure of the merit / strength of a population entry.

These standard operators as described by Holland 1975 [8] will act as the basis for my developing Optimized genetic operators more suitable for the class of NP-Hard problems that I will be investigating within this Manuscript.

8. Holland, j. H., Adaption of Natural and Artificial systems, Ann Arbor: University of Michigan Pres.

3.0 EXPERIMENTATION INTRODUCTION

The examples / problems that I have chosen to investigate within the thesis start out as reasonably simple cases and progress to the main experiment of the thesis. I am developing the investigation in this form (simple to actual) in order establish a set of verified tools and examples from problems which I can expect to solve. By being assured that I can look at the solution of a moderately sized problem and empirically evaluate if the answer is correct, I can make inferences as to the efficiency and correctness of the software tools that I will be utilizing to develop the solution to the main experiment. This is, in a sense, building a strong foundation upon which I will grow the main system.

The minor development problem I will investigate within this thesis is:

1) Eight N Queens

Problem case number one is the challenge of taking an NxN chess board and placing N queens upon the board, one per rank, such that if any queen were to make one legitimate chess move she would not capture any other queen upon the board[1]. Figure 3.0.1 is an example of an arrangement that is invalid or a failure, because moving the queen from square (2,3) to square (5,6) will result in the capture of the queen on square of (5,6). Figure 3.0.2 is an example of a correct or successful placement of 8 queens upon an 8x8 chess board. In Figure 3.0.2 moving any queen one legitimate chess move will **not** result in the capture of any other queen.

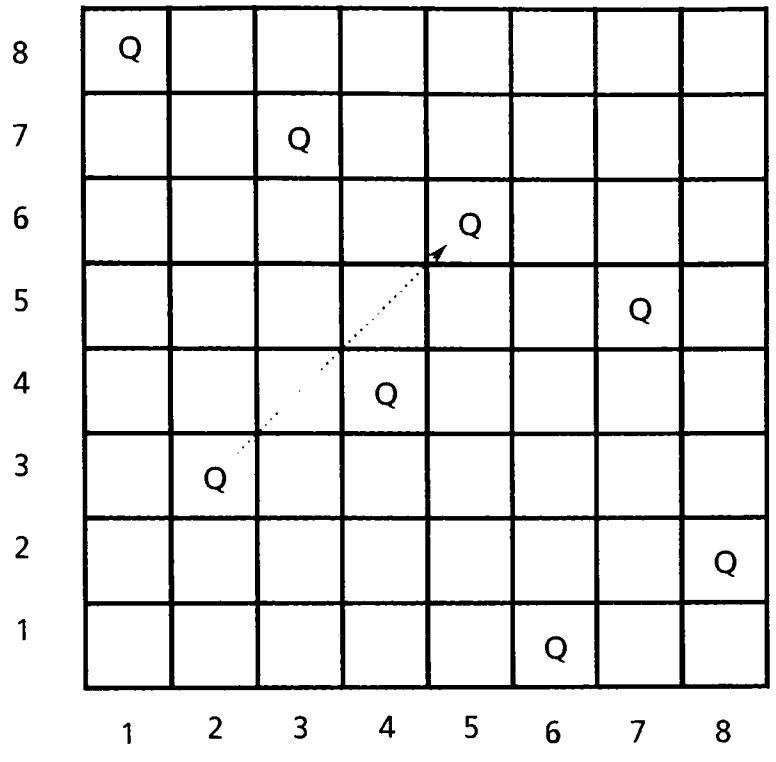
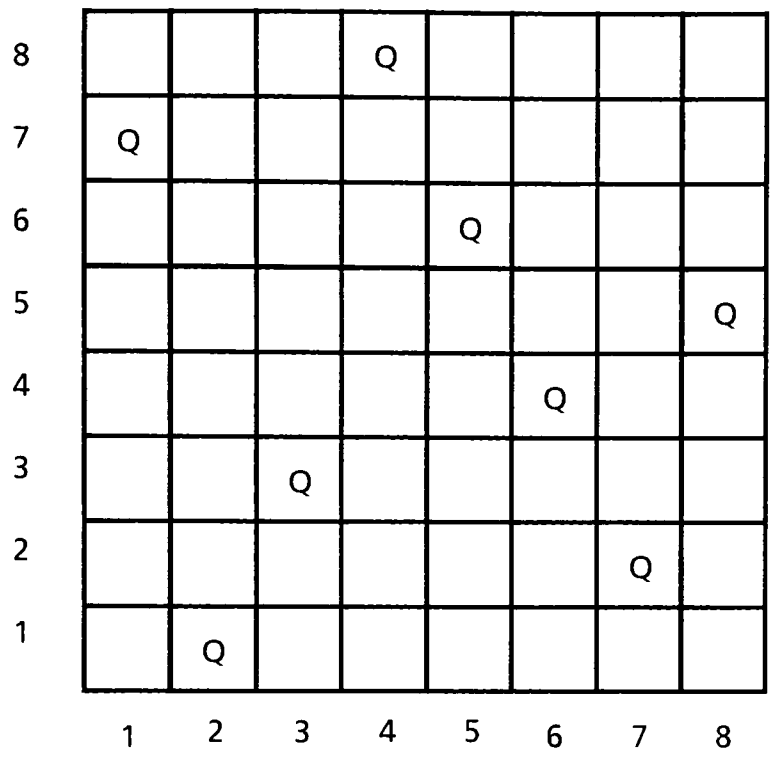


Figure 3.0.1
Example of a failed solution

3.1 N QUEENS PROBLEM

If we look back to the criteria of formulating a problem / solution methodology discussed in the introduction and apply this to the N Queens Problem, we find that we must have:

1) A well formed statement of what the problem / question is
2) Criteria for determining an acceptable solution
3) Characteristics of the problem.



The labeled squares are the positions occupied by queens

Figure 3.0.2
Example of a successful solution

For the N Queens problem, the above criteria are defined to be:

1) The N Queens problem is defined as a square of NxN positions, where each position represents one of two states, occupied or not. We further have the restriction that each square on the board has relevance / effect upon a select set of other squares on the board (refer back to the problem description in Section 3.0).

1. H.S.Stone, J.M.Stone, Efficient Search Techniques - An empirical study of the N-Queens problem, IBM J. Res. Development., pp464-474, vol.31, no.4, 1987

2) A solution is acceptable iff moving any one queen one legitimate chess move, she does not capture any other queen upon the chess board. All solutions not satisfying this criteria are invalid. Please note that this problem does not have a tolerance range for its solution acceptability as some problems do, but there is more than one correct / acceptable solution per board.

3) I will not detail the problem characteristics here but will discuss them below as I work through the solution to the problem.

For this example it was simple enough to assign a one or zero as occupied or not occupied, respectively. This representation scheme can be implemented as one location per bit, 8 locations per byte. I selected the bit per position scheme because it was convenient and saves resource space. Also, by having the board packed in this manner, I could more easily use boolean operators rather than algebraic operations to perform some of the genetic functions. I did, however, treat the 8x8 board as a vector of rank(8) bytes and the population as a vector of size P board vectors. Please refer to Figure 3.1.1 for further explanation.

Having selected a representation scheme, the next item of importance is to determine if there is any fundamental relationship between the board size and the ability to solve the problem. In other words, if there is a minimum board size (NxN), what is it? The goal here is to identify key factors and characteristics of the problem that might relate to implementing an optimal solution algorithm.

By searching for the minimal board, I believe that I can make inferences about schema [2 3 4] related to larger problem / solution sets. The fundamental / minimum solution can be utilized as a highly correlated predictor for making statistically

0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0

Example board for 8x8 problem.
8 bytes w/8 bits per byte

Within the solution algorithm this board is treated as a one dimensional array of 8 bytes e.g

unsigned char board[8];

The population is represented as a 2 dimensional matrix

unsigned char **population;

where each pointer in the population array points to a board array.

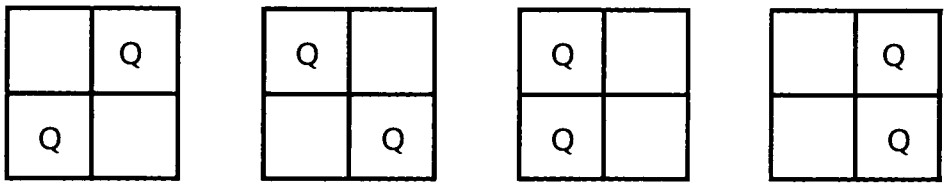
population[0] = 1 1 1 1 1 1 1 1 . . . . 1 1 1 1 1 1 1 1
population[1] = Byte 0 Byte 7
population[2] =
population[3] =
:
population[P] =

Figure 3.1.1 8 Queens representation

2. Goldberg, D., E., Optimal initial population size for binary-coded genetic algorithms (TCGA report #85001).
3. C.L. 8ridger, D.E. Goldberg, An Analysis of Reproduction and crossover in a binary coded Genetic algorithm, Proceedings of the Second International Conference on Genetic Algorithms, 7/1987
4. Holland, J., H., Genetic Algorithms and the optimal allocations of trials, SIAM journal of Computing, 2(2), 88-105

valid assumptions about logical, algebraic, and heuristic rules required to describe the problem and its solution algorithm.

The minimum board size in relation to the solution should be relatively easy to find. If necessary, we can use brute force and test boards of sizes 2x2 up through 7x7 to determine what is the smallest board size before the problem cannot be solved. We are able to set these bounds, 2 and 7, because we know the 8x8 solution exists and a 1x1 board is illegitimate. We can determine by inspection that a 2x2 board has no possible solution, as shown in Figure 3.1.2 and that a 3x3 board also has no solution, as shown in Figure 3.1.3.

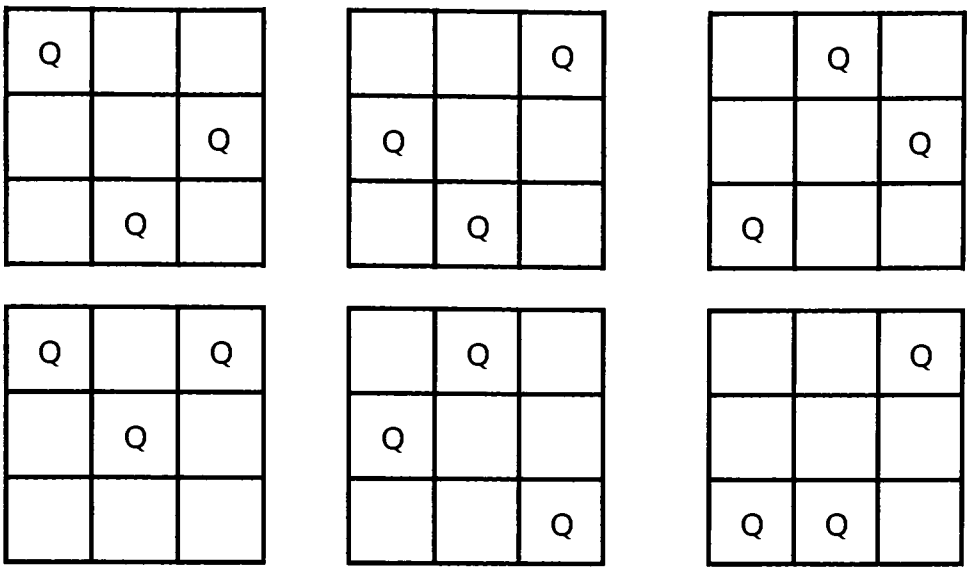


The labeled squares are the positions occupied by queens

Figure 3.1.2

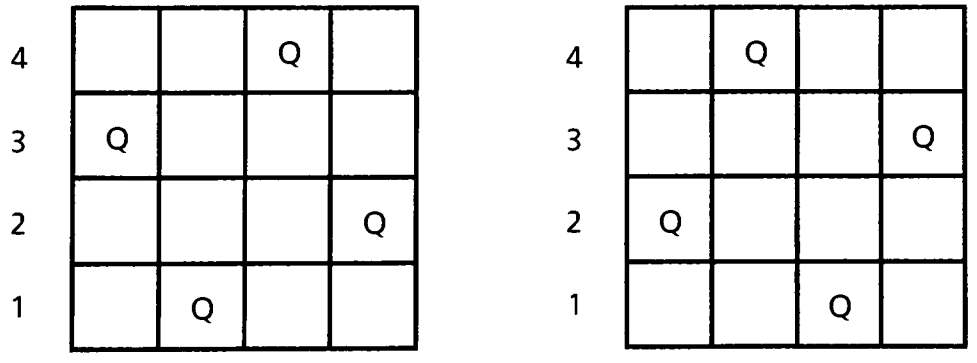
Other schema traits that we know by obvious inspection is that there can only be one queen per rank and one per file. I identify only the rank and file, not the diagonals because, these are very simple to identify and eliminate via single boolean software operations. By being able to eliminate these cases with minimal overhead, we are drastically reducing the invalid population entries that can occur within the working population thereby reducing the search space and making the problem more manageable.

The next size board to test is a 4x4 board. In a 4x4 board, Figure 3.1.4 there are



The labeled squares are the positions occupied by queens

Figure 3.1.3



The labeled squares are the positions occupied by queens

Figure 3.1.4
Examples of a successful pattern

2^{16} possible board combinations, but not all combinations are valid. By

eliminating the obvious (trivially identified) board patterns mentioned above for the 2x2 and 3x3 and 4x4 cases, we can reduce the possible board combinations to 2^8. This makes the search space very manageable even for brute force algorithms. This type of search space reduction[5] (an order of magnitude or more) is highly significant in the case of NP-Hard problems. In summary we have now identified the minimal board size for the N Queens problem to be 4x4, this was done by exhaustive example. Having the minimal board size (4x4) we can now base our schema design on this and develop optimized genetic evolution algorithms.

One of the reasons for searching for the minimum board size is to help in determining what the size and characteristics of a schema might be. The utility of identifying a set of schema is high because we can then direct the evolution routines of the genetic algorithm to generate entries that are statistically more valid[6] [7]. This kind direct computation is highly efficient and desirable; for example think of the algorithm for directly computing numbers that are perfect squares (e.g. 1, 4, 9, 16, 25, ...). The unintelligent method for computing these values would be to test each whole number to determine if it is the produce of a perfect square. The exhaustive testing algorithm might look something like:

1) assign X_1 the value 1; by definition this is a perfect square
2) add one to the previously tested value $S = X_n + 1$
3) $Y = \text{round}(S / 2)$
4) loop for 2 to Y test cases and test the divisibility of S

5. Suh, J., Y., & Gucht, D., V., Incorporating heuristic information information into genetic search, Proceedings of the Second International Conference of Genetic Algorithms 7/1987
6. Johnson, K, & Daniell, c., & 8urman, J., Feature extraction in the Neocognitron, Proceedings from the conference on Neural Network
7. Krishnan, G., & Walters, D., Psychologically plausible features for shape recognition in a neural network

5) if S is not divisible then $X_{n+1} = S$

6) loop around to step 2 to test another case

This looping and exhaustive testing of each number is very inefficient. Through inspection and reasoning we learn that the formula / schema for directly computing squares is:

1) assign X_1 the value 1; by definition this is a perfect square

2) assign Y the value 3

3) $X_{n+1} = X_n + Y$

4) $Y = Y + 2$

5) Loop to step 3

Please note that the X_n's are the perfect squares

It is these kinds of direct operations based upon the fundamentals of the problem that help to optimize solution algorithms. I intend to utilize techniques such as these to facilitate and optimize the genetic algorithms for my test problems (N Queens, and the PWB routing problem).

From the N queens schema investigation I found that the 4x4 size board is the smallest possible size with a solution, Figure 3.1.4. Knowing what the minimum solvable board size is, I then computed several 4x4 solution board sets as well as numerous 4x4 failure board sets. I then used this information in my evolution algorithm to filter out population entries that have known failure structures and promote solution entries with the 4x4 solution schema structure.

This is a simple technique of restricting the search space by rejecting the known failures and promoting the entries with the most potential[8]. Having added this

8. DeJong, K., A., (1981) Adaptive search procedures for large complex spaces., (technical report #81-2), University of Pittsburgh

information to my solution algorithm I was able to cut the number of generations required to find a solution about in half for most of the tested cases.

3.2 Determining Mean Population Size MPS

At this point the problem fundamentals have been reviewed, and I refer the reader back to Section 3.1 for a discussion on problem characteristics and solution optimization. This information will be incorporated in both the generation of boards for the initial population as well as in the evolution functions of the genetic algorithm.

The algorithm, in order to generate the working population, requires that an initial population of size MPS be generated, where MPS is defined either by the user or the estimator function MPS().

$$MPS(BS, ETS) = \left(\frac{BS * ln(\frac{2048}{ETS}) * ln(2^{BS})}{2 * ln(BS)^2} \right) \quad : eqn\,10$$

Where BS is the Board Size (for example and 8x8 board is Board Size 64), and ETS is the number of expected Evolutions Till Solution (for example 25, 50, 75, 100, ...). An example of an MPS calculation would be:

let BS = 64

let ETS = 100.

$$MPS(64, 100) = \left(\frac{64 * ln(\frac{2048}{100}) * ln(2^{64})}{2 * ln(64)^2} \right)$$

Which would simplify to:

$$MPS(64, 100) = \left(\frac{64 * 3.0194 * 44.3614}{2 * 17.2963} \right) = 246.312$$

And rounding this off will give us a MPS of 246.

This function, MPS(), will yield the mean population size. During the evolution process both the mutation and annealing operators will evaluate the current population and adjust the Mean Population Size by some percentage. The actual population size is allowed to fluctuate in order for the genetic algorithm to be able to control the evolution process. For example, if the population appears to be stagnating, then the algorithm will increase the population size, hence infusing "new blood" into the population to revitalize the evolution.

There are additional factors by which the genetic algorithms would adapt themselves over the evolution of the population. One example is the Mutation function, I designed this function to be proportional to the population size as well as the average changing utility value of the most recent 3 evolution cycles. If the population size is relatively large (all or most of the population entries replicate at 10% or better than the CORE population size) then the mutation function will increase the probability of mutation. The theory here is that as the population size grows so does it ability to tolerate additional mutation without beginning to thrash.

3.3 Solution Algorithm Description of Genetic Operators

The solution algorithm for the N-Queens problem describe earlier is fairly simple and consistent with its application of standard genetic operators. The operators known as replication, mutation, and crossover are utilized. The algorithm is augmented with functions such as a population randomizer, an annealing feed back scheme, resampling of the population's parents, and a subsampling technique[9] [10].

9. Foo, N., Y., & Bosworth, J., L., (1972) Algebraic, geometric, and stochastic aspects of genetic operators, (CR-2099)

10. Grefenstette, J., J., Optimization of control parameters for genetic algorithms, IEEE Transactions on Systems, Man and Cybernetics, SMC-16(1), 122-128

The above mentioned genetic operators and functions are applied to the population at each evolution cycle. Depending upon the annealing temperature and mutation rate, it is possible that some population entries will not pass through all of the genetic operators at each evolution cycle. The genetic operators that are applied to solve this problem in the following order are:

1) Replicate current population_m yielding population^a
2) Shuffle* population^a
3) Crossover population^a yielding population^b
4) Shuffle* population^b
5) Mutate* population^b by $<<<\%$
6) Filter population^b according to valid schema rules yielding population^c
7) Add parents to population^c yielding population^d
8) Shuffle* population^d
9) Mutate* population^d by $<<\%$
10) Resample population^d yielding population_{m+1} for next generation

* Operation may not occur at each evolution or for every population entry

3.3.1 Initial Population Generation

Now that we can determine the Mean Population Size we know how many boards we need to generate to initialize the algorithm. In generating the initial boards for the population, I incorporated the schema information determined earlier in Section 3.1. This schema information about minimum valid board sizes and configurations as well as invalid configurations was captured into two sets. The set of valid schema configurations were denoted as set Δ and the invalid schema configurations were denoted as set τ.

The set Δ was generated via the schema processing algorithm and stored. Example entries are shown in Figure 3.3.1.

The set τ was generated from two input sources. One being the capture of invalid schema output put from the schema algorithms mentioned in Section 3.1 and the other being the simple generation of boards that have two or more queen entries per rank and file. Example entries to this set are shown in Figure 3.3.2.

These two sets were then used in the board generation function Board().

These examples will represent the board as it is being stored within the computer, a vector of bytes with each bit representing one board location.

For example, the valid chess board of Figure 3.0.2 is represented as:

0	0	0	1	0	0	0	0
1	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	1
0	0	0	0	0	1	0	0
0	0	1	0	0	0	0	0
0	0	0	0	0	0	1	0
0	1	0	0	0	0	0	0

The example boards below are some of the entries in the ∎ set

1 0 0 0 0 0 0 0	0 0 0 0 0 0 0 1	0 0 0 0 0 1 0 0	0 0 0 1 0 0 0 0
0 0 0 0 0 1 0 0	0 1 0 0 0 0 0 0	0 0 1 0 0 0 0 0	0 0 0 0 0 0 1 0
0 0 0 0 0 0 0 1	0 0 0 1 0 0 0 0	0 0 0 0 0 0 1 0	1 0 0 0 0 0 0 0
0 0 1 0 0 0 0 0	1 0 0 0 0 0 0 0	0 0 0 1 0 0 0 0	0 0 0 0 0 0 0 0
0 0 0 0 0 0 1 0	0 0 0 0 0 0 1 0	1 0 0 0 0 0 0 0	0 0 0 0 1 0 0 0
0 0 0 1 0 0 0 0	0 0 0 0 1 0 0 0	0 0 0 0 0 0 0 1	0 1 0 0 0 0 0 1
0 1 0 0 0 0 0 0	0 0 1 0 0 0 0 0	0 1 0 0 0 0 0 0	0 0 0 0 0 1 0 0
0 0 0 0 1 0 0 0	0 0 0 0 0 1 0 0	0 0 0 0 1 0 0 0	0 0 1 0 0 0 0 0

Figure 3.3.1 Example valid board schema

The example boards below are some of the entries in the ∎ set

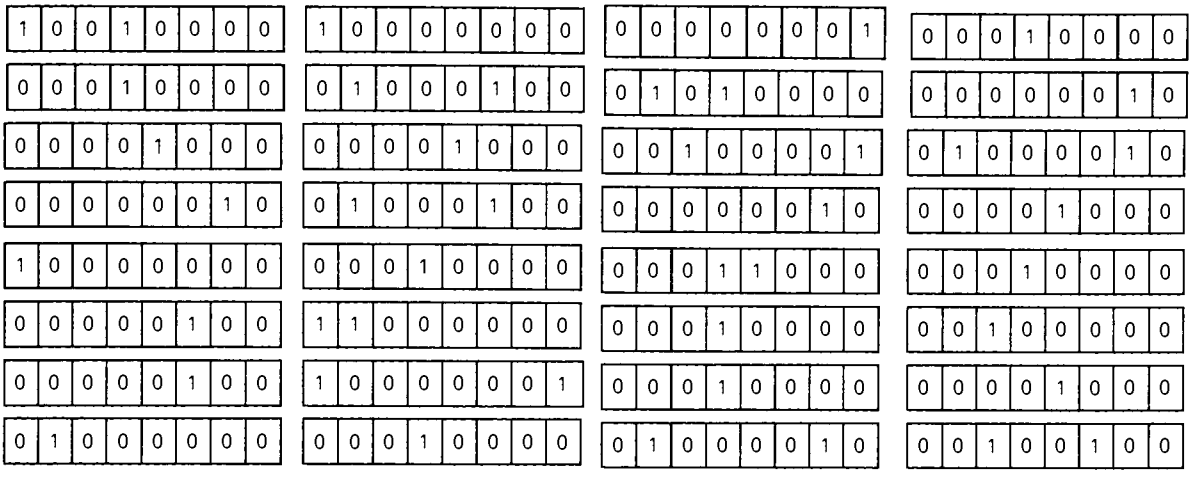


Figure 3.3.2 example invalid board schema

$$BOARD(\{\Delta\},\{\tau\},\{F\}) \quad = \{Vec(8,F) : (Vec(8,F) \cap \tau)\ ' * (\Delta \in Vec(8,F))\} \quad : \quad eqn\,11$$

Vec(N, F) function is a random number generator with a filter function that creates a vector of length n bytes appropriate for the problem.

$$Vec(N,F) = \bigcup_{i=0}^{i=N-1} F[Rand(seed) * Rank(F)] : eqn\,12$$

F is a set of bytes from which the initial chess boards will be generated. The set F consists of specially constructed patterns that account for the schema rules identified earlier in Section 3.1. N in the Vec() function is the rank of one row of the chess board, for example with an 8x8 board N = 8. Every time the set F is fed into the Vec() function, it is randomly shuffled to reduce correlations between set position and data content. This vector Vec() is then utilized by the board generation function, which will filter out identifiably invalid board formulations

based upon the predetermined characteristics and rules of the invalid board schema sets.

Utilizing the two functions Board() and Vec() the initial population for the system can now be generated, and this set is defined as eqn. 4 below.

$$\left\{ \{POP\} : \left[\bigcup_{m=1}^{m=MPS()} BOARD() \right] \bigcup \left[\bigcup_{m=1}^{m=\phi} Vec() \right] \right\} \quad : eqn\,13$$

The set POP can be visualized as a vector of length MPS() + ϕ, where ϕ is a quantity relative to the amount of randomness the algorithm will utilize and the annealing characteristics of the solution algorithm. Each entry in the vector is a byte string that represents one chess board (please refer back to Figure 3.1.1 for a more detailed description of the encoded board entries). The set POP is fed into the genetic algorithm as the starting population.

3.3.2 The NQC() Success Function and the Replication Operator

Each of the population entries from $population_m$ are first evaluated for success, e.g. is this entry a valid board. If the answer is yes, then the board is displayed to the user and the evolution process is suspended. The success evaluation function is very simple; it is denoted as NQC() which stands for Number of Queens Correct upon the board. If the NQC() function returns any value less than the rank of one board row then that board is not a success. For example, with an 8x8 board the NQC() function should return 8 for a correct / acceptable board.

Successful boards are displayed to the user. The user is allowed to either accept the solution and terminate the search, or reject the solution and continue the search. In the event that the user rejects the currently displayed solution, the

algorithm will randomly decide to either mutate the board and leave it in the population or remove the board from the population.

The replication operator is used to replicate the population entries according to a predetermined function REP().

$$REP() = \frac{NQC(POPE)^{ln(SQRT(BS))}}{3} \quad : eqn\,14$$

Each population entry that fails the NQC() test is passed through the REP() function to determine how many times the entry should be replicated for the genetic evolution functions.

For example if we evaluate an 8x8 board (BS = 64) with a NQC() of 5, we have:

$$REP() = \frac{6^{ln(8)}}{3} = 13.8356$$

This gives us a REP() = 13.8356, which, when rounded to an integer, indicates that the population entry should be replicated 14 times going into the evolution process. These replicated population entries are then added to population[a].

3.3.3 The Mutation Operator

This operator is split into several sub-functions that are customized for the particular problem.

1) Whether to mutate an entry or not.
2) Where to mutate the entry.
3) How to mutate the entry.

Case one, to mutate or not, is a simple Random number generator and a threshold test. In other words case one is simply a frequency or probability function that returns true or false based upon user specified values and population conditions. Case two randomly selects one or more locations on the board to mutate. Finally,

case three selects from a set of allowable mutation operations. For example some of the possible type of mutation possible are: is the board reordered; do we add another queen, do we subtract a queen; do we assign one of the valid schema onto the board, etc.

The reason for mutation cases two and three is to help optimize the evolution algorithm. By customizing the mutation[11] operation, I can force the evolution algorithm to make random changes with some confidence level that the change is helping to evolve the board in the proper direction towards a solution.

When this operator is invoked, an entire population is passed through the operation and some percent of the population is changed according to the mutation rules. Below in Figure 3.3.3A is a graph showing the standard mutation success rate versus my hybrid mutation success rate. Figure 3.3.3B in the appendix is the corresponding data table to Figure 3.3.3A. The input population was of average size 40 and the board size was 12x12.

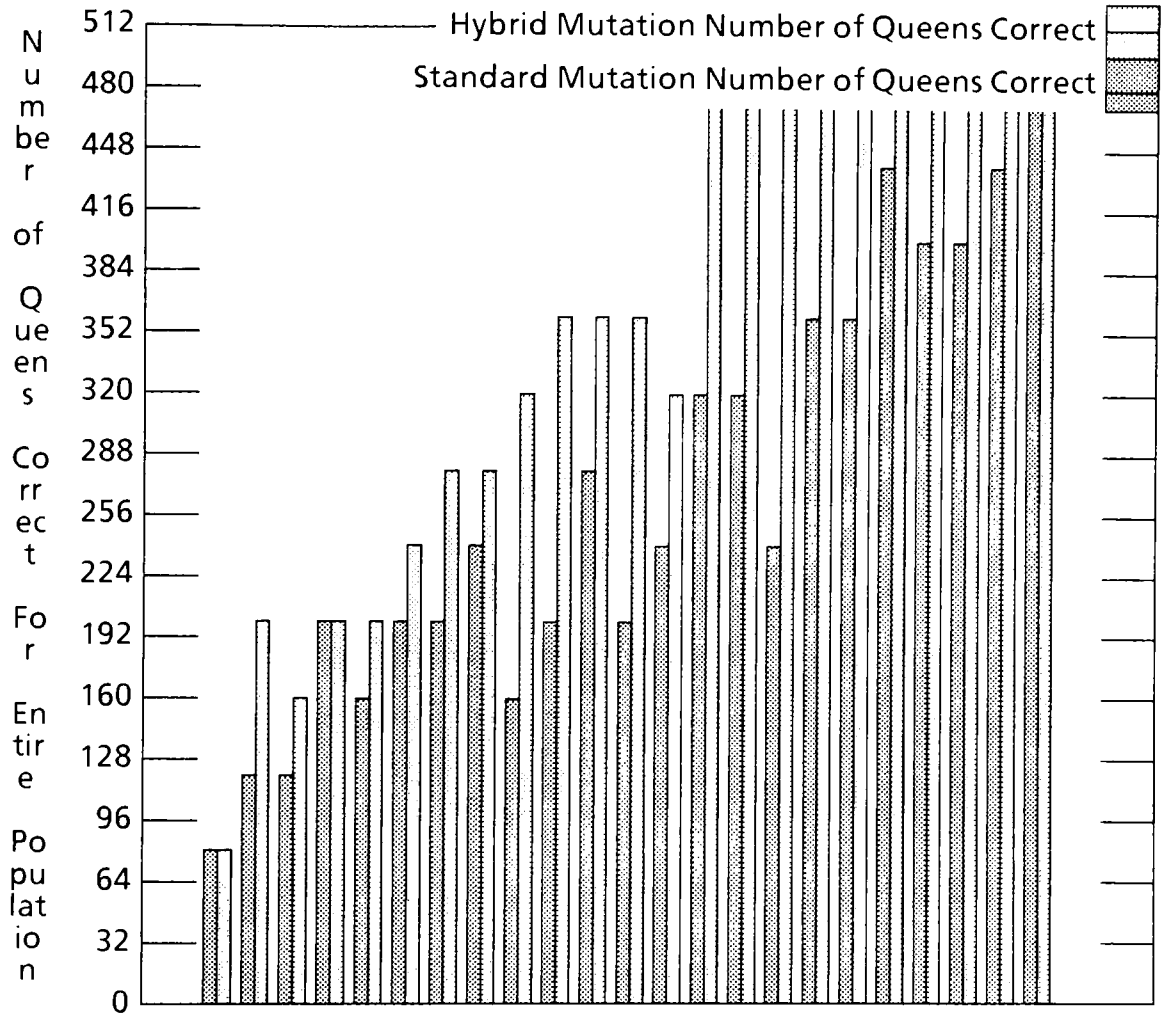
3.3.4 The Crossover Operator

The crossover operator[12] is also customized for the specific problem as is the mutation operation. Some of the restrictions of this operation are:

1) Most boards are crossed over at either row or column end points.
2) A board can be crossed over with itself (e.g. rows or columns are swapped)
3) The crossover must not leave a row or column without any queens.

Again, the reason for restricting the function is to help insure that only valid and statistically optimal entries are produced for the population[b] going into the next evolution cycle.

11. Bosworth, J., & Foo, N., & Zeigler, B., P., Comparison of genetic algorithms with conjugate gradient methods (CR-2093) National Aeronautics and space administration



Histogram plot of efficiency of hybrid genetic Mutation operators
Figure 3.3.3A

The standard genetic crossover operator is defined such that the cross over point is a randomly selected location along the string representing a population entry. This simple definition of crossover does not account for any of the structure of the

12. Goldberg, D., E., (1987) A note on the disruption due to crossover in a binary coded algorithm, (TCGA report #87001).

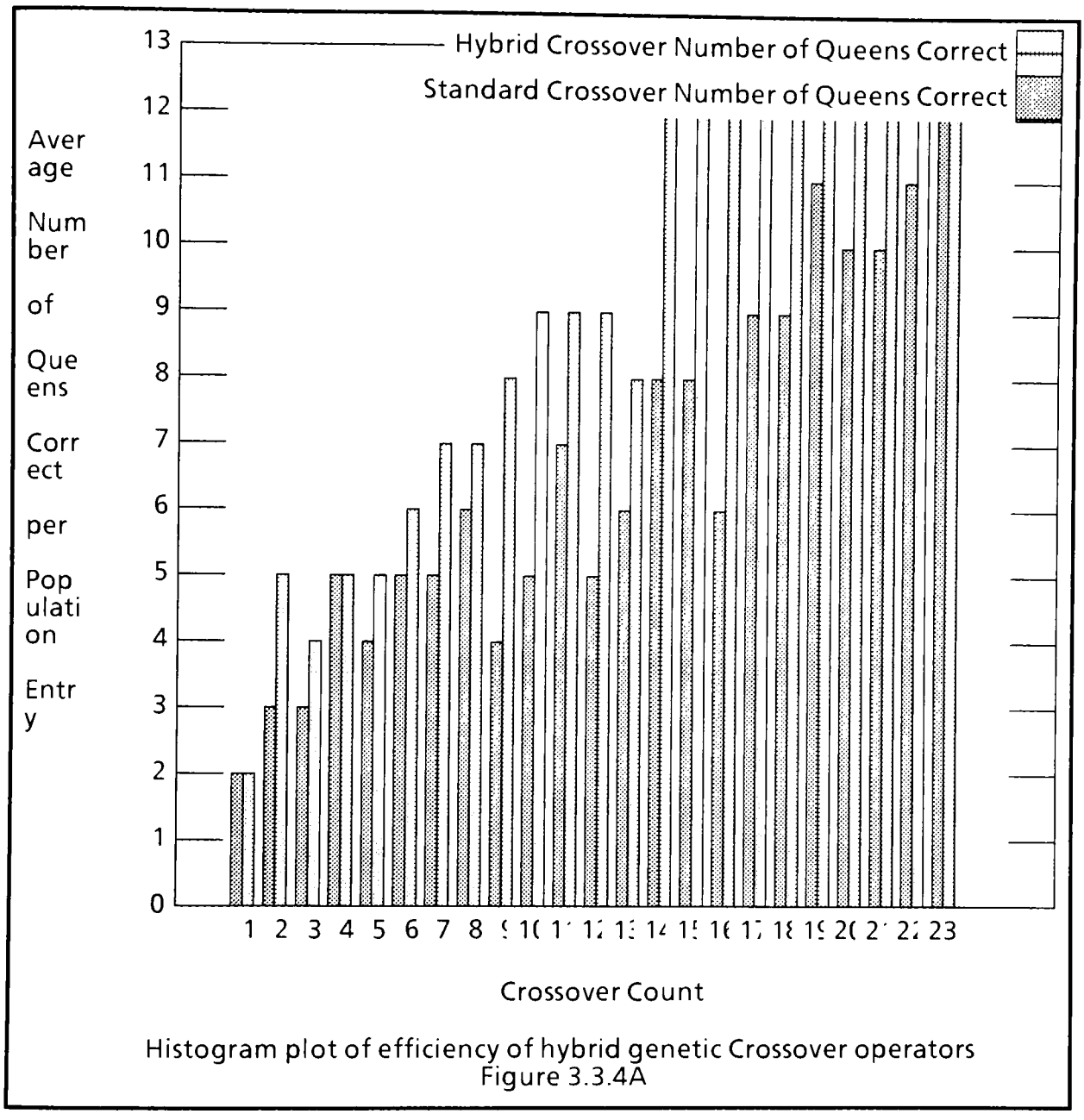
problem or the relationship between the implementation representation and natural problem structure. My intent is to restrict the crossover operator to recognize the inherent structure of the problem and its computer representation. In doing so I contend that I can optimize the crossover operator to combine population entries and produce more statistically valid entries. Below in Figure 3.3.4A is a graph showing the standard crossover success rate versus my hybrid crossover success rate. The exact data table for Graph 3.3.4A can be found in the appendix as Figure 3.3.4B. The input population was of average size 40 and the board size was 12x12.

3.3.5 The Filter Operator

As intermediate populations are generated, they are passed through a filter function to insure that the number of obviously invalid population entries are kept to a minimum. Some of the filter operations that this function implements are:

1) Checking for greater than 2 queens per row or column
2) Rows and columns missing a queen
3) Boards that have a high correlation with the valid schema set Δ
4) Boards that have a high correlation with the schema set τ.

The above set of conditions as well as others are tested for against the population entries. The boards that have negative characteristics are either passed through the mutation function, or the algorithm will apply a heuristic and change the board to be more correlated with characteristics of the Δ set. The intent here is to filter out some of the invalid population entries and coalesce them to have a higher utility values. The filter operation will also promote the board entries that have high correlations with the set of valid schema rules.



Histogram plot of efficiency of hybrid genetic Crossover operators
Figure 3.3.4A

3.3.6 Selecting and Adding Parents Back Into the Evolving Population

This function is designed to reintroduce some of the population entries from the population prior to the current evolution cycle. In other words this operation will add back some of the parents from the prior population to the evolving population. The function NPTA() returns the Number of Parents To Add back into the evolving population. Once this number is determined the system then will randomly select NPTA entries from the prior population and add them back into the current evolving population.

$$NPTA() = \frac{MPS()}{ln(BS)^2} + \frac{Rand(BS)}{10} Rand(BS) * 2 * ln(BS)^2 - DPPU \quad : eqn\,15$$

The DPU value is maintained by the population character function. This value, DPU, represents the Δ Percent in the Population Utility from the prior two populations. All of the other function parameters have been previously identified and will not be explained again here.

An example of the NPTA function would be:

Let MPS() = 200

Let BS = 64 (which is an 8x8 board)

Let DPU = -5 (meaning that the total utility of the prior two populations has decreased by 5%

$$NPTA() = \frac{200}{17.29} + \frac{0.2}{10} * 2 * 17.29 - (-5) = 14$$

3.3.7 The Average Utility Function AUF

This function simply computes the average utility of all of the boards in the current population.

$$AUF(POP, N) = \frac{\sum_{i=1}^{i=N} NQC(POPE_i)}{N} \quad Eqn: 16$$

3.3.8 The Resample Operator

RPS stands for Resample Population Size. This operator performs two tasks[13][14]. One is to determine how many population entries (X) of the evolving population will be carried forth into the next population. The second Task is to randomly sample / select (X) entries from the evolving population and define them to the next population. In other words $population_n$ is submitted to the genetic operators and is expanded and evolved; the resample operator selects (X) of the evolved entries and produces $population_{n+1}$.

Back in Section 3.2 we defined a function called MPS() for Mean Population Size. This value is set as the average size of the population through the evolution process. The exact size of the working population is allowed to fluctuate within some tolerance range determined by a combination of the genetic classifier functions such as character function and annealing temperature, population size, etc.

RPS() represents the number of population entries that will be selected from the evolving population and used to define the next population. The RPS() function is defined as:

$$RPS() = MPS() + NPTA() - AUF() \ : eqn\ 17$$

Once we have determined the value of RPS, the function then randomly selects RPS number of population entries from the evolving population and defines them

13. Wetzel, A., Evaluation of the effectiveness of genetic algorithms in combinatorial optimization, Unpublished manuscript, University of Pittsburgh (1983).

14. Booker, L., B., Improving performance of genetic algorithms in classifier systems, Proceedings of an international conference on genetic algorithms and their applications, pp80-92

to be the population for the next set of evolution operations. The output of this function is the next population or $population_{n+1}$.

There are advantages with being able to subsample an expanded population as a separate step, rather than having the population created by the crossover operator be the input to the next evolution cycle. Some of the advantages are that we can now easily control the size of the population going into the next generation. This added control can be utilized as a parameter similar to annealing. The concept is that as the population begins to stagnate or converge toward false optima, we can allow the size of the population to grow (increased population size typically allows for increased mutation probabilities). This has the advantage of increasing the potential for population entries to converge to the correct answer or at least break out of the false minimums without the need for increasing the mutation rate such that the the system begins to thrash.

Another advantage to the post subsampling is that it allows the evolution process an additional degree of freedom to either statistically, randomly, or by design select population members that should exist in future generations. For example, some algorithms may need or find it beneficial to have the parents of certain children remain in future evolutions.

3.3.9 The shuffle Operator

This operator is a simple shuffle operation. It can be likened to shuffling a deck of cards prior to dealing the cards for playing. The purpose for designing this operator is to be able to pass the evolving population through this operator at any time in the evolution process and randomize the order of the population entries.

For example, this is useful for reducing the correlation between sequential population entries subsequent to the replication operator. The replication operator simply accepts a population and reproduces the population entries some determined number of times. In doing so the replicated population contains groupings of the previous population.

For example:

1) If we let a X_n represent the n^{th} population entry we could describe a population by the set $\{X_1, X_2, X_3, \ldots, X_{m-1}, X_m\}$ were there are m entries in the population.

2) After the population under went replication my data management routines of the population would hold the replicated population entries as such:

   $\{X_1, X_1, X_1, X_1, X_1, X_2, X_2, X_2, X_3, X_3, \ldots, X_{m-1}, X_{m-1}, X_{m-1}, X_m, X_m\}$

   We can clearly see that the replicated population now has a positional relationship amongst the population entries

In order to decorrelate the order of the population entries we simply pass the replicated population through the shuffle operator, and now the population entries have no location / position correlation.

For example after the replicated population under goes the shuffle operator the shuffled population might look something like:

$\{X_3, X_2, X_1, X_{m-1}, X_1, X_2, X_1, X_2, X_m, X_1, \ldots, X_m, X_{m-1}, X_1, X_3, X_1, X_{m-1}\}$

3.3.10 The Character Function

For this problem case the function is simple. There are two types of population information being maintained. One is the average population utility for each evolution cycle. The second is the annealing temperature for the current evolution.

For the average population utility this is a simple function that is executed at the end of every evolution cycle. The result is stored within an array for use by other genetic operators. The array storage allows for a history of results to be maintained throughout the solution generation. The Average Utility Function AUF() is shown below:

$$AUF() = \frac{\sum_{i=1}^{i=N} NQC(POP_i)}{N} \quad : eqn\ 17\ A$$

Where N is the number of entries in the population. POP is the entire population for the current evolution. And NQC() is the previously defined function returning the Number of Queens Correct for an individual population entry.

3.4 N-Queens Solution Algorithm

For this problem case the function is simple. There are two types of population information being maintained. One is the average population utility for each evolution cycle. The second is the annealing temperature for the current evolution.

For this experiment we can conclude that the modified genetic operators are successful in optimizing the solution algorithm based upon the improved results shown in the previous figures. We can additionally conclude that the basic genetic operator functions are correct and can be utilized as building blocks to investigate more complex functions.

By way of the successful examples and solutions presented earlier I am also concluding that the data structures and data management routines developed to manage the populations are correct and do not adversely effect the solution algorithm. Factors of concern here were the possible interaction between the sequential linked lists of population entries. The shuffle operator appears to minimize / remove detrimental effects of sequential correspondence otherwise I do not believe that we would observe the excellent results.

We can also conclude that the hybrid crossover and hybrid mutation functions improve the convergence performance of the algorithm. This is demonstrated by the data of figures 3.3.3A and 3.3.4A.

4.0 Routing Problem and Genetic Algorithm Introduction

In Chapter 3 I developed the genetic algorithm fundamentals as well as several building blocks for implementing solution algorithms. This work was done using the N-Queens problem as the focus for development. I selected the N-Queens problem for ground work because of the magnitude of information available related to solving the problem, and also because the problem and solution can be made tractable.

In this Chapter I will begin discussions of the main investigation, Printed Wire Board (PWB) routing. I intend to utilize and build upon the fundamental information developed for the N-Queens problem to solve the PWB routing problem.

Section 4.1 and 4.2 are a brief introduction to the PWB routing problem. In subsequent Sections I will describe the genetic operators I designed to solve the PWB routing problem. The genetic operators described will be implemented for all solution algorithms with only slight modification to the utility function that tailors it to the individual solution algorithm being implemented and tested.

Chapters 6, 7, 8 will present the specifics of each solution algorithm; each Chapter describes a new solution algorithm. I attempted to utilize information learned in the prior experiments to best optimize a final solution algorithm. As the experiments progressed I enhanced the initial set of genetic programming tools that I developed to solve PWB routing problem.

4.1 Routing Problem Description

If we look back at the criteria for formulating a problem / solution methodology discussed in the introduction, we find that we must have:

1) A well formed statement of what the problem / question is
2) Criteria for determining an acceptable solution
3) Characteristics of the problem.

For the PWB routing problem these criteria are defined as:

1) Characteristics of this investigation is to model a rectangle of MxN cell positions, where each position represents one of two states, occupied or not. Each occupied state has a neighbor relationship, "connected to" or "terminator". By connecting carefully selected MxN cells, the algorithm will route all PWB traces.

2) A solution is acceptable if the algorithm is able to route all of the connections specified by the netlist or some specified percentage of the connections. Please note that this problem does have a tolerance range for its solution acceptability; hence, by definition there is more than one acceptable solution per net list.

3) For this problem there are three initial requirements.

   One: a net list exists for the circuit.

   Two: Parts placement has been performed.

   Three: a board of adequate dimension is defined.

4.2 PC Board Algorithm Model

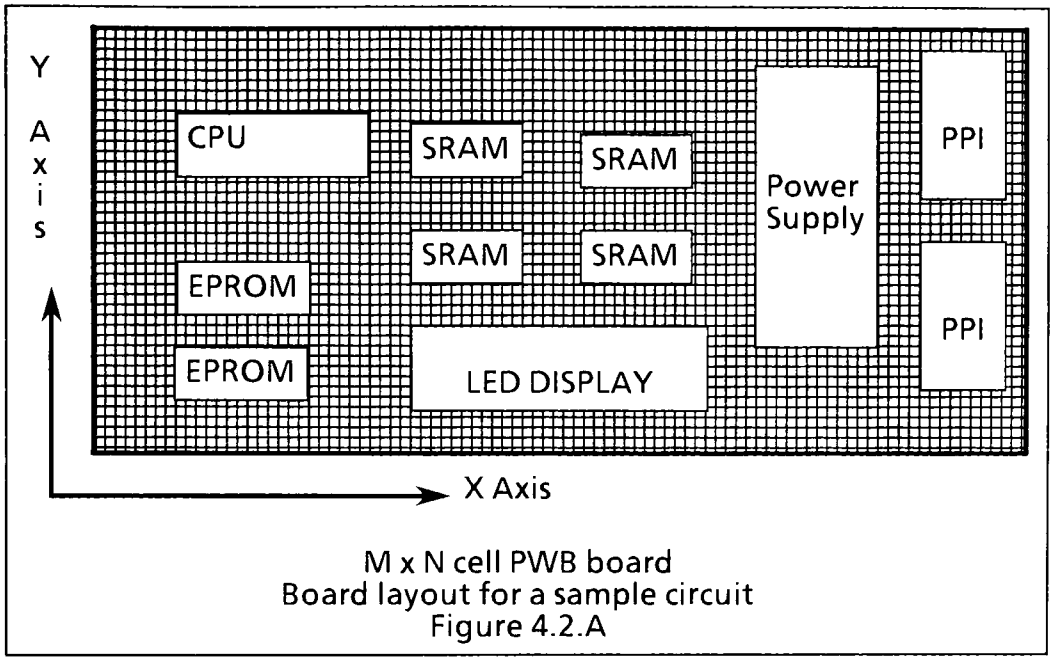
The first assumption required for all of my routing algorithms is that there exists a net list for the circuit to be routed and that the parts placement has already occurred. An example netlist is Figure 4.2.1:

This will give me a working board size upon which I can route the traces. I will treat the PWB as a rectangle of size MxN positions upon a cartesian grid. By using the analogy of a cartesian grid, I can associate trace starting points, trace ending points, and the trace path itself as a series of connected (X, Y) coordinates. Please refer to Figure 4.2.A as a sample board layout and grid overlay. This type of a layout is similar to the formats utilized in many of the solution algorithms for the Traveling Salesman problems and the euclidean distance minimization problems[1] [2]. Examples of a simpler board and its potential trace path routings are presented in the appendix as figures 4.2.B and 4.2.C.

Having the initial starting data, a netlist, a board size, and parts placement, I associate each trace starting point with an (X, Y) coordinate and each trace ending point with an (X, Y) coordinate. With these two data points for each trace, starting and ending point, the algorithm knows where the routing paths start and where they terminate. A routing path is deemed complete when two conditions are satisfied for the trace. Condition one is that there are a set of (X, Y) coordinate cells that can be traversed starting from a trace's starting coordinate and ending at the traces ending coordinate. The second condition is that all of the (X, Y) coordinates of the trace path are unique to the trace; the coordinates composing the path are not required or held by any other trace. From these criteria the algorithm can evaluate with certainty which routing traces are successful,

```
; a circuit for calculating a parity bit for a 16-bit word (an xor tree)
dimension (29,37)
; chip definition -- quadruple 2-input xor gates
chip type = ttl7486 pins = 14 horizontal = 2 vertical = 6
    vcc = 14
    gnd = 7
    a1 = 1
    b1 = 2
    y1 = 3
    a2 = 4
    b2 = 5
    y2 = 6
    y3 = 8
    a3 = 9
    b3 = 10
    y4 = 11
    a4 = 12
    b4 = 13

; power and ground are supplied here
hole (3,20)
hole (3,25)

; the 16-bit input word
hole (26,5)
hole (26,7)


; the output (parity) bit
hole (3,11)

; four instances of the above chip
chipat (6,5) name = xor0 type = ttl7486 orientation = normal
chipat (16,21) name = xor3 type = ttl7486 orientation = normal

; connect power and ground to all chips

connect (3,20) and xor1.vcc
connect (3,20) and xor2.vcc
connect (3,20) and xor3.vcc
connect (3,25) and xor0.gnd
connect (3,25) and xor1.gnd


; condense 16 bits into 8 bits
connect (26,5) and xor2.a1
connect (26,7) and xor2.b1
connect (26,9) and xor2.a2
```

Figure 4.2.1 Simple Net List Example



M x N cell PWB board
Board layout for a sample circuit
Figure 4.2.A

incomplete, or unsuccessful. Hence, the algorithm has a mechanism to measure its progress.

Each of the three algorithms designed and discussed attempt to evolve the population entries (trace paths) toward acceptable valid solutions. The evolution process is designed to evaluate, select, and compete for intermediate (X, Y) coordinates in order to evolve the trace paths to successful completion, connecting starting point to ending point. A highly active population will have all of its trace entries advancing one coordinate position per evolution, though it is not expected that all trace entries will advance during every evolution cycle.

The algorithm monitored and characterized evolving populations. Population entries that cannot progress any further, those that have either terminally

1. Moopenn, A., & Thakoor, A., P., & Duong, T., A Neural network for Euclidean distance minimization
2. Van Den Bout, D., E., & Miller, T., K., A traveling Salesman Object function that works, North Carolina University

stagnated or lost all utility, are removed from the evolving population. Population entries that are demonstrating progress towards completion are promoted during future evolutions.

To summarize, initial algorithm requirements are:

A netlist exists (Trace starting and ending points are defined)

Parts placement has occurred

PWB size is known

From these initial data points, the algorithm will evolve a population of PWB traces to successful completion.

4.3 Core Population

Each population entry, hereafter referred to as a POPE, is equated to a trace path attempting to be routed. The POPE assigned value can be one of three types:

1) (X, Y) trace starting coordinate found in the netlist / placement data.

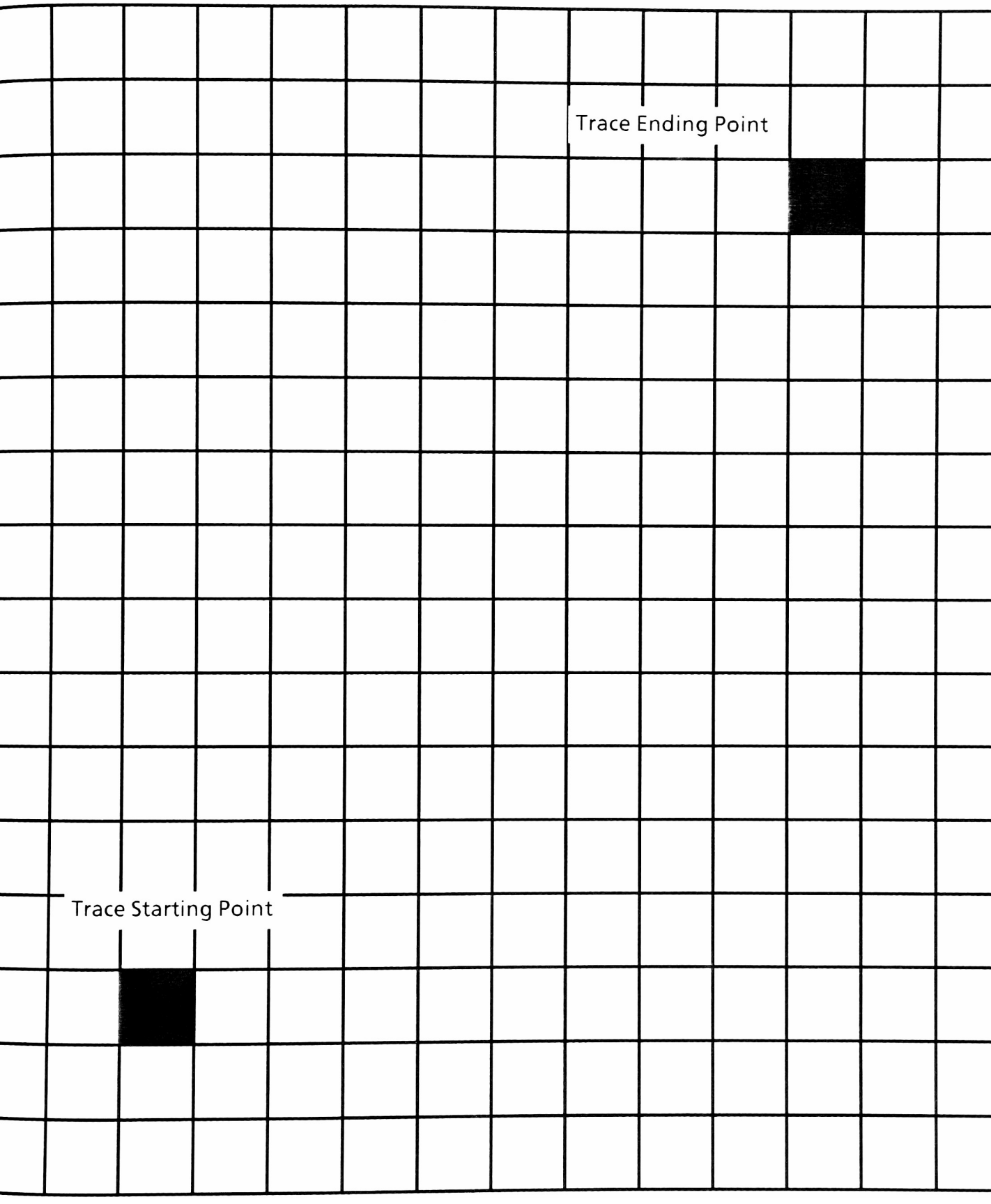
2) (X, Y) trace ending coordinate found in the netlist / placement data.

3) Set of (X, Y) coordinates that represent a trace's quantized ratnest path. Please refer to Chapter 7 for definition of a ratnest path.

Prior to the start of the algorithm, a core population is created. The core population is simply a list of one POPE per PWB trace, as identified in the circuit's netlist, and is labeled COREPOP. The POPEs of the COREPOP are considered the start of a family or blood line. POPEs from the core population are replicated and gathered to form the initial population for the genetic algorithm.

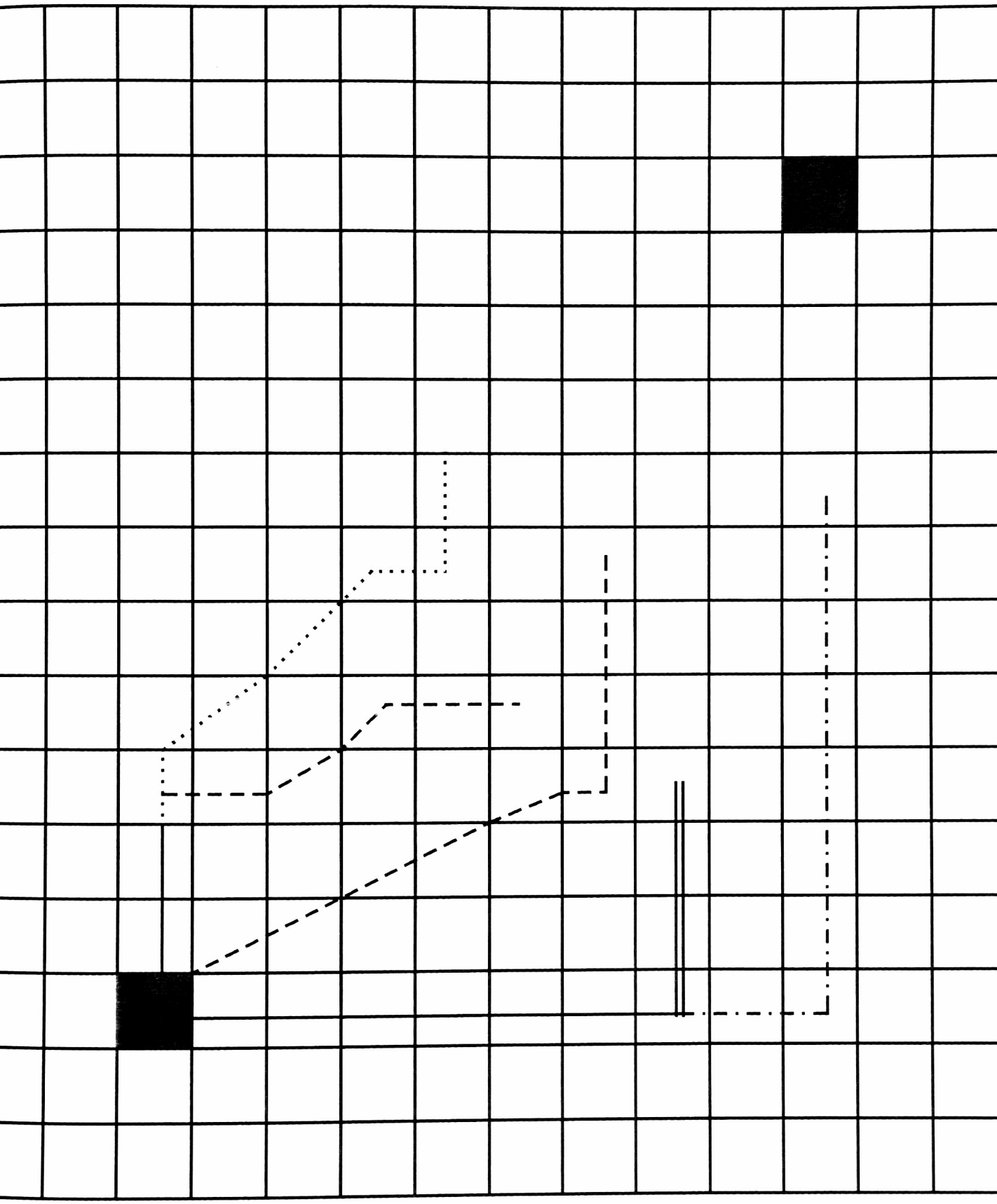
This process and the definition of an initial population will be discussed in Chapter 5, Section 5.2.

I use the notion of family / blood line to connote the relationship of the offspring that evolve during the evolution process to their parents from the COREPOP. Each trace entry to be routed represents a family / blood line, and the offspring of each family work collectively to solve each trace routing path. The two figures below illustrate what is means by a blood line. The two blackened cells in Figure 4.3.1.A are the two end points of a trace to be routed. The trace end points are what make up the population entries (POPEs). Figure 4.3.1B show the POPE of Figure 4.3.1.A after several generation cycles where intermediate cells on the way towards the trace end point have been captured. Figure 4.3.1.B shows multiple paths being established that are developing their way towards the single end point. These multiple trace paths being explored are what I refer to as a POPEs family / bloodline.



Example of a Blood line for one routing trace

Figure 4.3.1.A



Example of a Blood line for one routing trace

Figure 4.3.1.B

4.4 Fundamental Characteristics of Solution Algorithm

For the solution algorithms presented here, an initial population of POPEs is generated from the core population and contains one or more POPEs for each trace to be routed. In other words at least one representative for each trace to be routed is in the initial starting population and is active at all times right from the start.

The algorithm evolves the population towards a solution. During the evolution process there are only two ways in which a POPE is removed from the population, by either completing its trace path successfully (finding the trace's end point coordinate), or failing and dying. No matter what the condition is, success or failure, at least one single POPE is removed from the evolving population. Following is a detailed discussion of the two ways in which a POPE can be removed from the evolving population; they are:

- One, by a POPE successfully completing its routing path.

  In the case of success, the POPE's coordinates are marked as routed and remain unavailable to other POPEs. Upon successful completion, the entire blood line of the successful POPE is removed from the evolving population. If a POPE is successful in finding a routing path to its end point, then the POPE is removed from the active evolution list; its coordinates / trace path are left marked as a valid trace, and all its other family members are removed from the active population. This is because there has been a successful path found and will be preserved; therefore, the other family members are no longer needed for searching a valid path. Coordinates occupied by the other family

members of the successful POPE are freed up and placed upon the available neighbor list for other POPEs to utilize.

- Two, by a POPE failing to progress during the course of evolution. Failure to progress is characteristic of a POPE stagnating and / or losing all its utility value.

  The ways in which POPEs die are numerous. For example, a POPE may route itself into a position where there are no available neighbors and it has not reached its destination point. In this case, only a single POPE is removed, not all of its family members. A POPE may bid all of its money / utility away before reaching its destination. This death is dealt with similarly to the above stagnation case.

  In the case of failure only the failed POPE is removed from the population, not its entire blood line, as in the successful case. Also in the case of failure the POPE's coordinate positions are returned to the available list of neighbors for the board; other POPEs may begin to utilize the freed up coordinates.

Solution algorithms investigated within this thesis do not perform any "backtracking". What I am referring to here is that as POPEs are removed from the population there are board cells that become available. The algorithms I will present have no mechanism to go back and reevaluate the merit of freed up board cells to existing POPEs. The algorithm does not backtrack k through prior evolutions and reevaluate trace path decisions based upon the newly freed board cells. However, the newly freed board cells are available for evaluation and use in future population evolution cycles.

POPEs, in trying to rout a path from starting point to ending point, are able to wind in any possible direction (move at any available angle, full 360 degrees). This means that it is possible for a POPE to loop back and begin pursuing a direction opposite that of where its destination end point is. For example in

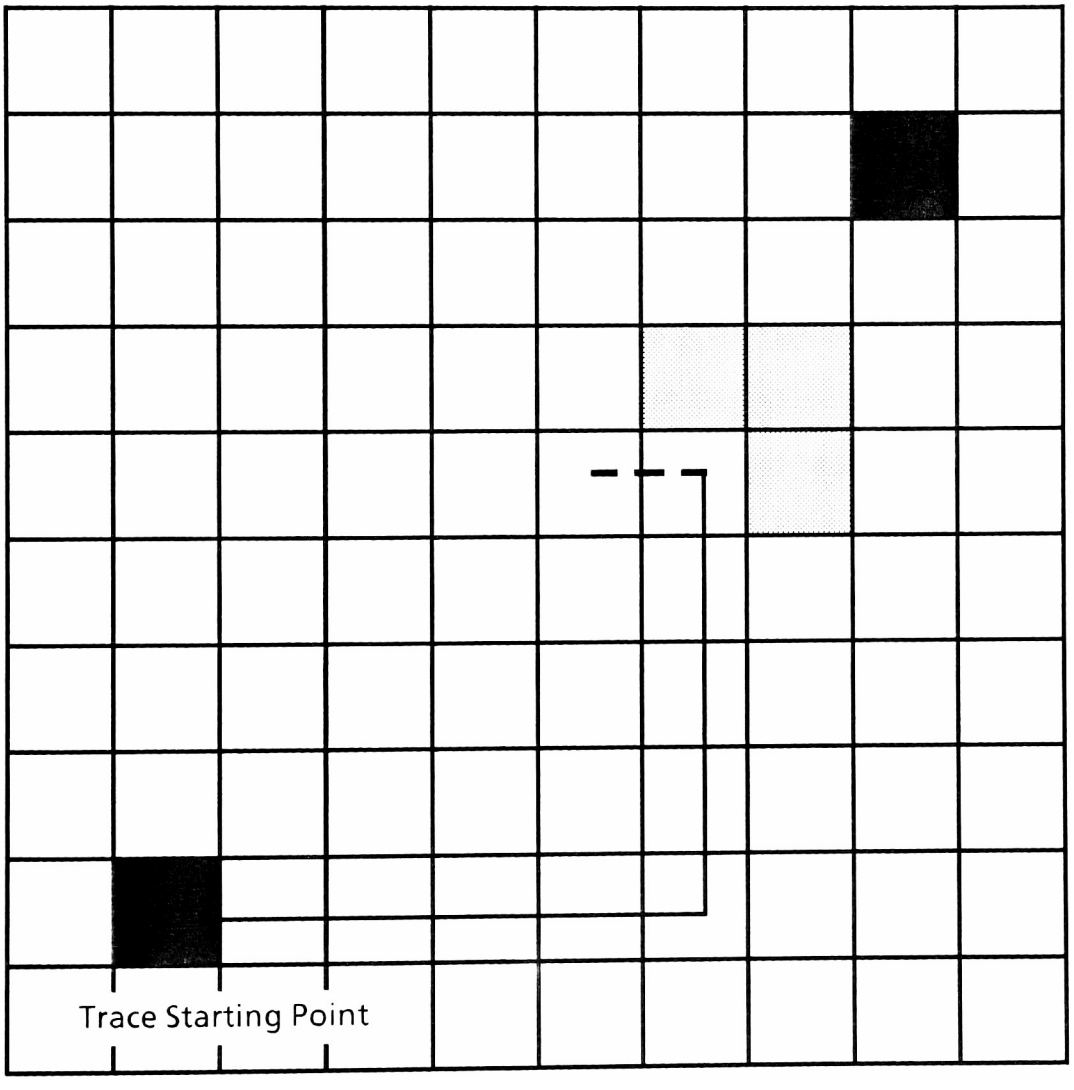


Figure 4.4.1
Trace paths reversing directionality

Figure 4.4.1 the trace direction turns back upon (see the dashed trace segment)

itself because forward motion is no longer possible. The shaded squares are indicate squares that are not available to the current trace path.

At this point we have talked about the board layout and the algorithm representation of the POPE's. We have also mentioned briefly some of the set up characteristics of the input population to the algorithm as well as general characteristics of the individual POPEs.

Another algorithm characteristic is that as POPEs die unsuccessful deaths (a trace path can not be routed to any other board cells yet the trace has not completed in routing path start to finish), they are not restarted into the evolution process. The potential problem here is that if a family blood line is so unsuccessful that all the POPEs of the family die of failure, there is no mechanism to retry and route that trace path. This trace path is marked as unsuccessful and left out of the routing process.

Another characteristic of the algorithm is that the total size of the population at each evolution cycle is allowed to fluctuate within a user or algorithm specified range. The population entry count fluctuates due to the removal of traces, due either to success or failure. The adding of a POPE's parents at the end of each evolution is also a factor in fluctuating the population size. The population is capable of growing during genetic replication, evolution and resampling stages.

4.5 Algorithm Initial Requirements

- Netlist of the PWB exists.

  A net list for a circuit is the listing that describes all of the pin to pin connections for the system. Refer to Figure 4.2.1

- Parts placement for the system is done.

  This body of information identifies where all of the circuit components are to reside on the given PWB. For example the placement information identifies where all of the power and ground lines are to be. It also identifies where all of the chips of the circuit are to be placed and what their orientation is to be. Refer to Figure 4.2.A.

- Sufficient PWB board size MxN is defined.

  This is the size of the PWB board it self. The only requirement of this value is that the placed circuit must fit within the given dimensions with 1" surround on all edges. Refer to Figure 4.2.A.

These initial requirements are essential to all of the solution algorithms investigated. From this supplied information the user can run the system and generate solutions to the given routing problem.

4.6 Genetic Solution Algorithm Functional Flow Description

Please refer to the appendix section 11.4.6.X for several drawings of the major components of the solution algorithm. They are provided to give a high level description of the components of the solution algorithm and their relationships within the solution evaluation. The figures 11.4.6.X within the appendix are a graphical representation of the algorithm flow of operation.

Diagram 4.6.1 of the appendix shows the main solution generation routine. This set of modules represents the components of the genetic algorithm that evolve the population towards a solution. The current population (set {POPE}) is fed through

each of the algorithm modules in sequence. One evolution cycle has occurred every time the currently evolving population has completed a full cycle of the genetic algorithm modules (Figure 4.6.1).

The following are high level procedural descriptions for each of the genetic solution algorithm components. The actual function definitions will be presented in detail later in Chapter 5:

- *Replication Operator*:

$$\left\{\{Replicated\,Population\}_a\right\} = \sum_{m=POPE_1}^{m=POPE_n} Replicate(POPE_m) \quad EQN\,18$$

This function accepts the current input population and replicates each POPE some number of times. The actual number of times that any POPE is replicated is based upon three primary criteria:

1) Utility of the $POPE_m$

2) Characterization of the current $POPE_m$ relative to the entire {POPE} set

3) Randomness, some small random factor

The replicate function evaluates the utility and character of each POPE and then adds a random component to generate the number of times that a POPE is to be replicated. The POPE is then replicated and inserted into the replicated population set $\{POPE\}_a$.

- *Crossover Operator*:

$$\left\{\{Crossover\,Population\}_b\right\} = \sum_{m=1}^{m=Number\_to\_cross(POPE_n)} Crossover(\{Replicated\,Population\}_a) \; EQN\,19$$

The replicated population set, $\{POPE\}_a$, is then fed into the crossover operator.

This function is implemented in two steps:

- step one is to select two POPEs to be entered into crossover from the working population set $\{POPE\}_a$(less any previously selected POPEs).
- Step two is the actual crossover of the two selected POPEs, hence creating a new POPE, which is placed into the evolving population $\{POPE\}_b$.

The actual crossover operation can be one of two types: 1) single point crossover or 2) dual point crossover. Factors considered by the crossover operator are:

1) Purely random selection

2) POPE blood line relationships

3) POPE grid coordinate relationships

The crossover operator evaluates the input population set $\{POPE\}_a$ and selects two POPEs from the input set based upon POPE relationships, given the above three categories. By filtering the POPEs to be crossed, we limit the number of invalid POPEs that will be generated or placed into the evolving population. The result is to focus / direct the solution algorithm to operate primarily upon POPEs that have a statistically higher correlation with the final solution set of POPEs.

This type of restriction of population entries in order to reduce the search space can be visualized, in terms of set theory, as follows. The entire possible solution space can be modeled as shown in Figure 4.6.0:

Knowing the sets that comprise the entire population, we can begin to derive simple set theory equations that define the population by its entities. For example, based upon Figure 4.6.0, we can write the following equation for the entire population:

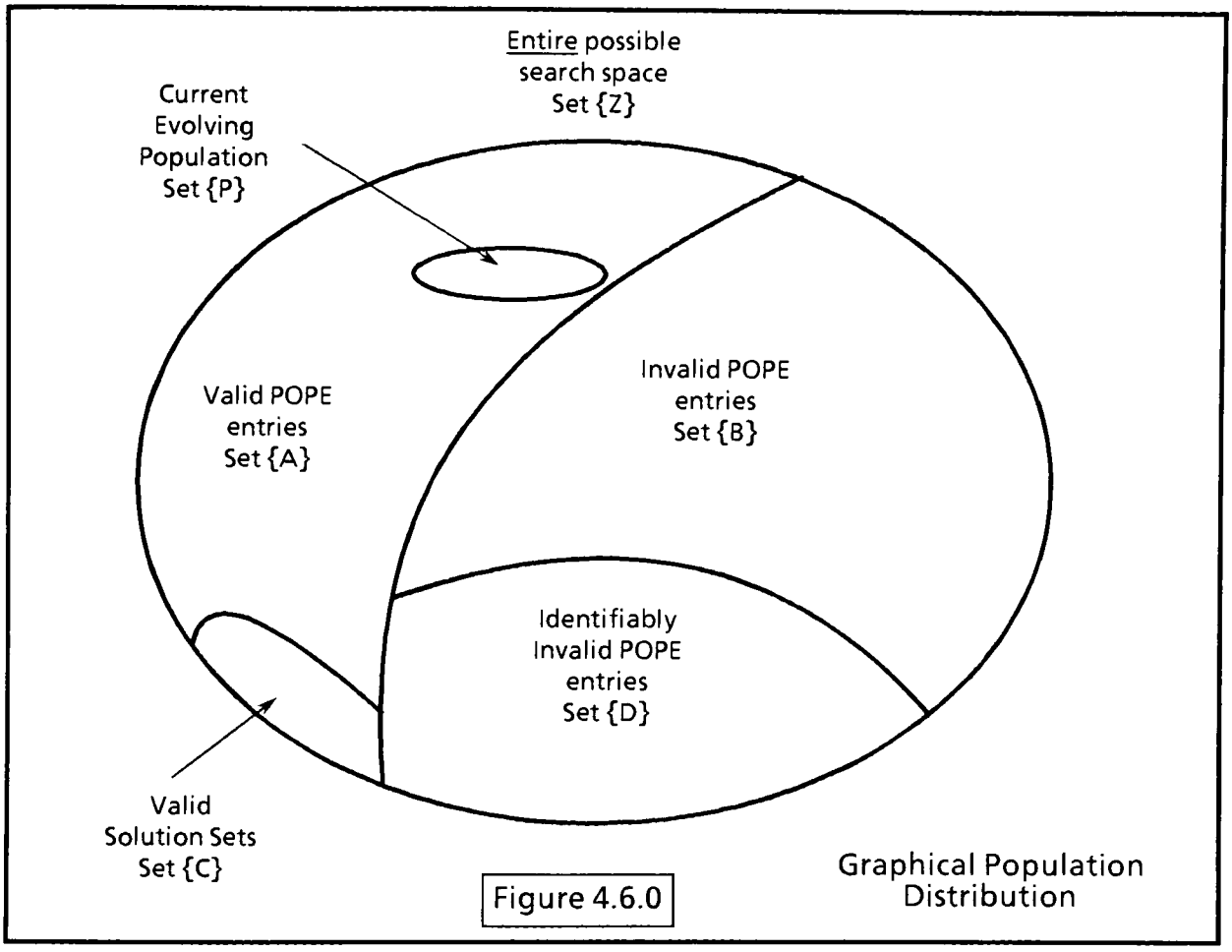

Entire possible
search space
Set {Z}
Current
Evolving
Population
Set {P}
Valid POPE
entries
Set {A}
Invalid POPE
entries
Set {B}
Identifiably
Invalid POPE
entries
Set {D}
Valid
Solution Sets
Set {C}
Graphical Population
Distribution

Figure 4.6.0

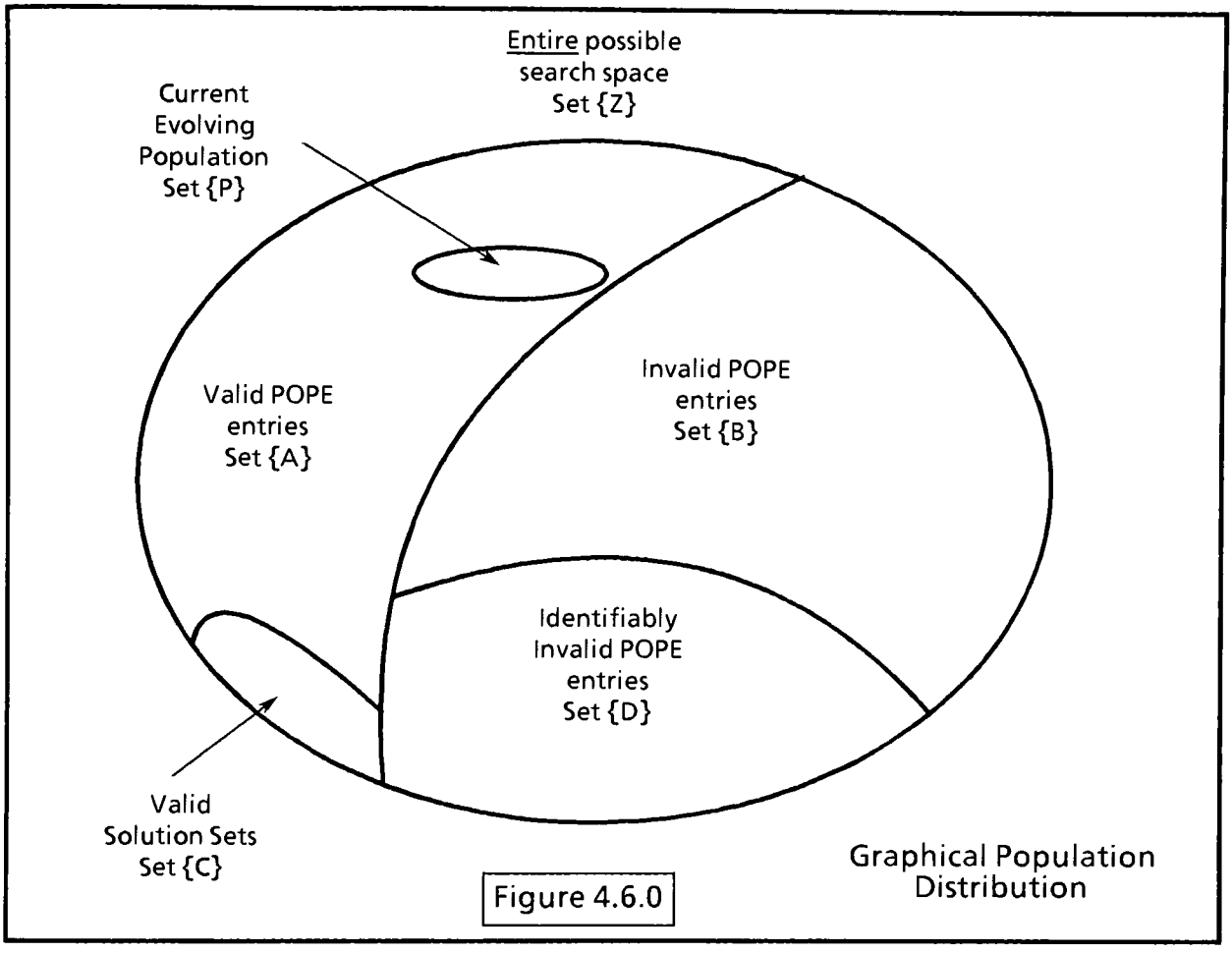


Figure 4.6.0

$$Population\ Set\{Z\} = \{A\} \cup \{B\} \cup \{C\} \cup \{D\} \quad EQN\,20$$

With out any type of population / POPE filtering we would not be able to eliminate some of the invalid POPE entries. Therefore, our working population also would be required to search the trivially invalid POPE entries, e.g. those of set {D} within Figure 4.6.0. Hence without filtering, the search space is equivalent to the size of the entire possible population set {Z}.

$$Population\ Set\{Z\} = \{A\} \cup \{B\} \cup \{C\} \cup \{D\} = Unfiltered\ Algorithm\ Search\ Space \quad EQN\,21$$

With the ability to filter out some of the trivially invalid POPE entries from the search space we can write the equation below, which describes the possible search space:

$$Filtered\ Algorithm\ Search\ Space\ \{F\} = \{Z\} \cap \{\overline{D}\} \quad EQN\,22$$

By inspection set {F}, is a smaller set than {Z} hence we are already optimizing the algorithm by eliminating some of the trivially invalid POPEs.

As discussed earlier in Chapter Three, Section 3, the algorithm designer needs to be cautious not to cause "inbreeding" within the evolving populations, which causes in stagnation of the evolving populations. The way this is prevented is:

1) Allow for purely random crossovers to occur.

2) Monitor the variance of the population and adjust the mutation rates accordingly

3) Monitor the growth rate of the population via the character function and dynamically adjust the algorithm parameters to avoid stagnation.

These filters / evolution-monitoring routines are designed to compensate the above mentioned parameters in order to prevent stagnation or convergence upon a false minimum. As these filters determine that the evolution algorithm is stagnating or the rate at which new cells are being captured is declining, etc., the mutation rate may be increased. Likewise the population size may be increased and / or additional parents may be added back into the population. All of these compensations are performed in order to keep the solution algorithm proceeding towards finding a solution.

- *Mutation Operator*:

$$\left\{\{Mutated\,Population\}_c\right\} = \sum_{m=POPE_1}^{m=\{POPE_n\}b} Mutate(POPE_m) \quad EQN\,23$$

This operator utilizes the trace distance estimator function, population characterization function, and the annealing function. All of these inputs are utilized to characterize the state of the evolving population. The mutation function determines the condition of the current evolving population and the condition of each individual POPE. It then determines whether the POPE is to be entered into mutation. In deciding to mutate individual POPEs, the mutation operator attempts to insure that the population is not stagnating to false solutions, as well as insuring that the population does not begin to thrash.

For this solution algorithm the mutation operator cannot be simple random bit flipping. What I did was to design a mutation operation that would introduce random change in a manner that was more suitable for the problem and its representation.

For additional descriptive information on the mutation function, refer to Chapter Five, Section 5.9.

- *Resample Operator*:

$$\left\{\{Resampled\ Population\}_d\right\} = \sum_{m=POPE_1}^{m=POPE_n} Resample(\{POPE_m\}_c) \quad EQN\,24$$

The resample operator has two modes of operation.

1) Purely random resampling

2) Blood line filtering mode

In mode one above the resample operator is fed an entire current working population set $\{POPE\}_c$. From this set a predetermined number of POPE entries are selected, purely at random, and placed into the set $\{POPE\}_d$. The new set $\{POPE\}_d$, is then augmented by adding some of the parents from the immediately

preceding evolution cycle. This newly formulated set of $\{POPE\}_d$ then becomes the input population to the next genetic algorithm cycle.

In mode two the resample operator does pseudo-random resampling. The difference is that in this mode the resample operator will make predetermined choices as to which POPEs from the set $\{POPE\}_c$ to carry forth into the next set $\{POPE\}_d$. The predetermined choices are made by rules such as:

- Insuring that there are at least two POPEs from each blood line (trace representative).
- The utility of a POPE relative to the average set $\{POPE\}_d$ utility value, as well as the statistical correlation of a POPE relative to the set $\{POPE\}_d$.
- Estimated trace distance to completion (e.g., augment with traces that have very low estimated completion distances).
- Parents from the previous population set $\{POPE\}_a$ are added back into the set $\{POPE\}_d$

These directed selections are done with care so as to not redirect the population evolution onto false solutions. The basis for directing the resample operator is to guide / restrict the POPEs that enter into the next evolution cycle to POPEs that are of high potential and not trivially invalid. I also need to insure that a blood line does not get lost in the evolution process. This would be a false death, and the trace would never route.

- *Shuffle Operator*:

$$\left\{\{Shuffeled\ Population\}\right\} = \sum_{m=POPE_1}^{m=N} Shuffel(\{POPE_m\}) \quad EQN\,25$$

This operator performs a simple random shuffling of the set of POPEs that are handed to it, analogous to shuffling a deck of cards. This operation is utilized because the genetic algorithm, as I implemented it, serially concatenates POPEs into a list that becomes the next set of $\{POPEs\}_n$. Because of the way the list is generated, adjacent entries are highly correlated. This correlation could cause "in breading," which leads the evolving population to stagnate and / or converge to false minimums.

4.8 Genetic Characterization Function

For these algorithms I implemented simple population character functions and individual POPE character functions that monitor vital statistics of the evolving population. The character function looks at statistics of both individual POPEs and the population as a whole. Some of the parameters considered for the character function are:

1) Number of POPEs that advanced in the current evolutionary cycle.
2) The average utility of the entire population.
3) Estimated distance required to route the remaining traces.
4) Average number of evolution cycles for population POPEs.
5) Current and past annealing temperature.
6) Average number of POPEs that advance per evolution cycle.
7) Population skew, Kurtosis, and variance.

The character function scans the current population and keeps a history of past data items, which is utilized to evaluate trends of the population. From data gathered, the characterization function then sets certain condition flags and adjusts some of the biasing and randomization constants. These condition

variables are used by the other genetic operators such as crossover and mutation in order to control the evolution algorithm and optimally direct it to converge upon a solution.

For example, the character function evaluates and compares the mean of past populations. This information is evaluated and used to monitor the population growth rate (up, down, stagnate, thrashing). A population can be assumed to be thrashing if consecutive population means fluctuate by large amounts. Similarly, a population may be considered to have stagnated if its mean does not change after many evolution cycles.

Other information that is maintained by the character function will be listed in Chapter 5, Section 5.2. The way in which this information is utilized by the genetic operators is:

- If a population is negatively skewed, the REP() and NPTA() operators will modify their characteristic equations to attempt to compensate for the poor populations that are evolving.

- If a population's kurtosis is spread too long and or if the variance is too great, then this is a sign that the evolution algorithm is causing thrashing. The algorithm is exploiting / thrashing through the solution search space rather then effectively exploring it for a solution.

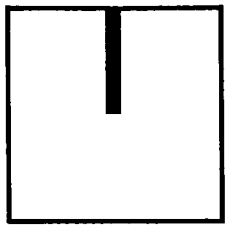
The goal is to collect and monitor the characteristic evolution information and utilize this to optimize the genetic operators. Operators such as annealing, replication, mutation all are designed to utilize the character function information to try and adjust their behaviors.

4.9 Routing Map Overview

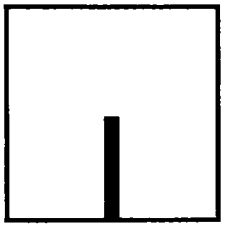
The Routing map is managed as a cartesian grid composed of rectangular cells. These cells are filled with the primary schema symbols that represent trace path components, connection pads, trace joints, etc. The solution algorithm selects cells from the grid according to the genetic algorithm rules. The selected cells then are filled in with the schema symbols that join together to form the routing trace from the net list.

- Figure 4.9.1 illustrates the schema symbol set for constructing trace paths in any of the 90 degree rotations out of the 360 degree circle.
- Figure 4.9.2 illustrates the schema symbol set for constructing trace paths in any of the 45 degree rotations at 90 degree intervals out of the 360 degree circle.
- Figure 4.9.3 illustrates the schema symbol set for constructing trace path mounting holes and connection joints.
- Figure 4.9.4 illustrates the schema symbol set for constructing a trace path through the edges / corners of cells. These are designed to better utilize cells when there are diagonal paths through them.

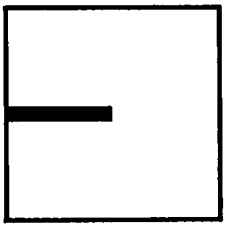
Each of the schema symbol blocks are sized to fit entirely into one cell of the routing board (a cartesian grid, as discussed earlier). The algorithm is designed to logically combine the schema blocks in order to build the routing trace paths required to solve the problem. Figure 4.9.5 through Figure 4.9.12 show example diagrams of how the schema blocks are combined in order to connect a trace path.



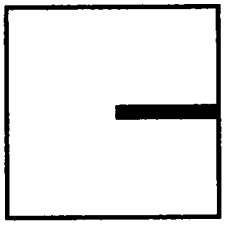
Schema A
Vertical line segment upper half



Schema B
Vertical line segment lower half



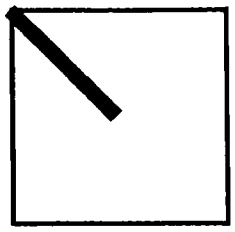
Schema C
Horizontal line segment left half



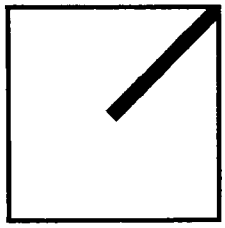
Schema D
Horizontal line segment right half

Figure 4.9.1

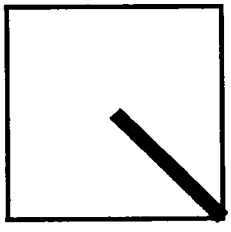
In the example of Figure 4.9.5 our PWB is a 5x6 cell board, and we wish to connect the three darkened cells. An 'animation' that shows the combining of schema blocks used to complete a trace routing path is provided in the appendix as figures 4.9.6 through 4.9.12. This combining of blocks is how the routing algorithm builds a trace path in order to complete the routing problem.



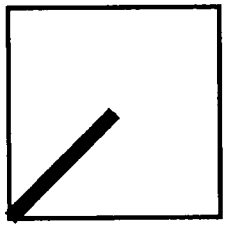
Schema E
Left -45° line



Schema F
Right +45° line



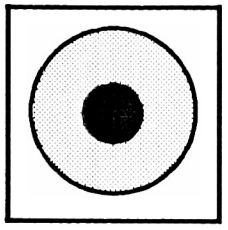
Schema G
Right + 135° line



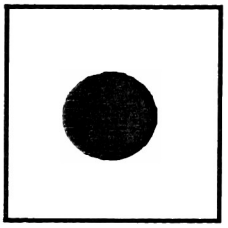
Schema H
Left + 225° line

Figure 4.9.2

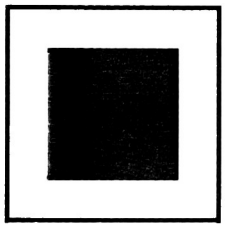
One caveat that needs to be pointed out here is that there are precautions that need to be taken when determining the availability of cells for occupancy. For example, one does not want trace paths to occur as shown in Figures 4.9.13 through 4.9.14. Therefore, in order to insure that anomalies like this do not occur



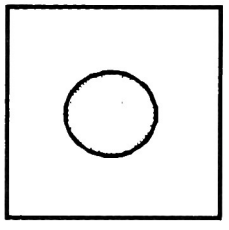
Schema I
Hole for connection



Schema J
Via for layer transition



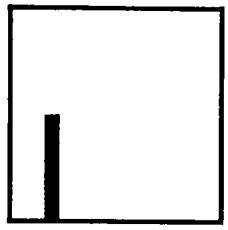
Schema K
Solder pad for connection



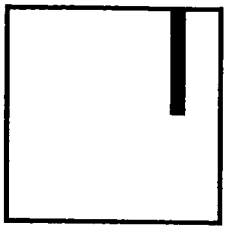
Schema L
Trace connection joint

Figure 4.9.3

the algorithm has multiple evaluations it performs when determining the eligibility of its neighboring cells for occupancy.

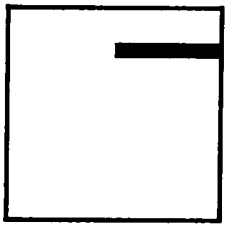


Schema M
Left Vertical

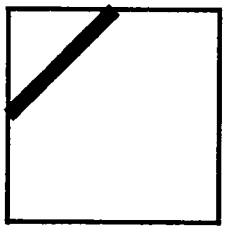


Schema N
Right vertical

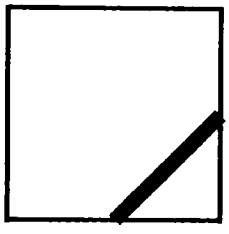
Schema O
Lower Horizontal



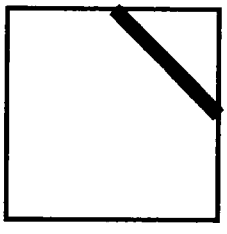
Schema P
Upper Horizontal



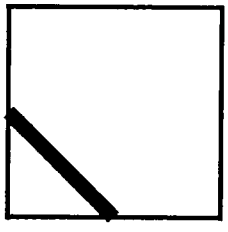
Schema Q
Diagonal



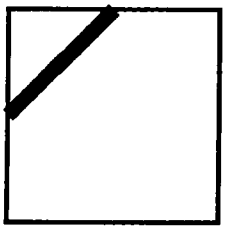
Schema R
Diagonal



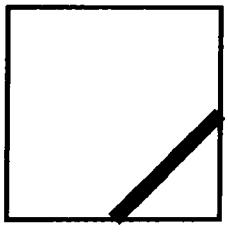
Schema S
Diagonal



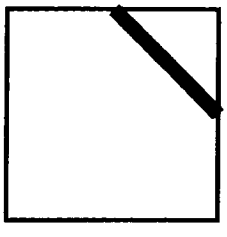
Schema T
Diagonal



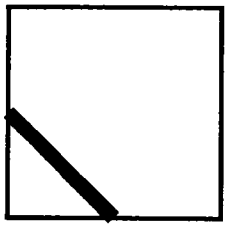
Schema Q
Diagonal



Schema R
Diagonal



Schema S
Diagonal



Schema T
Diagonal

Figure 4.9.4

These are the remaining Schema Cell blocks that are utilized to construct trace paths. For the rotations that are not shown it is implied that they are available by simple cell rotations.

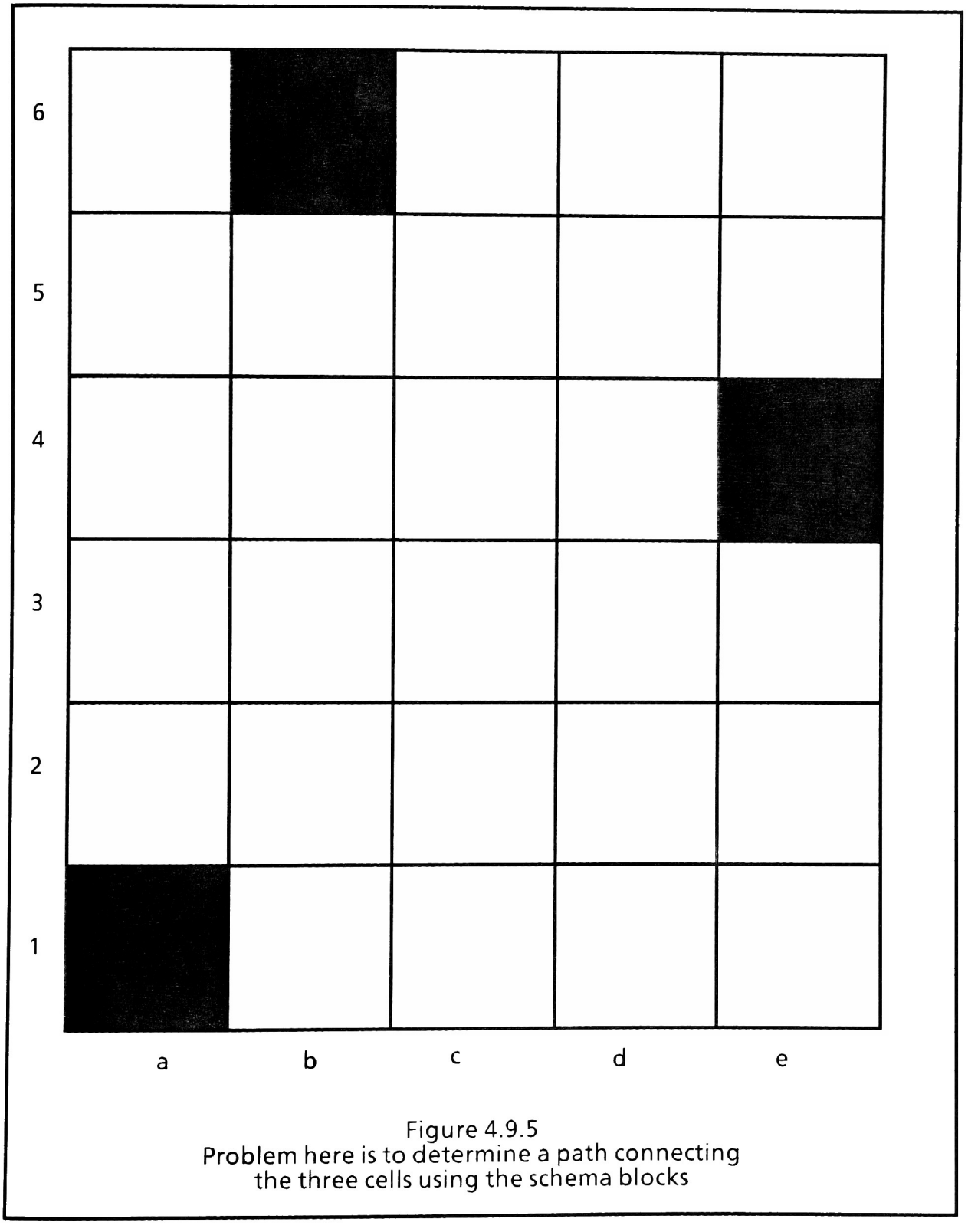


Figure 4.9.5
Problem here is to determine a path connecting
the three cells using the schema blocks

In this example the problem was to connect the two sets opposing cell blocks (horizontally / vertically)

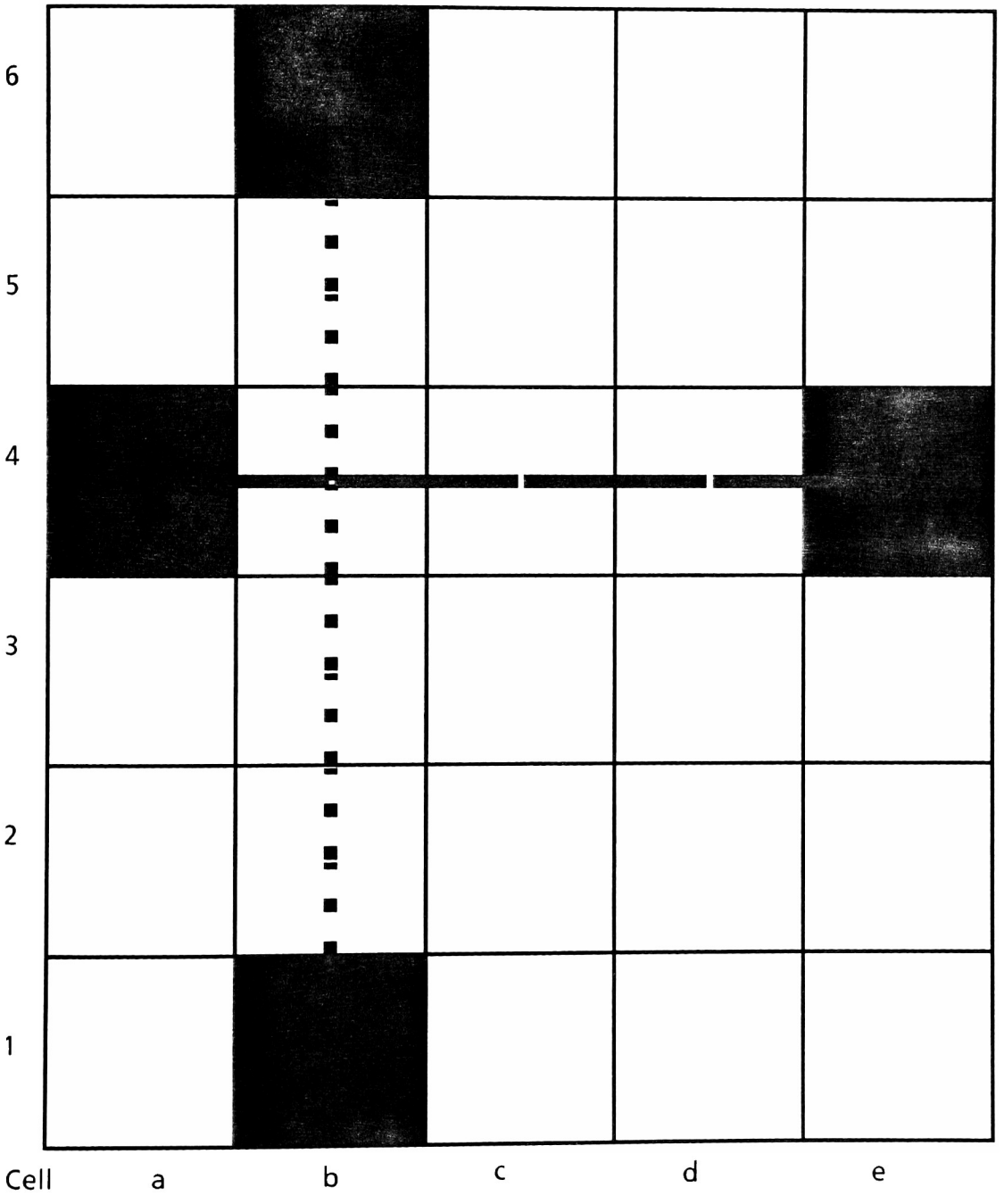


Figure 4.9.13
Here there are two traces that should not be overlapping because they are two independent traces and yet they share one PWB cell in common

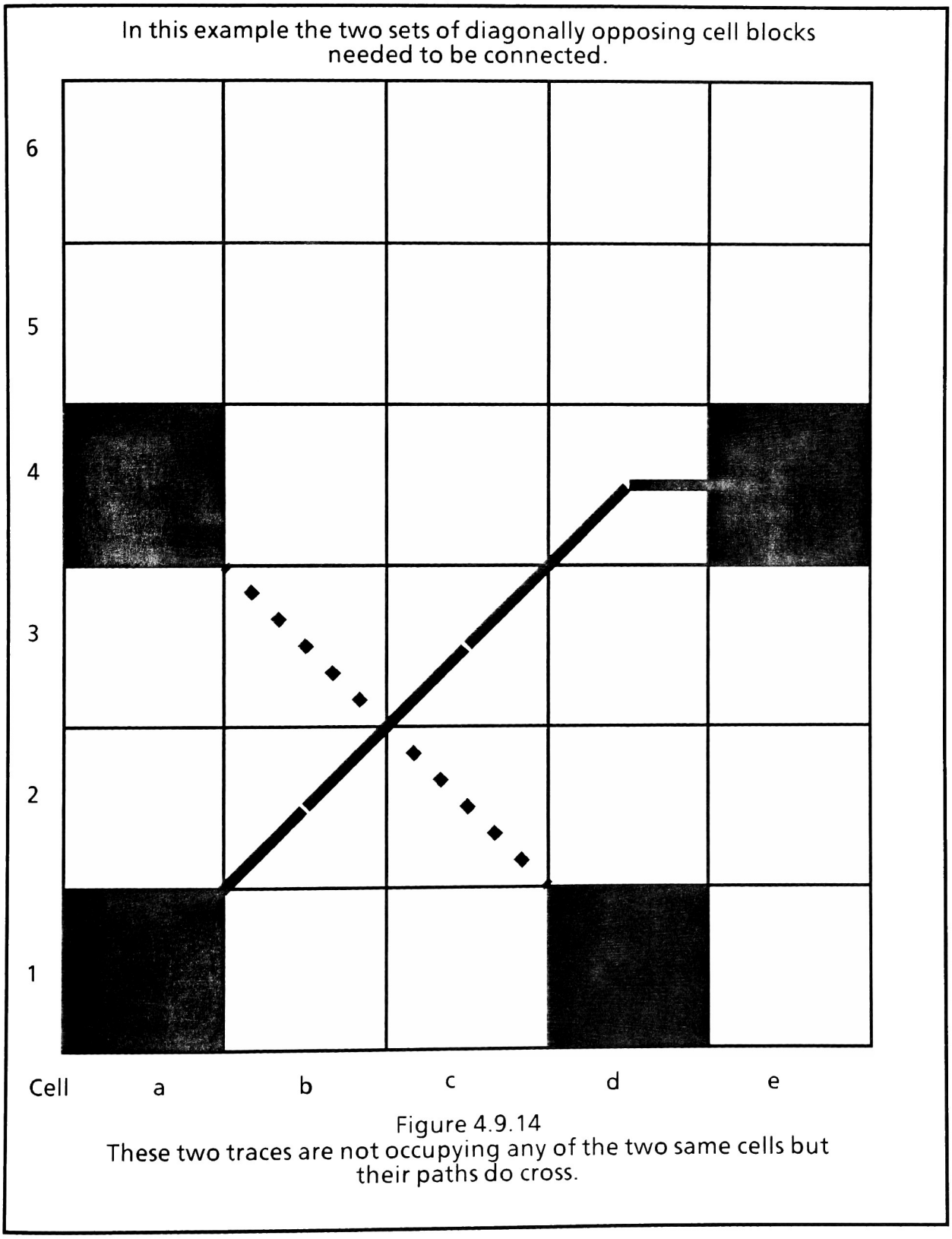


Figure 4.9.14
These two traces are not occupying any of the two same cells but their paths do cross.

5.0 Genetic Algorithm Routing Equations

In Chapter Four, I presented a general overview and high level description of the routing algorithm and genetic operators. In this Chapter I will present the solution algorithm equations and a description of their function for the routing problem. The algorithm equations presented here are derivatives of the solution equations discussed in Chapter Three and Four; I recommend that the reader refer back to Chapter Three or Four for any additional information on the genetic operators / functions not repeated here. The solution to the N-Queens problem served as ground work for the development and characterization of the solution equations to be utilized for the routing problem.

As in Chapter Four, the functions presented here are utilized for all of the genetic routing algorithms developed in Chapters, Six, Seven, and Eight.

5.1 Genetic Character Function

This function is utilized to monitor the characteristics of the evolving population. The specific features of the population that are maintained / tracked by this utility are:

- Population average : see Chapter 2 eqn # 2

  This information is maintained as a vector of the last N values for the average POPE utility, average number of trace jogs, estimated average distance for trace completion.

- Population standard deviation : see Chapter 2 eqn # 3

This information is maintained as a vector of the last N values for the standard deviation re: POPE utility, number of trace jogs, estimated distance for trace completion.

- Population variance : see Chapter 2 eqn # 1

This information is maintained as a vector of the last N values for the variance re: POPE utility, number of trace jogs, estimated distance for trace completion.

- Population Skewness : see Chapter 2 eqn # 4

This information is maintained as a vector of the last N values for the population skewness re: POPE utility, number of trace jogs, estimated distance for trace completion.

- Population Kurtosis : see Chapter 2 eqn # 5

This information is maintained as a vector of the last N values for the population Kurtosis re: POPE utility, number of trace jogs, estimated distance for trace completion.

- Estimated average distance for trace completion

This function is not updated every evolution cycle. the frequency with which this is updated is either set by the user or defaults to every 5 population evolution cycles. There are special cases that will force this function to be updated they are:

1) Three or more traces complete their path
2) The average population utility plateaus and / or falls for five consecutive population evolution cycles

- Annealing Temperature

Depending upon how the population average utility grows and the estimated trace distance to completion falls, this value is updated. If the population is evolving positively at a steady rate then the annealing temperature is reduced; otherwise it is increased.

The actual annealing temperature is calculated by the following formula:

$$Anneal\,Temp = \frac{Average\,Estimated\,Remaining\,Trace\,Distance}{Average\,Population\,Utility} \quad EQN\,26$$

Most of the mutation and random functions utilize the annealing temperature to determine just how much variability (randomness) the population can tolerate.

In summary, the characterization function is a major data bank that stores historical characteristic data describing how the evolution is proceeding. Most of the genetic operators solicit information from this data management function in order to perform their operations.

5.2 Genetic Utility Function

This algorithm was set up to use a weighting scheme that considered the following as some of the criteria in order to determine which neighbors to bid for and how much to bid: the element of probability, the merit gained from the prior evolutions / biddings, the number of "jogs" in the path, the general direction (is it towards the destination or not), how much strength does the entry have to compete with, current traveled distance, and approximated distance to ending point. All of these factors plus others are combined as factors into the utility polynomial. This Polynomial has the form:

$$U_i = \sum_{m=1}^{m=i} A_i * F_m(X_m) \quad EQN27$$

Where A is a normalizing / scaling constant and $F_m( )$ is a function that evaluates and bounds the characteristic. An example of F() could be as simple as a MAX(), MIN() function, a COS() function, or a polynomial itself. The intent is to be able to define a function yielding a single value that considers all of the characteristics required to bid.

As a simple example of this technique, the definition of U_i is:

Bidding criteria for this example will be:

$F_1(X) = \text{strlen}(X)$	:	Trace length of X
$F_2(X) = U_{i-1}$	:	Utility of the prior generation
$F_3(X) = Z * \text{Rand}(X)$	:	Random percent Z with X as the Seed
$F_4(X) = \text{Rdist}(X)$	:	Estimate of remaining distance to end point

Please note that not all the string length functions will return the same value at each iteration. This is because some traces will terminate / complete before others and some traces will lose entirely in the bidding process; hence, for a given generation a trace may not advance past its current position. If the latter occurs, it is known as stagnation, and this genetic algorithm currently will increase the Z value of the Rand() function. As mentioned earlier the Z value is determined by a combination of factors; user input data, Kurtosis of the population recent population average utility trends, etc.. If this enhanced randomness does not correct the stagnation, then the population entry is removed after a time limit, and all of its occupied cells become available for other traces to bid for.

The following are examples of population entries over N iterations using the above utility factor. This series of examples is supplied to show the reader how this function is implemented.

Example calculation of U_i let:

$F_1(X)$ = strlen (X) = 5 cells

$F_2(X) = U_{i-1} = 10$

$F_3(X) = Z * \text{Rand}(X) = 10 * (0.4)$

$F_4(X) = \text{Rdist}(X) = 12$

Then the U_i value would be:

$$U_i = \sum_{m=1}^{m=4} 0.4 * \left[5 + 10 + 4 + 12\right] = 12.4$$

5.3 Genetic Replication Operator

The replication operator is used to replicate population entries according to a already defined function REP().

$$REP() = \frac{\left(UTIL(POPE)^{ln(SQRT(BS))}\right)^{-2}}{ln(BS)} \quad : eqn\ 28$$

Each POPE of the population is passed through the REP() function to determine how many times the entry should be replicated for the genetic evolution process.

For example if we are working on a board of size 100x50 cells (Board Size, BS = 5000) and the UTIL(POPE) function returns a 10 for the supplied POPE, then we would have:

$$REP() = \frac{\left(10^{ln(70.71)}\right)^{-2}}{ln(5000)} = 15.65$$

This gives us a REP() = 15.65, which, when rounded to an integer, indicates that

the population entry should be replicated 16 times going into the evolution process. These replicated population entries are then added to the population[a].

5.4 Mean Population Size

The algorithm requires that an initial population of size MPS (Mean Population Size) be generated, where MPS is defined by either the user or the estimator function MPS(). The algorithm's MPS() estimator function is comprised of two primary components, one being referenced as MPSA(), which utilizes a range of problem specific characteristic information combined with a small degree of randomness as well as a normalizing factor. The second major component of the MPS() function is referenced as MPSB(). This component calculates the estimated population size based upon two very stable user supplied factors, the PWB board size and the number of expected Evolutions Till Solution (ETS).

The MPSA() function is defined as:

$$MPSA(\{\alpha\},\{\beta\},\{\zeta\}) = \left(\sum_{m=1}^{m=RANK(\alpha)} \beta_m \times \alpha_m + (Rand(1.0) \times \alpha_m \right) \quad : eqn\,29$$

with β defined as:

$$\beta_m = \frac{1}{ln(\alpha_n)} \quad EQN\,30$$

where alpha α is a set of data containing information describing the current problem to be solved. For example the set α contains the PWB board size, a suggested number of generations within which the solution should be found, information about minimum solution schema, mutation rate, annealing data, number of traces already routed, number of trace left to be routed, current population size, etc.

The set β contains real-valued biasing terms, which will scale the estimated value to within a range for the population size estimator function MPS(). The rank of

the β set is equal to the rank of the α set. Each of the terms in the β set $\{\beta_0, \beta_1, ..., \beta_n\}$ are selected such that they are correlated to the data type in the corresponding α data set.

The MPSB() function is defined as:

$$MPSB(BS, ETS) = \left(\frac{BS * ln(\frac{2048}{ETS}) * ln(2^{BS})}{ln(BS)^2} \right) \quad : eqn\,31$$

where BS is equal to the Board Size. For example, if the PWB is 100x50 tap holes, then the Board Size would be defined as 100 times 50 or 5,000

ETS represents the user specified value of Evolutions Till Solution.

These two equations, MPSA() and MPSB(), are combined and averaged to yield the MPS value for the working population size. This is given by:

$$MPS(MPSA(), MPSB()) = \left(\frac{MPSA() + MPSB()}{2} \right) \quad : eqn\,32$$

5.5 Initial Population Generation

The initial population fed into the algorithm is generated by replicating the POPEs of the core population. The algorithm for determining the number times each of the core POPEs should be replicated is a combination of the REP() function discussed in Section 5.5 and the MPS() function from Section 4.5.1.

The first calculation in creating the initial population is to generate the RVEC() vector. This vector contains one entry for each POPE in the core population. The RVEC() function is defined as:

$$\sum_{i=1}^{i=CPS} \left[\overline{RVEC(i)} = REP(POPE_i) \right] \quad EQN\,33$$

where CPS is the Core Population Size, number of POPEs in the core population.

The next calculation is to determine the value of RTOT, which is done by summing all the entries in RVEC(). This gives a size for the population according to the replication function REP() in Section 5.5. The following equation is how the RTOT value is determined.

$$RTOT = \sum_{i=1}^{i=CPS} \overline{RVEC(i)} \quad EQN34$$

Having the RTOT value and the MPS value, we now determine the scaling factor that each of the RVEC() entries should be scaled by. The formula to determine the RSF Replication Scale Factor is given by:

$$RSF = \frac{MPS}{RTOT} \quad EQN35$$

The next step is to multiply each entry in the RVEC() vector by the RSF scale factor. This operation adjusts each of the RVEC() values to represent the actual number of times that the corresponding core population POPE's should be replicated for entry into the initial population. The function to scale the RVEC() vector is defined as:

$$\sum_{i=1}^{i=CPS} \left[\overline{RVEC(i)} = \overline{RVEC(i)} * RSF \right]$$

The RVEC() entries now represent the actual number of times the corresponding POPE from the core population should be replicated for insertion into the initial population.

The initial population is now generated by cycling through the core population and replicating each POPE entry by the number of times specified in the RVEC() vector. This can be visualized by:

$$INIT\_POP = \bigcup_{i=1}^{i=CPS} \left[\bigcup_{j=1}^{j=RVEC(i)} COREPOP(i) \right] \quad EQN36$$

Where COREPOP is the core population entries and INIT_POP represents the resulting initial population going into the genetic algorithm.

In Section 4.3 I discussed the notion of a family line. The INIT_POP is the first generation of the COREPOP family line. Each POPE is replicated according to the RVEC() vector and placed into the INIT_POP. Each POPE and all of its duplicates represent a family / blood line.

5.6 Crossover operator

This is the primary operator for introducing new POPEs into the evolving populations. The primary job of this operator is to combine two POPEs into one and place the resulting POPE into the next population. The basic idea of my crossover operator is different from the standard genetic crossover operator. In the standard genetic crossover operator two POPEs are selected at random from an evolving population, and are then split at some randomly selected point. Pieces from the two POPEs are then jointed to form a new POPE.

Within the genetic algorithms I am developing, I do not allow quite this degree of randomness to occur. The way I attempt to regulate crossover is:

- My genetic cross over operator attempts to select POPEs from the same family line to engage in the crossover operation. The reason for this to reduce the number of obviously invalid POPEs that are created for the next generation. If POPEs from differing family lines are randomly and blindly crossed over, then we would be joining trace paths that statistically have little or no correlation and hence are absolutely useless towards generating a solution.

- The crossover operator does cross POPEs of different family lines. This is allowed to a small extent, based upon the current annealing temperature and

the current randomness factor. I do need to beware not to cause inbreeding in the population, insure proper search space exploration, and avoid stagnation. There is only one occasion when this type of crossover is performed. This is when a POPE has an (X, Y) coordinate in common with another POPE. This condition can occur, but is of very low probability. In this function there is a very small probability that a POPE will be allowed to capture an occupied neighbor.

- This Crossover operator also performs dual crossovers. This type of crossover operation is not very common because of the restrictions placed upon the POPEs that are valid to enter into crossover with each other. In attempting to perform a dual crossover operation the function will attempt to:
  1) Crossover the two current POPEs
  2) Crossover one or both of the current POPEs with a member from the evolving population.

I refer the reader back to Chapter Four Section 4.7 for additional explanation of this operator.

5.7 Mutation operator

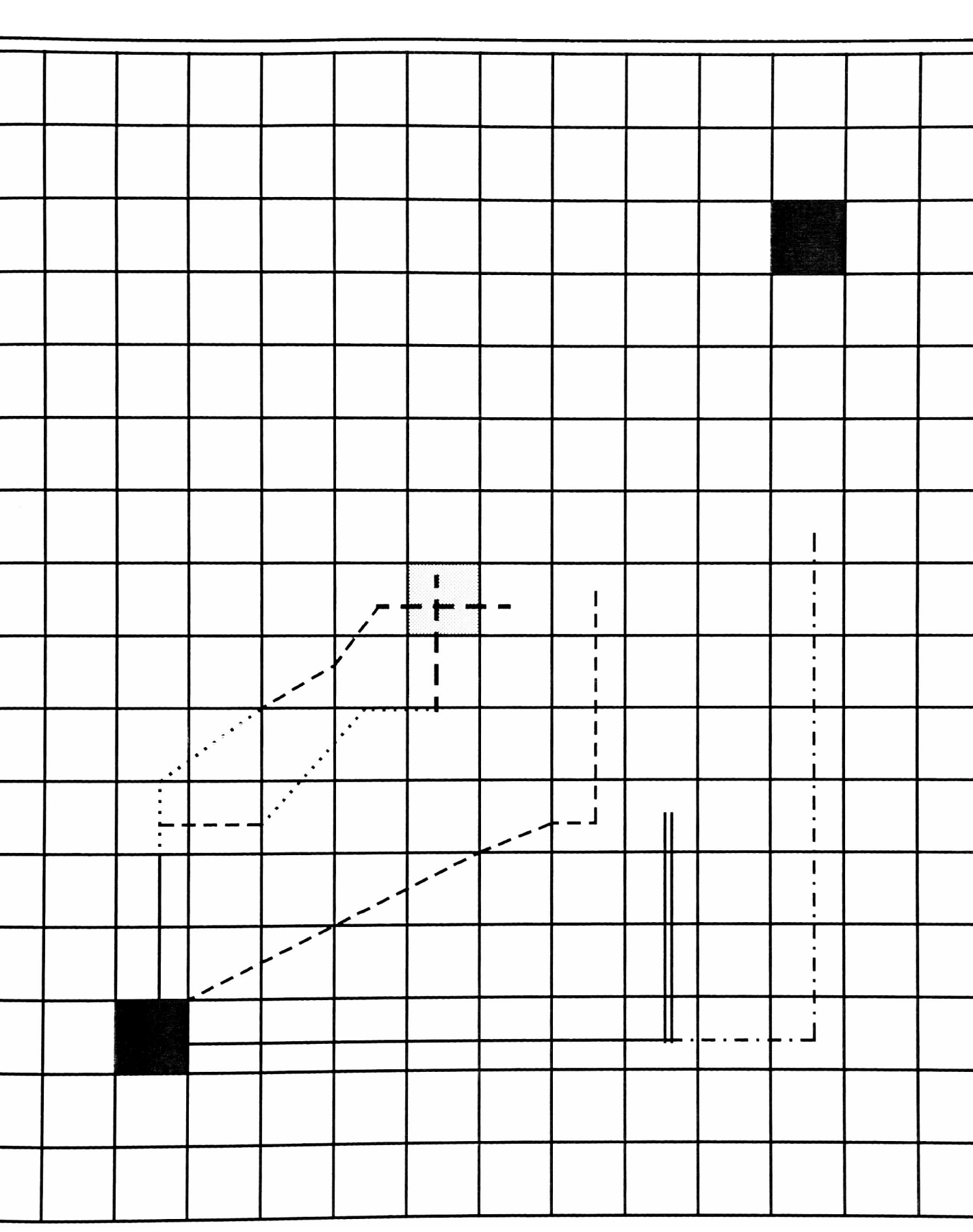
This operation will consult the population character function and determine how many POPEs are to be mutated from the evolving population. The Mutation operator then pseudo randomly selects POPEs from the evolving population and evaluates the utility of each POPE. This utility is compared against factors in the population character function, and a mutation probability is determined.

The mutation function then generates a uniform random number between 0.0 and 1.0. If the number is above the probability of mutation for the POPE then that POPE is changed by one of the following methods:

- A bias is added or subtracted to the strength value of the POPE
- The last cell that the POPE captured is removed from its path list
- The POPE is allowed to capture another cell without having to pass through the evolution process again.

The mutation operator for this algorithm does not trivially change the state of a POPE, as do most typical implementations of genetic mutation operators. I have chosen to implement the mutation operator as described above in order to decrease the number of trivially invalid POPEs introduced into the evolving population as a result of mutation.

For example, considering my implementation representation of the PWB board and POPEs, if I were to randomly change the (X, Y) cell values of a POPE, I would cause a discontinuity in the evolving trace hence immediately rendering it invalid, with an extremely small probability of it ever being corrected. If we refer back to Figure 4.2.1B we can see by inspection that it would not make sense to perform a crossover operation purely randomly on one of those traces. If we did this then we might cause the discontinuity or a cell collision as demonstrated in Figure 5.7.1 below:



Example of a Crossover Collision

Figure 5.7.1

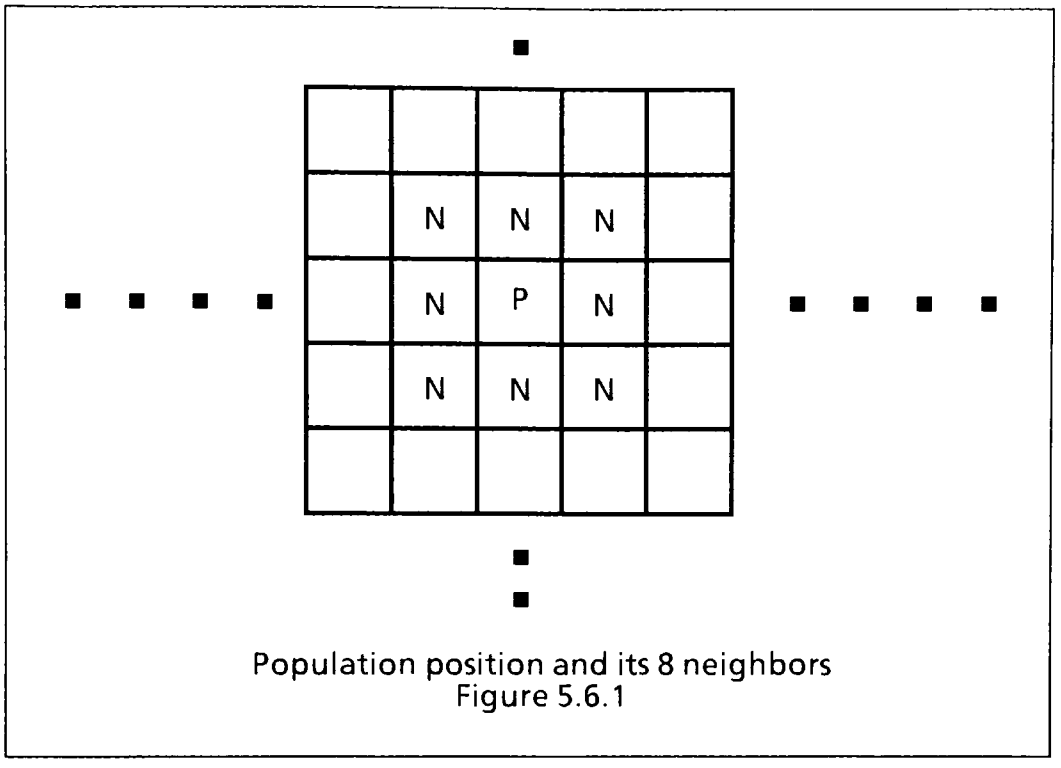
Another fundamental difference with the manner in which I implemented my genetic evolution algorithm is that I literally grow my population entries towards a solution. In many cases genetic algorithms work not to grow population entries but to change them (mutate) until their fundamental bit (representation) sequences are most optimal based upon the strength functions set up by the algorithm designer.

A visual difference may be gleaned by looking back at the N-Queens example in Chapter Three. In that experiment the mutation operator simply changed bits in the POPE representation. Each population entry already contained a full length definition of a row vector from the chess board, and the objective of the algorithm was to modify the row vector definitions (bit sequences) in order to produce the correct solution.

In the case of this PWB router implementation I designed the algorithm to "grow" into correct solution answers, not modify a full length entry into a correct state. By "grow" the population entries I literally mean that the POPE entries start out at length one and grow to length N, eventually occupying all of the necessary board cells to connect a trace path from starting point to ending point.

5.8 Neighbor Concept for Evolution

A POPEs immediate neighbors are the eight adjacent (X, Y) cell positions of the current POPE's position. This may be pictured by a 3x3 grid matrix, where the POPE's current position is the center location of the 3x3 matrix and the remaining 8 matrix positions are the immediate neighbors. (refer to Figure 5.6.1). Of these 8 neighbors it is possible for some or all of them to be occupied by other



Population position and its 8 neighbors
Figure 5.6.1

POPEs. If any of the immediate neighbors are occupied, then the POPE may not bid for those grid coordinates; occupied positions are considered unavailable.

In Figure 5.6.1, the neighbor relations are: P is the current population end point and N represents the 8 immediate neighbors. In this context neighbors refers to the grid coordinate positions. Each of the positions that I considered to be neighbors can be identified via the following formula.

$$Neighbors(X, Y) = \sum_{m=X-1}^{m=X+1} \sum_{n=Y-1}^{n=Y+1} Coordinate(M, N) \therefore m \neq x \,\&\, n \neq y \quad EQN37$$

As a POPE bids for its available neighbors, there are some criteria by which it attempts to prioritize the available neighbors into a most preferred to least preferred order. Some of the criteria that are used to asses the importance of a POPE's neighbors are:

Will the occupancy of this neighbor introduce more 'jogs' bends into the trace path? If the answer is yes than this neighbor is less palatable than one that provides a straight path continuance.

Does the neighbor move the trace closer towards its destination coordinate? An answer of yes is more favorable than no, or further away.

If the POPE were to capture the neighbor cell will the estimated distance until completion reduce or increase? If the answer is reduce the the neighbor is considered favorably.

These are some of the primary factors utilized in prioritizing a POPE's neighbor selection list.

Population evolution occurs by POPEs bidding upon immediate neighboring grid coordinates, attempting to win and occupy one of the coordinates. Hence, growing the POPE by one coordinate position towards its end point. In other words each POPE competes for its immediate neighboring gird positions in its attempt to find a valid path from starting point to end point. In an evolution cycle if a POPE is successful in bidding for one of its neighboring positions, the POPE is allowed to occupy the (X, Y) grid position. This movement / occupancy advances the POPE by one cell towards its final position. It should be noted that it is possible for a POPE during an evolution to lose the bidding for any of its neighbors and not advance in that evolution cycle.

The evolution process is continued until all POPEs have reached their destination positions or a timeout condition limit is reached.

5.9 Population Growth and Decay

The algorithm in attempting to route the POPEs and find a solution to the problem will grow and shrink the population size MPS(). At any point in time there are several factors which will regulate what the actual population size is, for example.

1) POPEs may route successfully and, hence, can be removed from the active population list.

2) POPEs may stagnate; all neighbors are occupied and hence can be removed from the population.

3) POPEs may simply loose their utility during bidding.

4) The genetic operators are designed to grow and shrink the population from evolution to evolution based upon current population characteristics.

These and other factors were considered in designing into the evolution algorithm to try and maximize its efficiency. Let's consider the case where POPEs complete their path successfully. They either find the trace end point as in case 1 above, or stagnate as in case 2 above, or they simply fail and die as in case 3 above. No matter what the reason for removal is, success or failure, the POPE is removed from the active population. In the case of success, the POPE's coordinates are marked as routed and remain permanently unavailable to other POPEs. In the case of failure, the POPE's coordinate positions are returned to the available list of neighbors and other POPEs may begin to utilize the freed up coordinates. These situations produce a shrinkage in the population size.

This shrinkage is expected by the algorithm and there are mechanisms to compensate for the shrinkage. First, however we will discuss more of the details of how and why POPEs are removed from the evolving population.

The way in which a POPE can die are numerous. For example, a POPE may route itself into a position where there are no available neighbors, but it has not reached its destination point. In this case, only the single POPE is removed, not all of its family members. A POPE also may bid all of its money / utility away before reaching its destination. This death is dealt with similarly to the above stagnation case; just the one POPE is removed.

If a POPE is successful in finding a routing path to its end point, then this POPE is removed from the active evolution list; its coordinates / trace path are left marked as a valid trace, and all its other family members are removed from the active population. The coordinates occupied by the other family members of the successful POPE are freed up and placed upon the available neighbor list for other POPEs to utilize. This is because there has been a successful path found that will be preserved; therefore, the other family members are no longer needed for searching a valid path.

Some characteristics worth noting about the algorithm pertaining to the removal of POPEs from the population are:

- POPEs do not back track and attempt to utilize any of the just freed-up coordinates / neighbors from POPEs being removed from the population.

- As POPEs die of unsuccessful deaths, they are not restarted in the evolution process. The potential problem here is that if a family blood line is so unsuccessful that all the POPEs of the family die in failure, there is no

mechanism to retry and route that trace path. This trace path is marked as unsuccessful and left out of the routing process.

- The algorithm is designed to allow the actual population size to fluctuate within a user / algorithm specified range at each evolution cycle. The population entry count fluctuates down from the death process of traces, successful or failure. The population entry count is capable of growing during genetic replication and resample operations during the evolution cycle.

During the evolution process the REP() function (Section 5.3) and the NPTA() function (Section 3.3.6) are compensated according the recent changes in the population size. This relation is established enabling the algorithm to compensate the size of the evolving population. This information is also utilized by the resample operator described in section 4.6 to also compensate for changes in the working population size. All of these interactions are established in order to optimize the algorithm for finding solutions to the routing problem.

6.0 Optimum Neighbor Solution Algorithm

In Chapters 4 and 5 I presented an overview of the routing problem as well as some specifics of the genetic solution algorithm. In this section I will present one of the three specific solution algorithms developed for this project. This algorithm is identified as the Optimum Neighbor Solution Algorithm. The title comes from the fact that the algorithm investigates a cell's 9 nearest neighbors (see Section 5.6 for definition) in attempting to determine a routing path for each trace in the netlist.

6.1 Optimum Neighbor Utility Function

Earlier in Section 4.6 I presented the concept of a cell's neighbors and the association of merit of the neighbors. This algorithm utilizes the concept to identify neighboring coordinates and rank them in order of most to least preferable. The way neighbors are ranked is to evaluate the POPE utility algorithm as if the neighbor is part of the POPE trace path. The path returning the greatest utility value is considered the highest potential neighbor for success. Being able to rank the neighboring coordinates allows the algorithm to isolate and select one or more coordinates which a POPE will bid upon and attempt to capture, thus advancing the POPE one coordinate further towards its termination coordinate as indicated in the net list.

This algorithm was set up to use a weighting scheme that considered the following as the criteria in order to determine which neighbors to bid for and how much to bid. There was the element of probability, the merit gained from the prior evolutions / biddings, the number of "jogs" in the path, the general direction (is it

towards the destination or not), how much strength does the entry have to compete with, current traveled distance and approximated distance to ending point. All of these factors are combined into the utility polynomial. This Polynomial has the form:

$$U_i = \sum_{m=1}^{m=n} ln\left\{ A_m * F_m(X_i) \right\}$$

where A is a normalizing / scaling constant, and $F_m( )$ is a function that evaluates and bounds the specific characteristic being weighted into a POPEs utility value. An example of F() could be as simple as a MAX(), MIN() function, a COS() function, or a polynomial itself. The intent of F() is to define a function yielding a single value that considers all of the characteristics required to determine a POPEs utility.

A simple example of this technique is as follows: The definition of U_i

Bidding criteria for this example will be:

$+F_1(X)$ = strlen (X)	:	Trace length of X
$+F_2(X) = U_{i-1}$	:	Utility of the prior generation
$\pm F_3(X) = Z * Rand(X)$	:	Random percent Z with X as the Seed
$+F_4(X)$ = Rdist (X)	:	Estimate of remaining distance to end point
$-F_5(X)$ = NJogs(X)	:	Number of Jogs in this POPE's trace path
$\pm F_6(X) = \Delta$PopUtil(X)	:	Δ population utility over last N evolutions
$\pm F_7(X)$ = SDevPop(X)	:	Number of STD Deviations this POPE is

Please note that not all the string length functions will return the same value at each iteration. This is because some traces will terminate / complete before others and some traces will lose entirely in the bidding process; hence, for a given generation a trace may not advance past its current position. If the latter occurs

it is a stagnation, and this genetic algorithm currently will initially increase the Z value of the Rand() function. If this enhanced randomness does not correct the stagnation, then the population entry is removed after some time limit and all of its occupied cells become available for other traces to bid for.

Also note that before each function F_n there is a $\pm$ sign. The + operator is achieved by directly taking the natural log of the function. the operator is achieved by first performing the (1/X) operation and then taking the natural log. In all cases, before the natural log operation is performed, a test for zero (0) is done. When a function returns zero (0) then both the (1/X) and the natural log function are not performed and zero (0) is added to the POPE's utility value U_i.

The following are examples of population entries over N iterations using the above utility factor. This series of examples is supplied to show the reader how this algorithm was designed.

If we look back at the example trace in Figures 5.4.8 and evaluate the utility function for the trace starting a cell (0,0) and routing towards cell (4,3) we would get:

$F_1(X) = \text{Strlen}(X) = 2$

$F_2(X) = U_{i-1} = 5.101$

$F_3(X) = AT * \text{Rand}(X) = 50 * 0.3565 = 17.85$

$F_4(X) = \text{Rdist}(X) \simeq 2$

$F_5(X) = \text{NJogs}(X) = 0$

$F_6(X) = \Delta\text{PopUtil}(X) = 8$

$F_7(X) = \text{SDevPop}(X) = -2$ which becomes (0.5)

The natural log of each of the functions above yields the following results:

$\ln\{F_1(X)\} = \ln\{2\} = 0.693$

$\ln\{F_2(X)\} = \ln\{5.101\} = 1.629$

$\ln\{F_3(X)\} = \ln\{17.85\} = 2.880$

$\ln\{F_4(X)\} = \ln\{2\} = 0.693$

$\ln\{F_5(X)\} = 0$: no operation is performed

$\ln\{F_6(X)\} = \ln\{8\} = 2.639$

$\ln\{F_7(X)\} = \ln\{0.5\} = -0.693$

When we sum all of these terms we get a U_i of 7.841

6.2 Optimum Neighbor Solution Algorithm Character Function

For this algorithm I implemented a simple population and individual POPE character function that was used to adjust the annealing temperature by monitoring the population's evolution rate. For this character function I would look at statistics of both individual POPEs and the population on a whole. Some of the parameters considered for the character function were:

1) Number of POPEs that advanced in the current evolutionary cycle.
2) The average utility of the entire population.
3) Estimated distance required to route the remaining traces.
4) Number of evolutions since the POPE Advanced.
5) STD Deviation of the POPE relative to the population.
6) Number of times POPE mutated vs number of times evolved.
7) Instantaneous slope of POPEs utility values (increasing / decreasing).

The function would scan the current population as well as keep a history of selected past data items with which to evaluate the trend of the population. From

the data gathered, the characterization function would then set certain condition flags and adjust some of the biasing and randomization constants. These condition variables would be used by the other genetic operators such as crossover and mutation in order to control the evolution algorithm and optimally direct it to converge upon a solution.

One of the largest problems with this solution algorithm was that it did not intelligently attempt to back track and incorporate any cells freed-up by traces that were removed from the population for whatever reason. The freed-up cells were used by traces only if they could be of benefit in their current routing path.

Another problem with this algorithm is that it was extremely difficult to design the utility function U_n such that as time went on and the population grew and shrank, it was difficult to manage the propagation or negation of prior U_i's and bids.

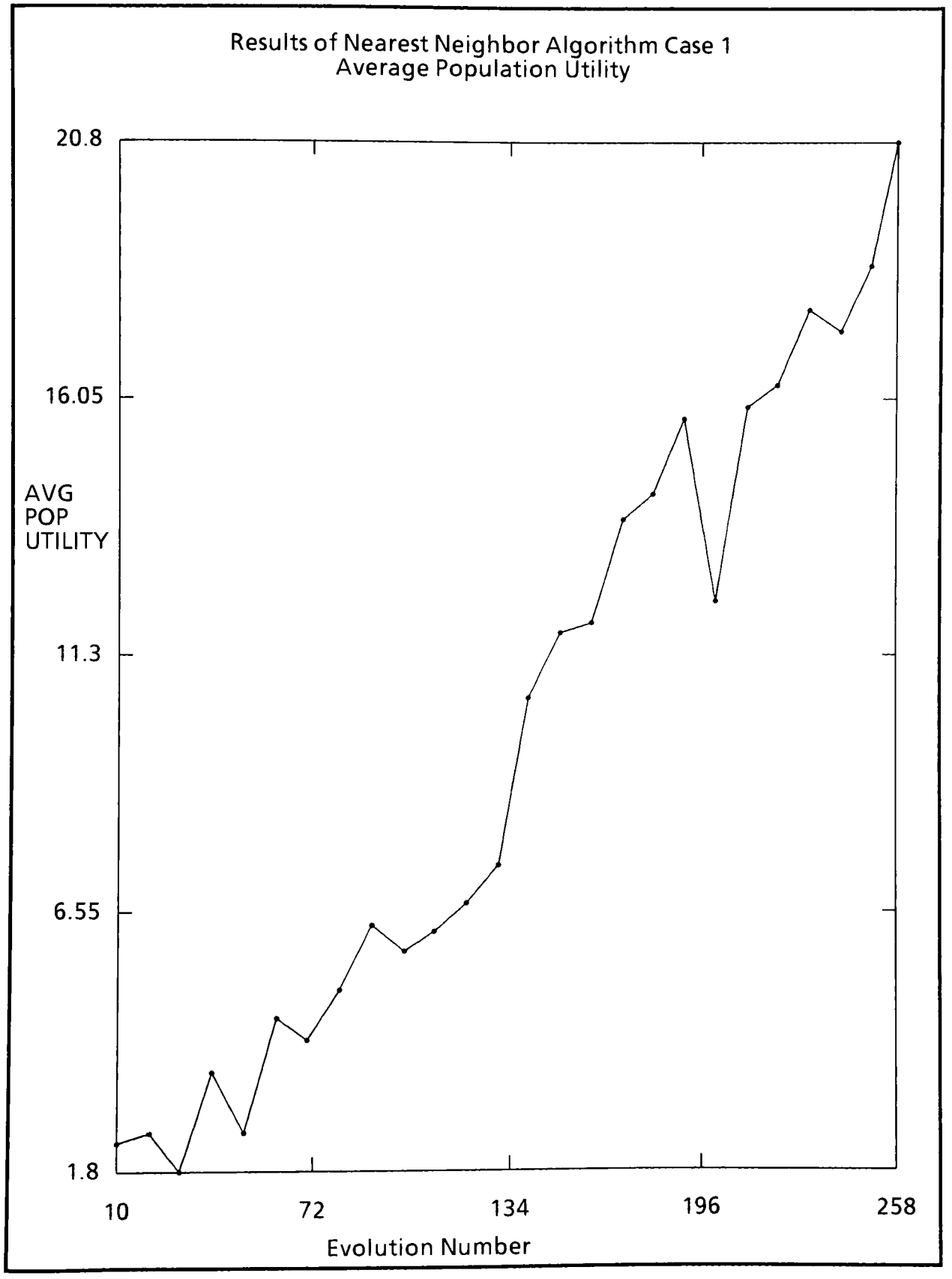
6.3 Optimum Neighbor Solution Solution Data

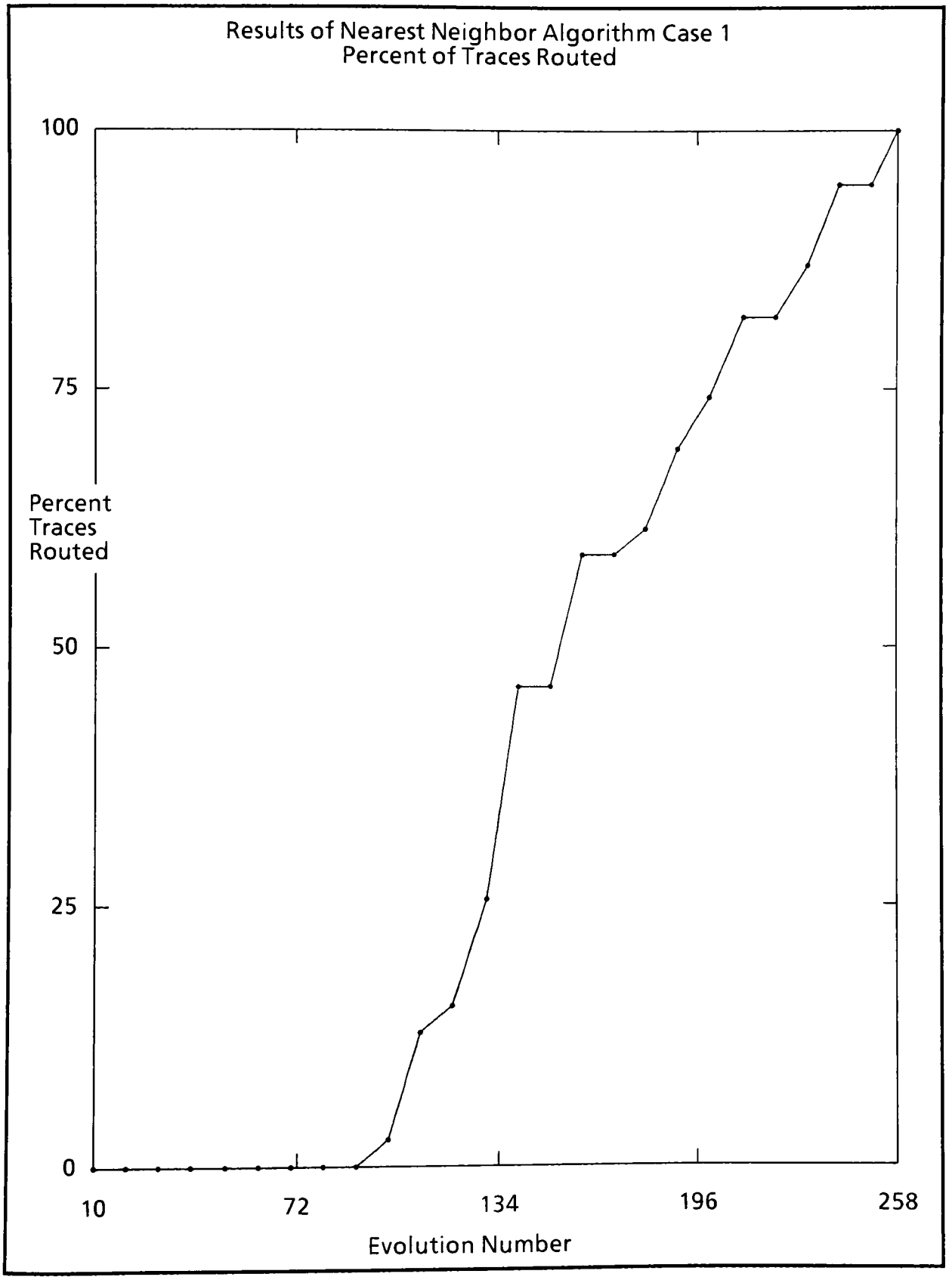
A table can be found in the appendix Table 6.3 that contains the tabular evolution data having run the genetic algorithm with the previously described evolution functions. For this simple example the algorithm was able to route all of the traces.

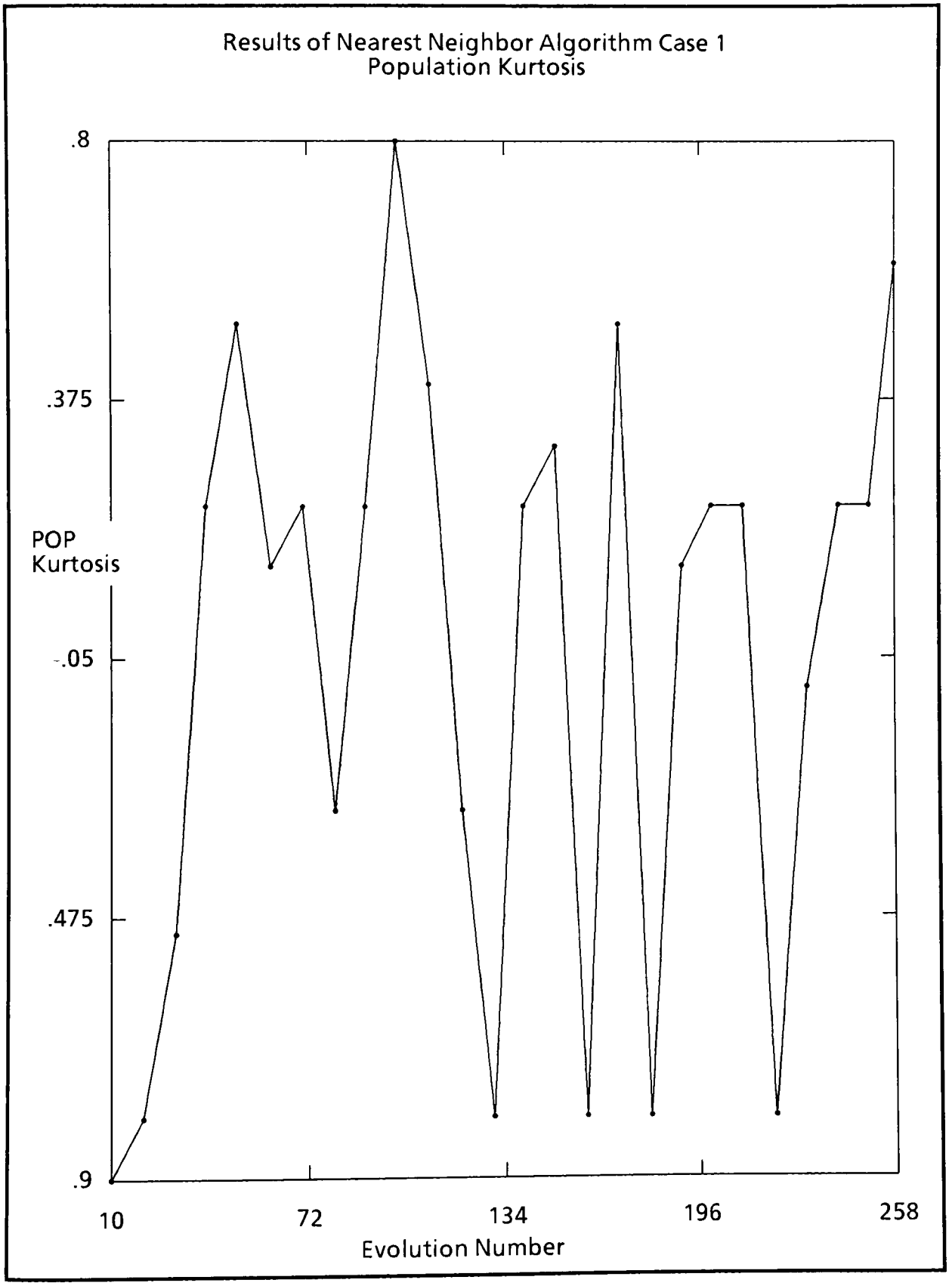
Graphically the results from the genetic algorithm of Section 5.7 are shown in the following charts section 6 results case #1.

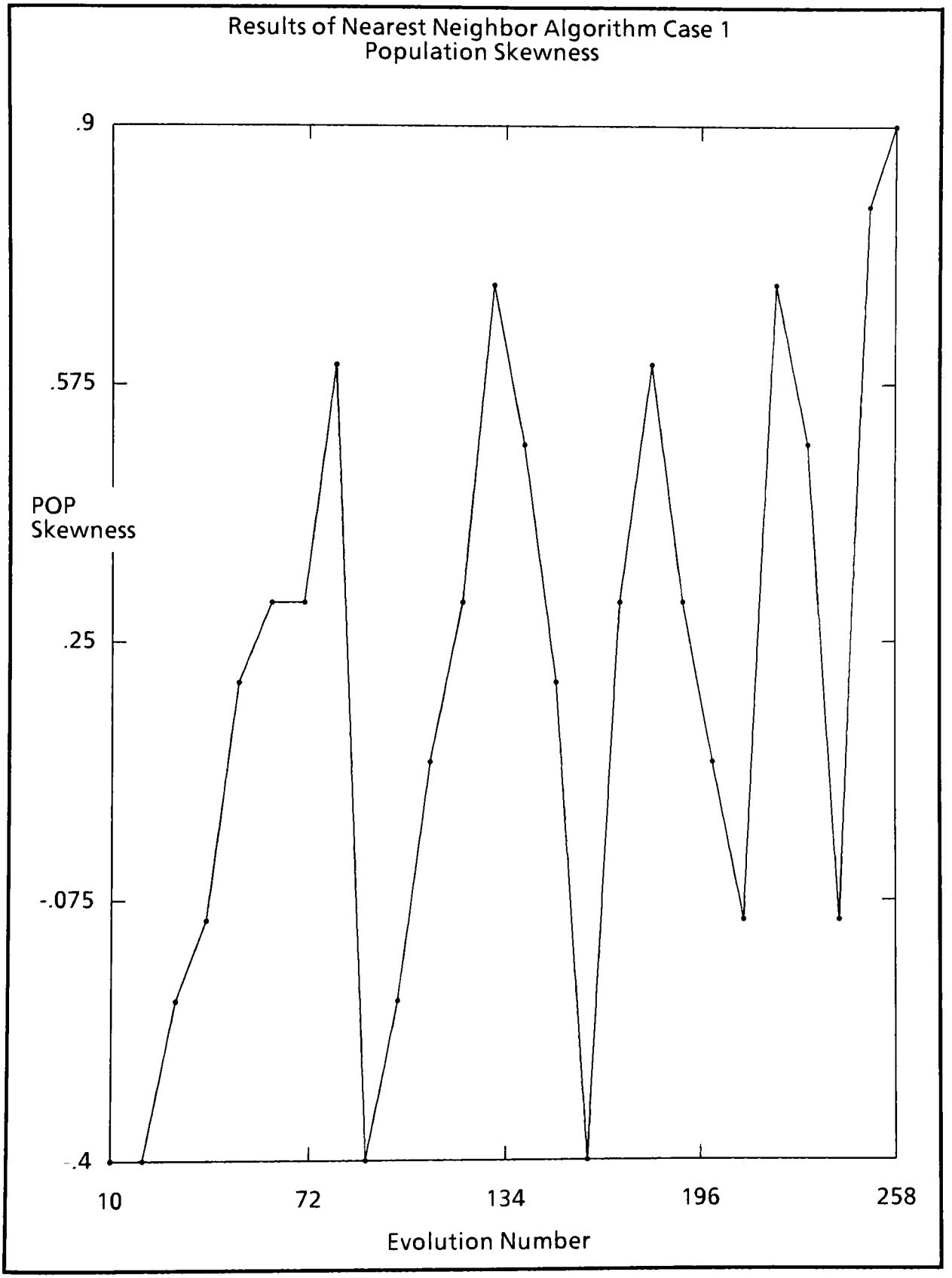
6.4 Optimum Neighbor Utility Function of 6.3 with Growth Modification

This utility function utilizes all of the characteristic information of the utility function described in Section 5.7 plus a factor based upon rate of neighbor growth.


Results of Nearest Neighbor Algorithm Case 1
Average Population Utility
20.8
16.05
11.3
6.55
1.8
AVG
POP
UTILITY
10
72
134
196
258
Evolution Number


Results of Nearest Neighbor Algorithm Case 1
Percent of Traces Routed
100
75
50
25
0
Percent
Traces
Routed
10
72
134
196
258
Evolution Number


Results of Nearest Neighbor Algorithm Case 1
Population Kurtosis
.8
.375
POP
Kurtosis
-.05
.475
.9
10
72
134
196
258
Evolution Number


Results of Nearest Neighbor Algorithm Case 1
Population Skewness
.9
.575
POP
Skewness
.25
-.075
-.4
10
72
134
196
258
Evolution Number

The neighbor growth factor is :

$F_8(X)$ = NGrowth(X) : This parameter increases directly proportional to the time since the last neighbor capture for the POPE.

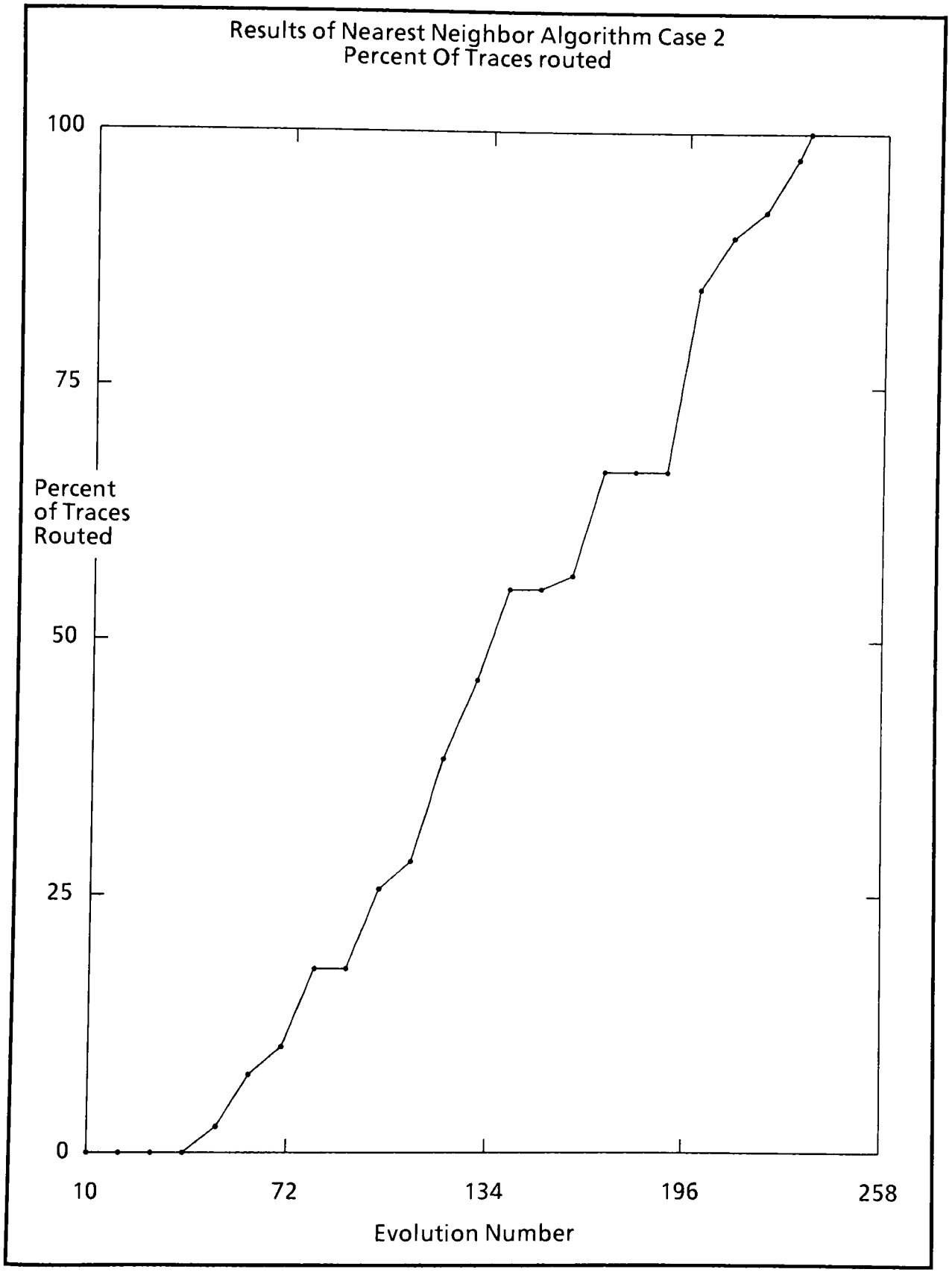
The goal of this function is to try and augment POPEs that are stagnating. As POPEs compete for neighboring cells several POPE may be bidding upon the same neighbor during the evolution process. This function is to bolster the week POPEs that may be competing for neighboring cells but loosing to stringer POPEs.

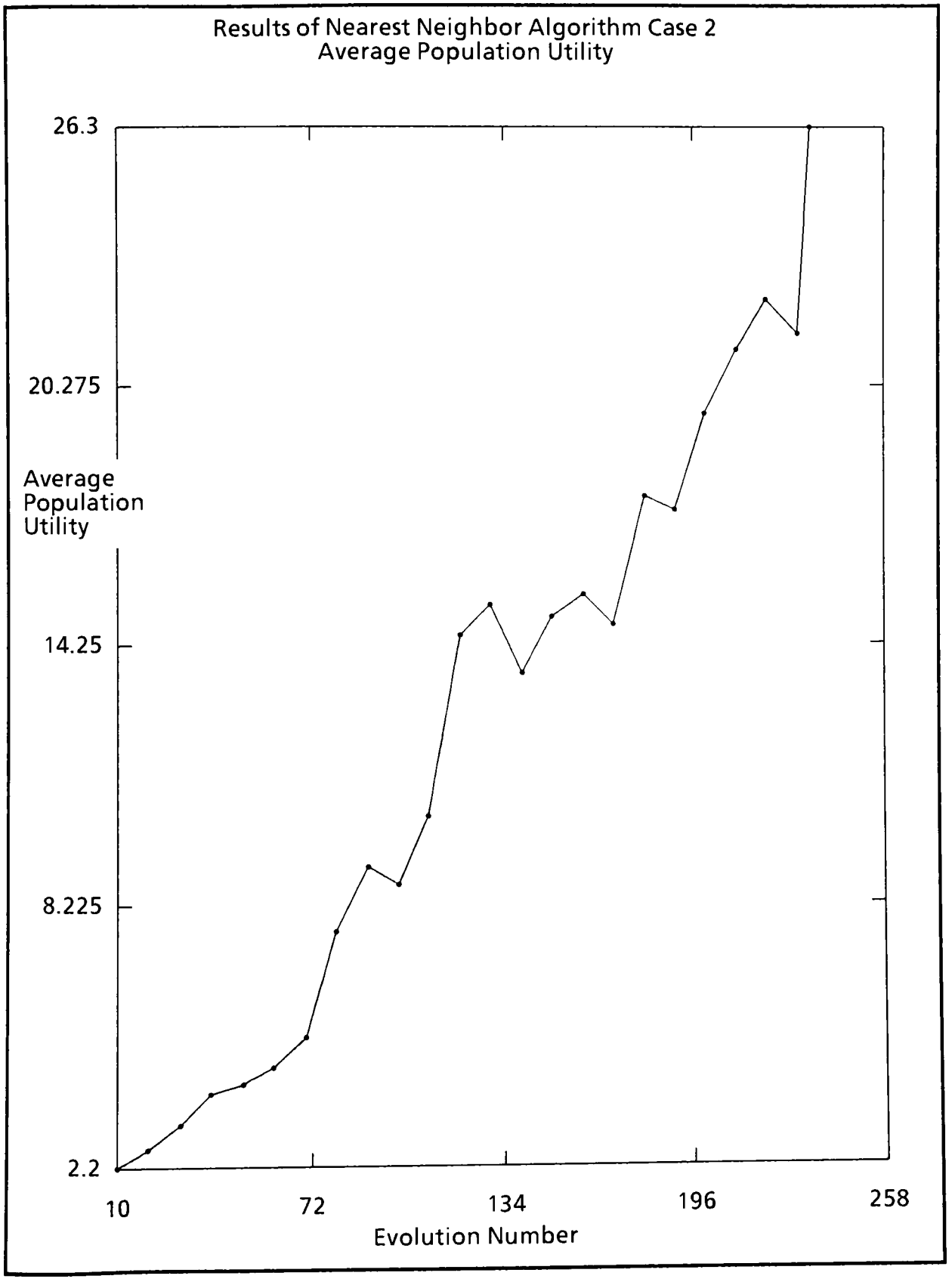
A table containing the evolution data from running the genetic algorithm with the modified POPE utility function as describe above can be found in the appendix Table 6.4. For this simple example the algorithm was able to route all of the traces.

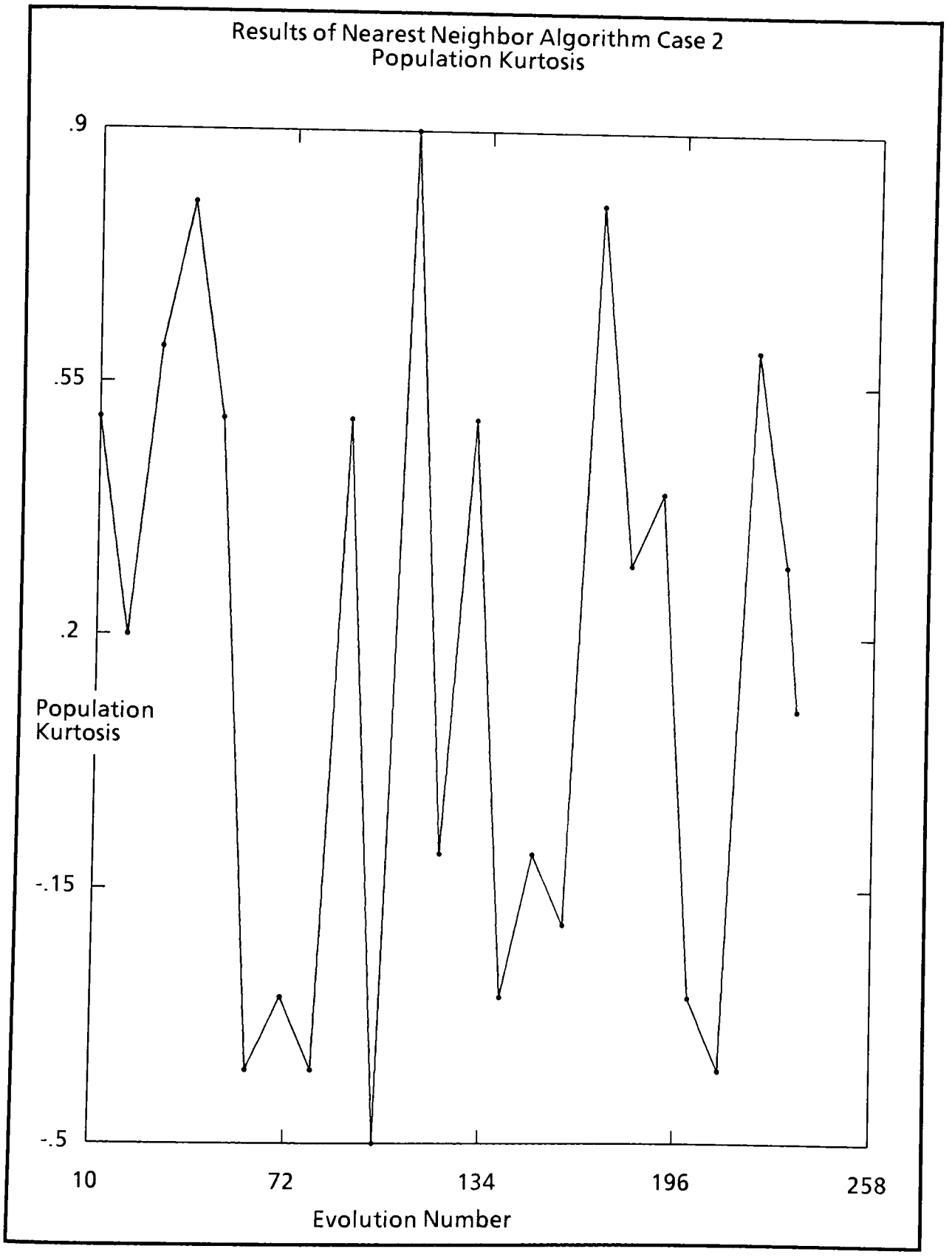
Graphically the results data from genetic algorithm test case 2 of Section 5.7 are shown in the following graphs.

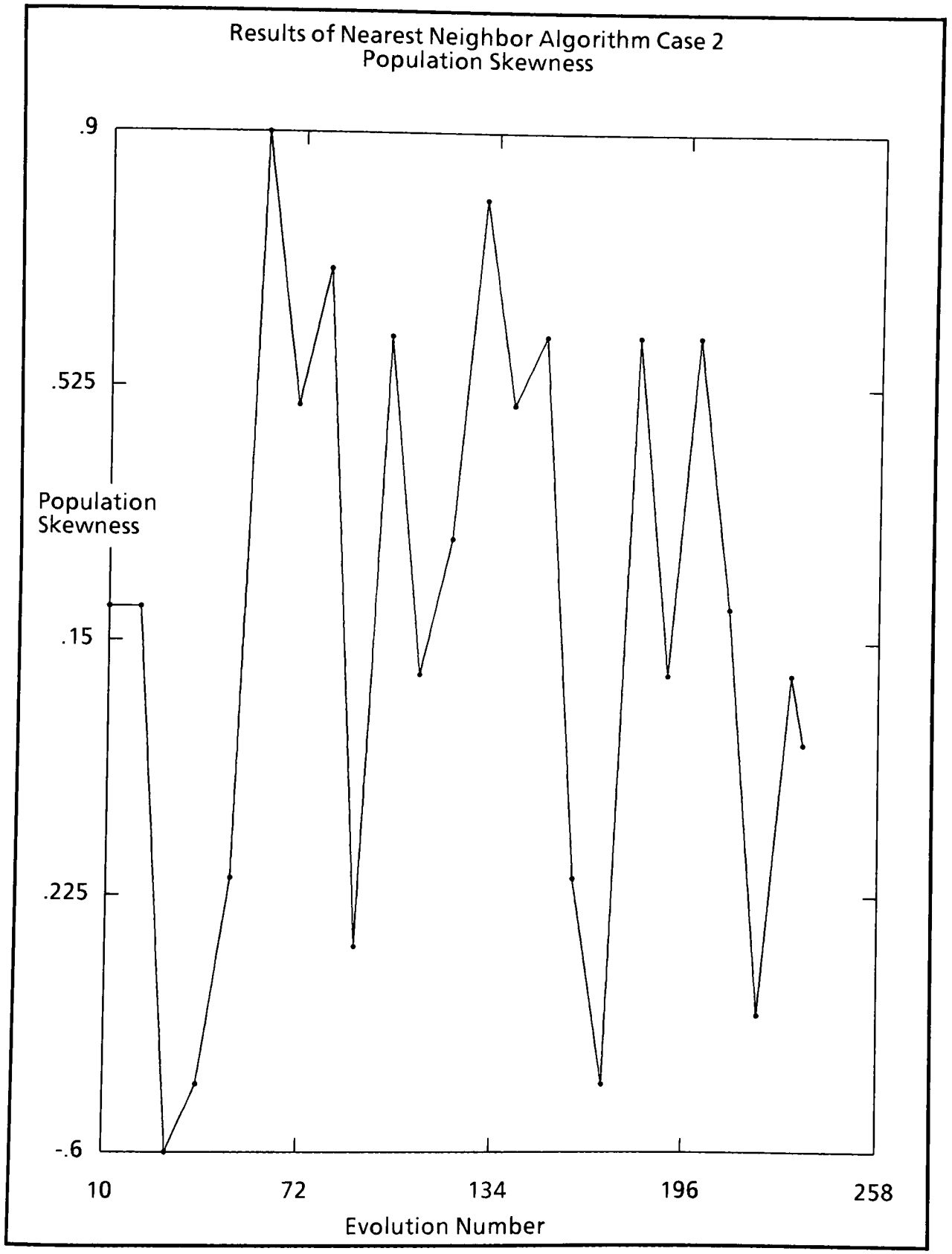
If we compare the results of this algorithm to the result of the previous algorithm we will see that by adding the parameter that augments a POPEs utility based upon the elapsed time that it has stagnated appears to be just sufficient catalyst to move the POPE into the active class for capturing neighboring cells. The table data show us that the number of evolutions before a trace routes has decreased, as well as the total number of evolutions required to complete the routing operation.

6.5 Optimum Neighbor Utility Function of 6.3 with Fewer Shuffle Operations


Results of Nearest Neighbor Algorithm Case 2
Percent Of Traces routed
100
75
50
25
0
Percent
of Traces
Routed
10
72
134
196
258
Evolution Number


Results of Nearest Neighbor Algorithm Case 2
Average Population Utility
26.3
20.275
14.25
8.225
2.2
Average
Population
Utility
10
72
134
196
258
Evolution Number


Results of Nearest Neighbor Algorithm Case 2
Population Kurtosis
.9
.55
.2
-.15
-.5
Population
Kurtosis
10
72
134
196
258
Evolution Number

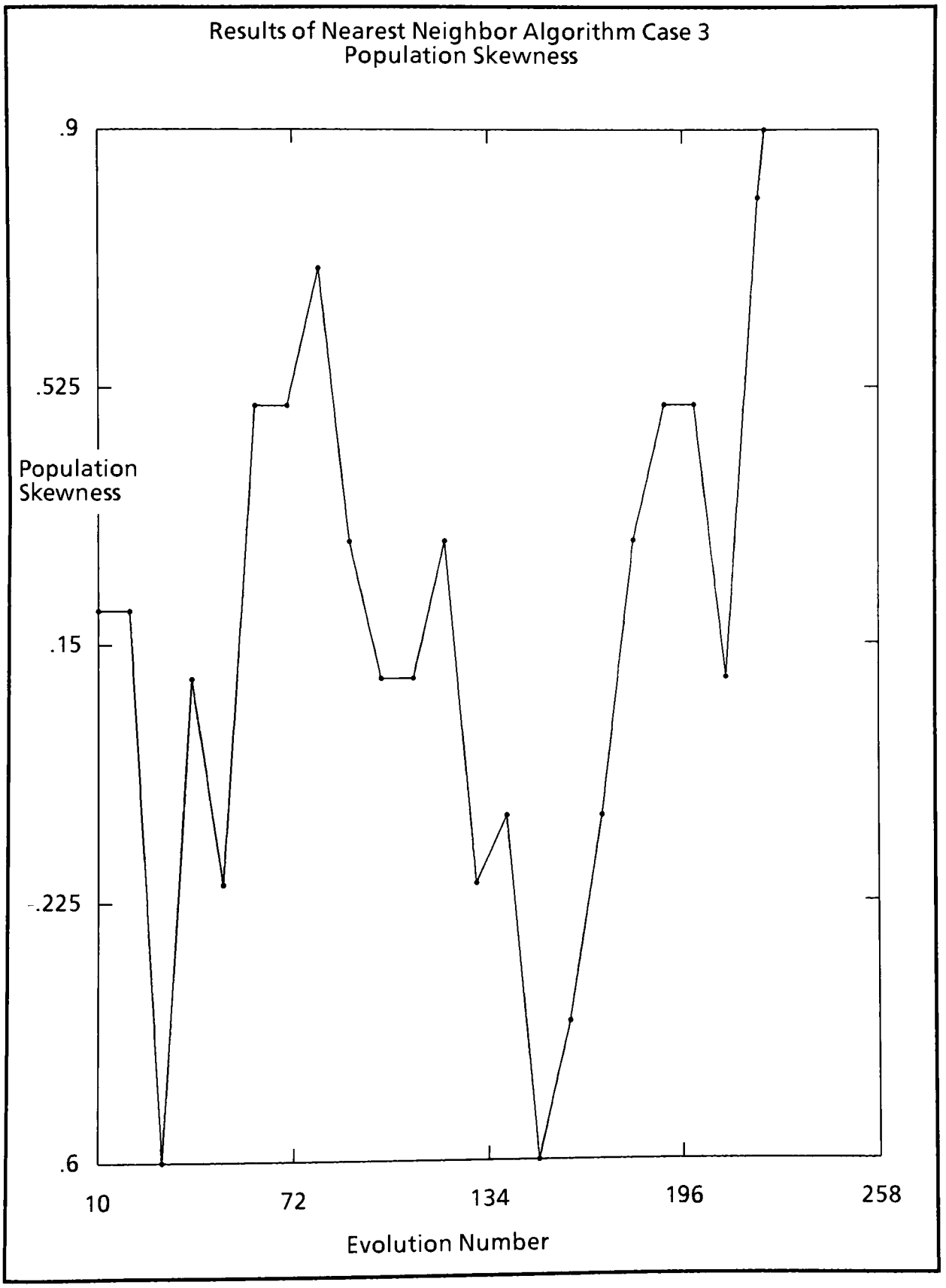

Results of Nearest Neighbor Algorithm Case 2
Population Skewness
.9
.525
Population
Skewness
.15
.225
-.6
10
72
134
196
258
Evolution Number

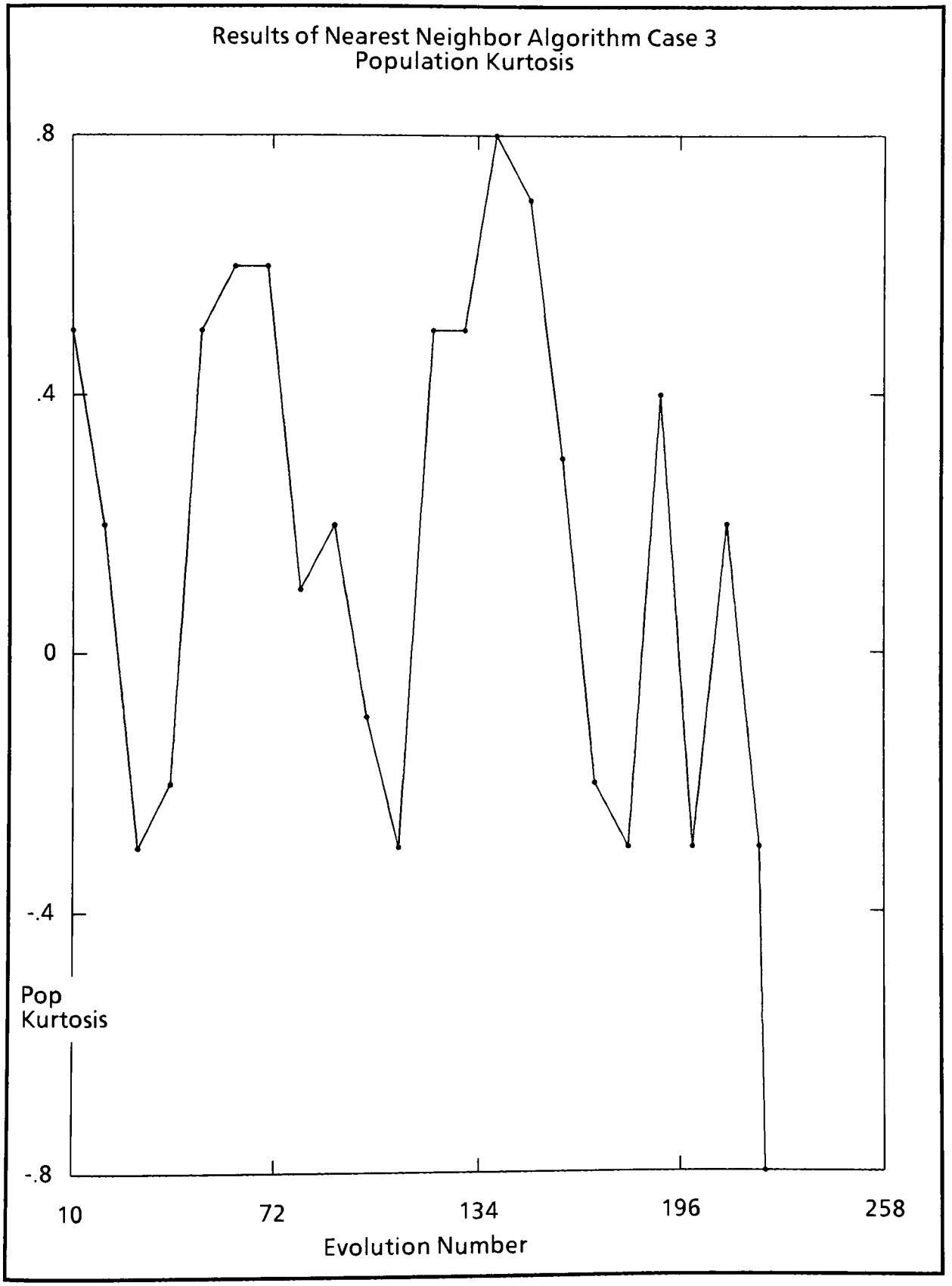
This algorithm test case utilizes the utility function of 6.3 exactly as it is shown earlier. The difference in this test case is that the shuffle operator is not applied to the population after the replication function. The reason for having the shuffle operator in the algorithm process after the replication operator is to minimize the positional correlation between POPEs as they are stored in the data structures.

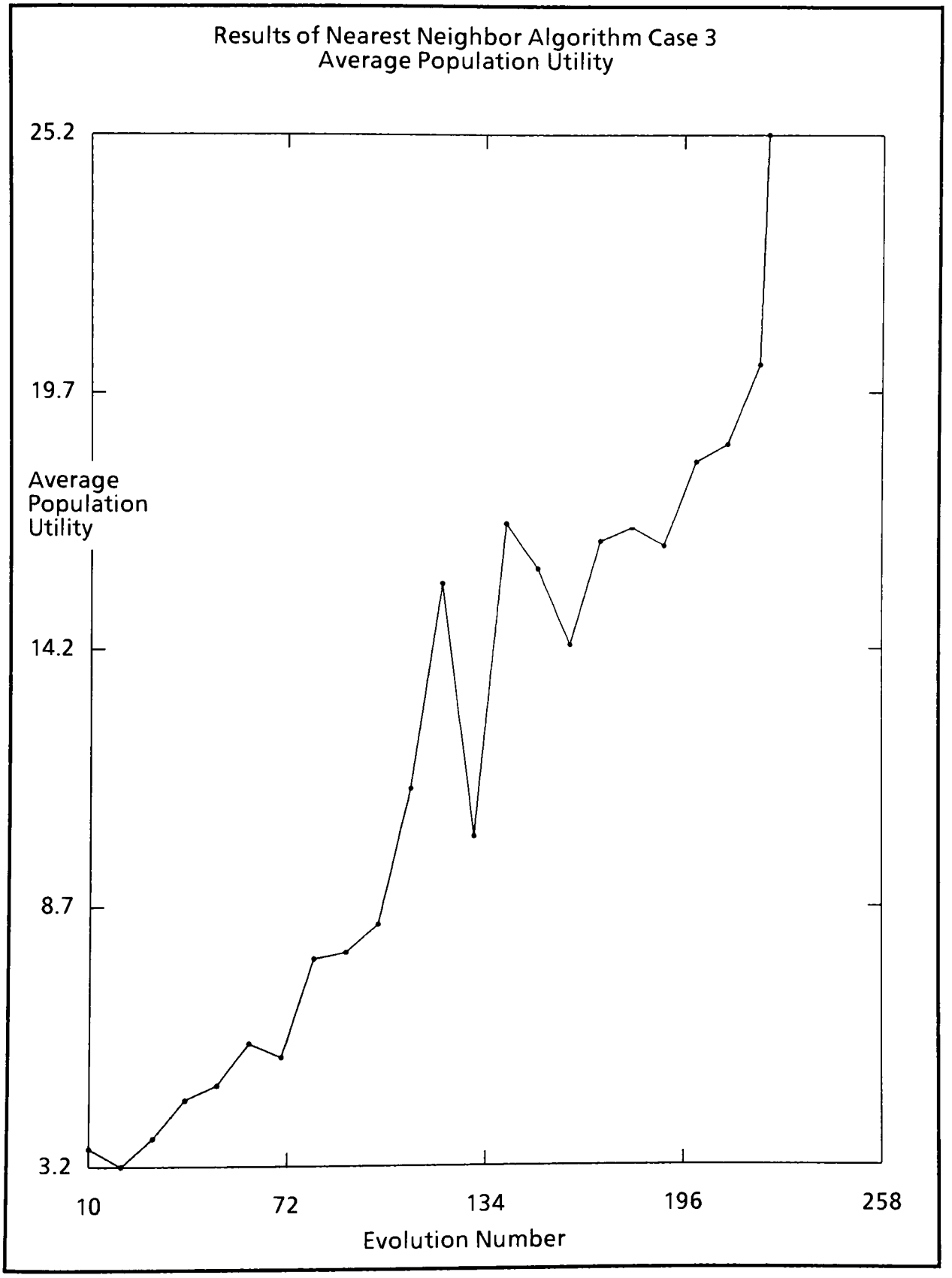
It was my assumption that the data structures, array vectors and their sequential loading and unloading tend to lead to negative effects in the evolving population. By applying the shuffle operator, it was my assumption that the negative correlation characteristics can be eliminated. In the appendix, Table 6.5 is the resultant data having removed the shuffle operators. The actual result was to decrease the number of evolutions required for solution generation. The time required to produce a solution also decreased.

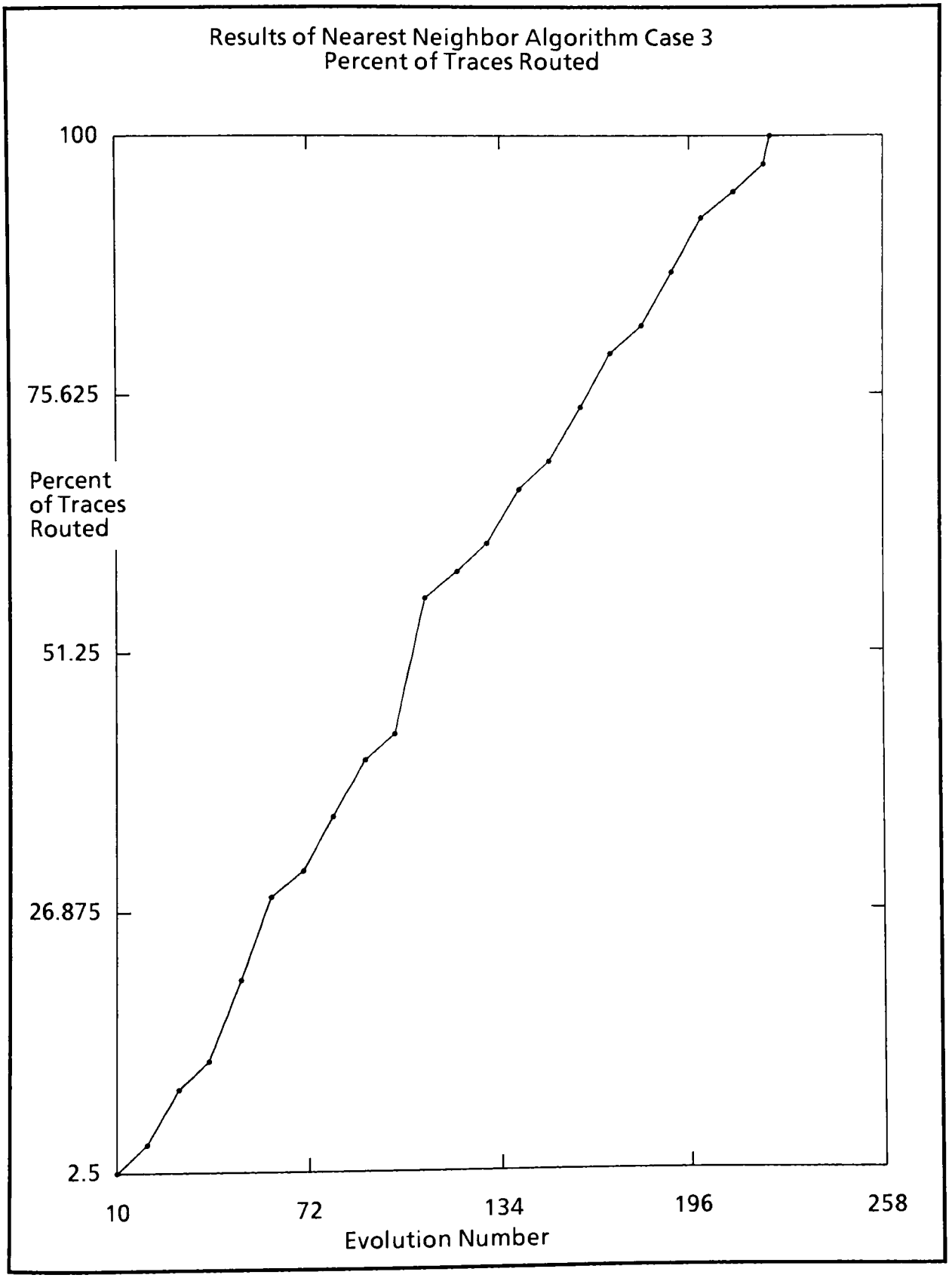
The time decrease was minimal and is attributed to the fewer operations being performed to the population entries at every evolution cycle.

The graph of these results is shown in the following four graphs


Results of Nearest Neighbor Algorithm Case 3
Population Skewness
.9
.525
.15
-.225
.6
Population
Skewness
10
72
134
196
258
Evolution Number


Results of Nearest Neighbor Algorithm Case 3
Population Kurtosis
.8
.4
0
-.4
-.8
Pop
Kurtosis
10
72
134
196
258
Evolution Number

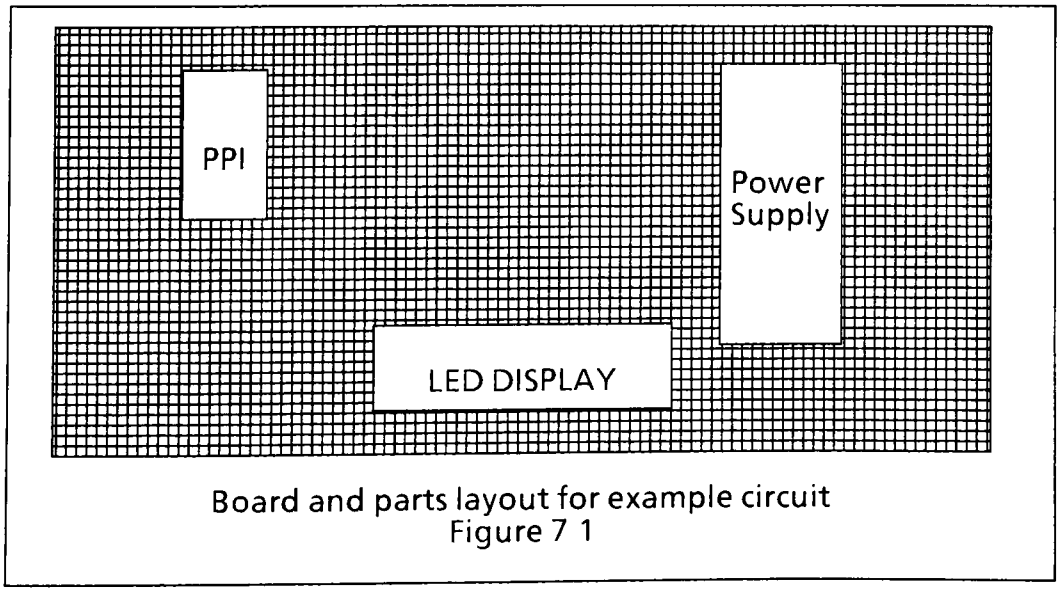

Results of Nearest Neighbor Algorithm Case 3
Average Population Utility
25.2
19.7
14.2
8.7
3.2
Average
Population
Utility
10
72
134
196
258
Evolution Number


Results of Nearest Neighbor Algorithm Case 3
Percent of Traces Routed
100
75.625
Percent
of Traces
Routed
51.25
26.875
2.5
10
72
134
196
258
Evolution Number

7.0 RATNEST SOLUTION TECHNIQUE

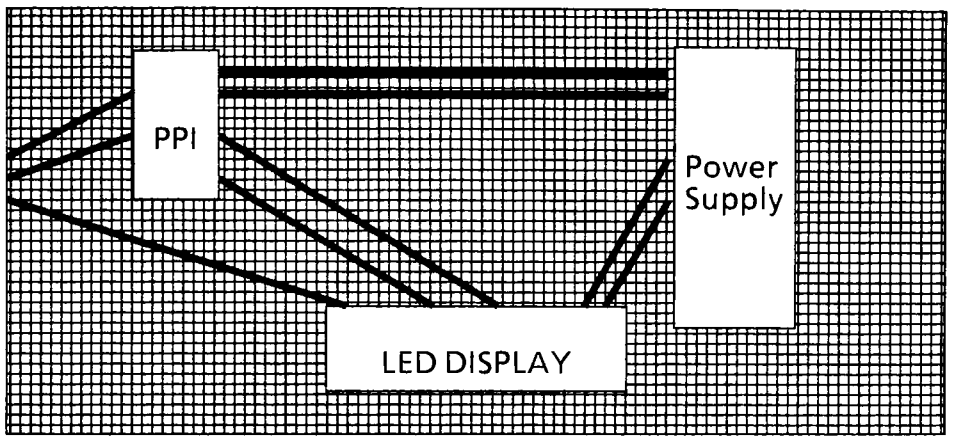
In Chapter 6 I described an experiment where the fundamental premise of the algorithm was to seek out a routing path for each trace within the netlist with the condition that each trace is not at all connected to its ending point. As an alternative algorithm this chapter presents a method of performing the trace routing with the each trace fully connected between its starting and ending point. The thought process here is that right from the start, the traces are provided additional information about their solution path. Also by having the traces connected the algorithm will know, right from the start, where the areas of high board contention are; these areas are the cells and neighboring cells that already contain trace path connections.

This solution algorithm starts out with the same initial requirements as the nearest neighbor solution technique (Chapter six) in that it assumes part placement has already occurred, a netlist is in existence, and an appropriate board size is known. Please refer to Figure 7.1 for a example board layout.



Board and parts layout for example circuit
Figure 7 1

The next item required for this technique is that a ratnest be run on the circuit to be routed. Just for clarification, a circuit's ratnest is a straight line drawing of all traces, starting point to ending point. Figure 7.2 is a sample ratnest. Before the

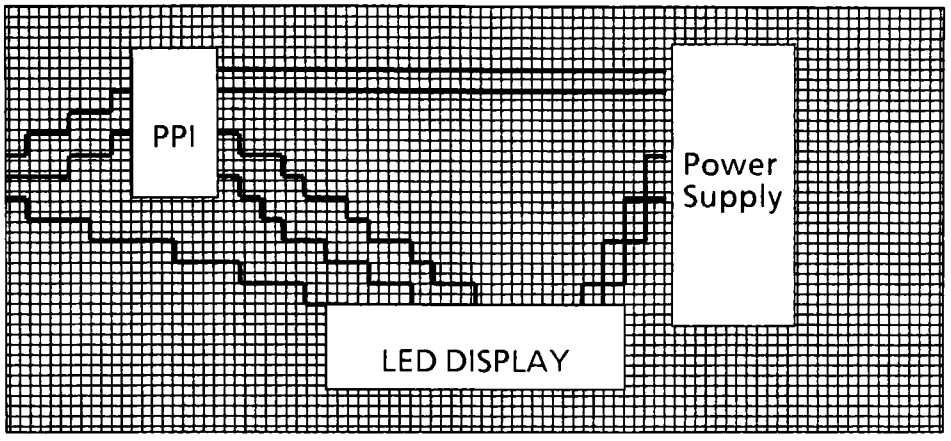


Ratnest for simple circuit
Figure 7.2

circuit's ratnest is utilized by the routing algorithm, it is preconditioned. The circuit's ratnest is then passed through a conditioning routine that quantizes each trace line to pass through the nearest (X, Y) coordinates of the unit grid superimposed upon the circuit board. This in effect shifts the straight line trace paths slightly such that they pass through integer (X, Y) coordinates, not real coordinate values. Figure 7.3 is a conditioned ratnest of Figure 7.2.

The quantizer function that allows us to develop the conditioned board from the ratnest board is as follows:

We know the function for a line is:



Conditioned ratnest for simple circuit
Figure 7.3

$$Y = MX + B$$

where M is defined as:

$$M = \frac{Y_2 - Y_1}{X_2 - X_1}$$

where (X_1, Y_1) is defined to be the Trace point origin and (X_2, Y_2) is defined to be the trace end point. and B is the Y intercept point at X = 0.

Given that we have the above data, the following pseudo code describes the algorithm that performs the quantizing function on the ratnest circuit board.

Test $\Delta X = 0$, if true then Free variable is Y

Test $\Delta Y = 0$, if true then Free variable is X

Test if both ΔY & $\Delta X = 0$ then a problem with trace end points, both are same

Determine value of M

If M > 1 then Free variable is Y Else Free variable is X

Loop on Free variable

For loop runs from Free variable trace Start point to Free variable trace end point increment = 0.5 units

Calculate variable

Round both Free variable and ____ variable up to next integer

Set next (X, Y) coordinates to the above corresponding values

End Loop

Result is a vector of conditioned / quantized values for the ratnest trace path.

There are some unique characteristics of the conditioned ratnest.

- Almost all traces have the maximum number of 'jogs' in them.
- Multiple traces may share the same grid coordinates (X, Y).
- Typically each trace length in the conditioned ratnest will be longer than the trace path in the solution network. By length I refer to the number of (X, Y) coordinates required to define the trace path.

As with the nearest neighbor solution algorithm, the initial core population starts off with one entry for each trace defined in the ratnest. Each of these traces are then replicated some number of times according to their utility values specified by the replication algorithm.

To restate an important characteristic of this algorithm, each POPE in the CORE population is greater than length 1. Unlike the Nearest Neighbor algorithm of Chapter six where each POPE in the core population is equal to length one, a POPE of the ratnest algorithm contains all of the coordinates required to run a path from starting point to ending point.

The fundamental idea of the ratnest algorithm is to evolve the population by modifying the POPEs such that they no longer have any of their board cells / coordinates shared in common with any other POPEs. This is different from the concept of the nearest neighbor solution. Because the nearest neighbor solution attempts to evolve its POPEs by growing them in length, capturing / occupying (X, Y) coordinates towards the traces ending point.

The evolution concept for the ratnest algorithm is for each POPE to identify and select neighbors of the existing trace path that:

- Eliminate / minimize 'jogs' in the paths, and minimize each trace distance (number of cells per trace and geometrical distance).
- Find paths for all traces that do not share (X, Y) coordinate pairs.

Essentially the technique here is to massage the invalid ratnest trace paths such that they become valid paths not sharing (X, Y) coordinates with other trace paths.

7.1 Utility function for solution case one

In this experiment I utilized the exact utility and character functions of the nearest neighbor algorithm, as described in Section 6.2. My intention here was to be able to hold the genetic operators consistent across the various solution methods being investigated.

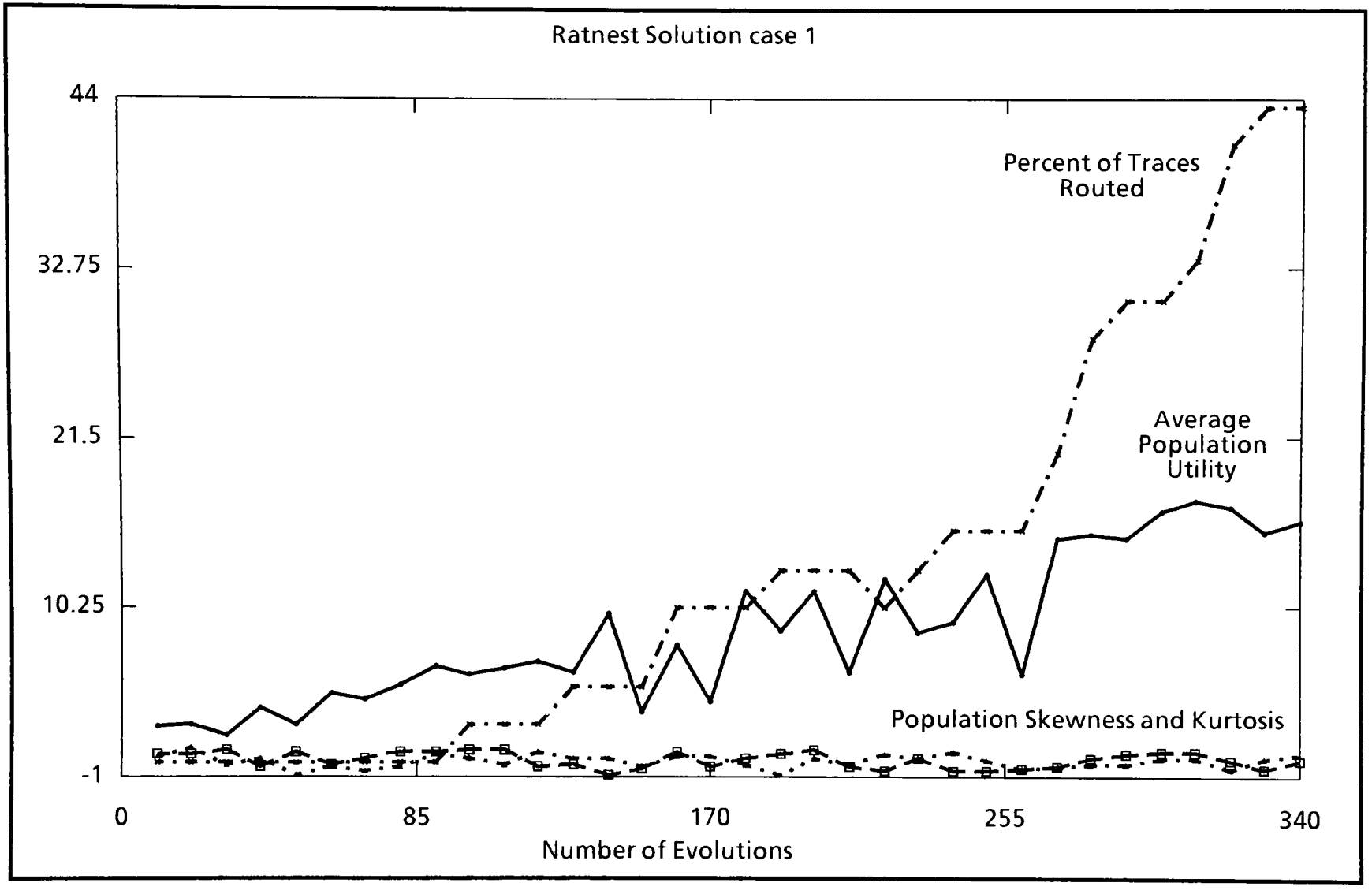
7.2 RATNEST Solution Algorithm Solution Data Case One

Within the appendix a table is provided showing the evolution data having run the genetic algorithm with previously described evolution functions. Please refer

to Table 7.2.1. For this simple example, we never achieved an acceptable routing path solution. After 300 plus evolutions the population percentage of successful routing paths was extremely low.

As a result of the very poor performance this solution algorithm was abandoned and the utility function upgraded to be like that of the nearest neighbor algorithm of Section 6.4.

A graph of the collect data for this set of genetic parameters is as shown in Figure 7.2.1

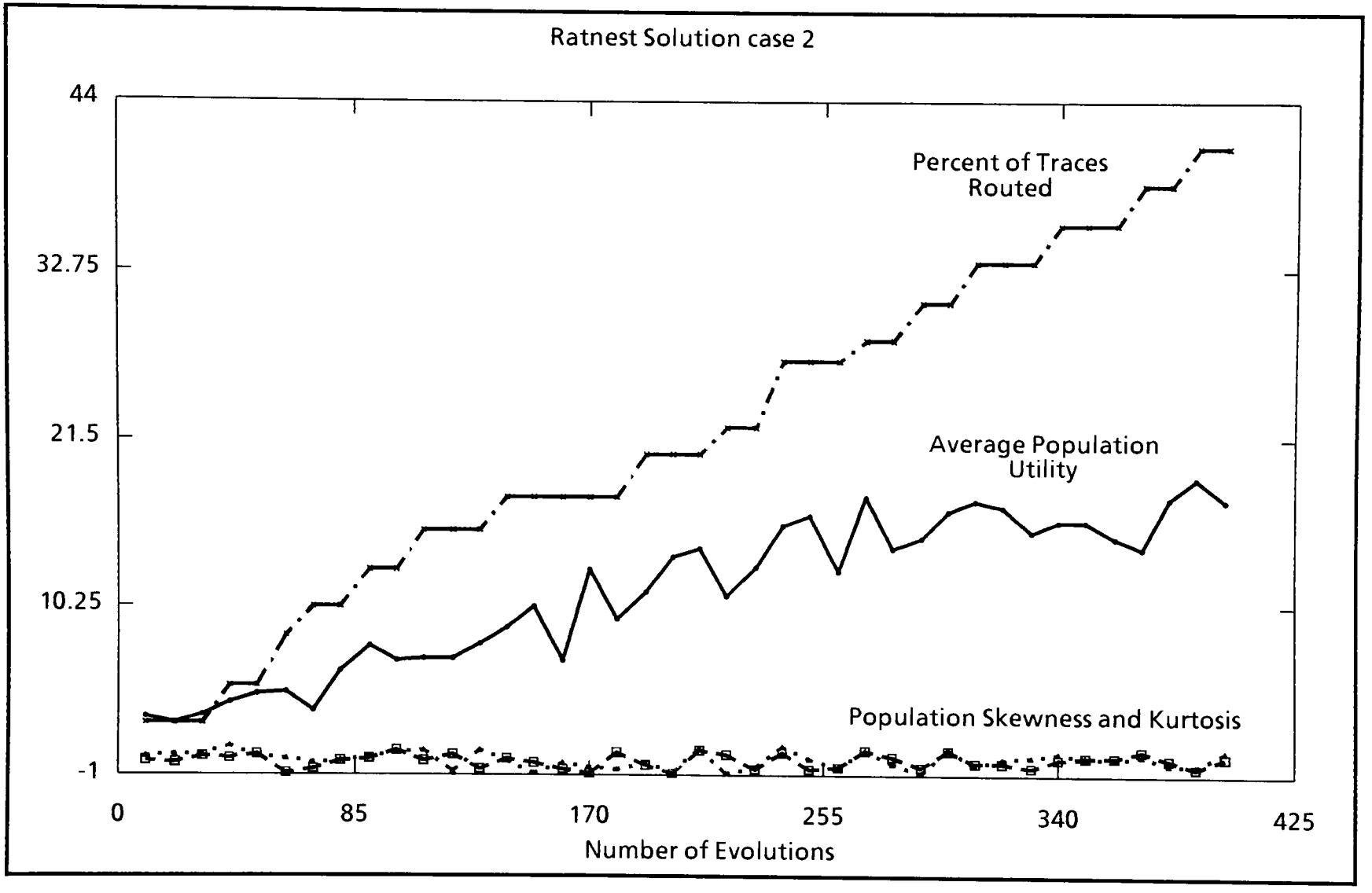


7.3 RATNEST Solution Algorithm Solution Data Case Two

The following table is the evolution data having run the genetic algorithm with previously described evolution functions. Please refer to the Table 7.2.1 in the appendix. For this simple example the we never achieved an acceptable routing path solution. After 400 plus evolutions the population percentage of successful routing paths is extremely low.

As a result of the very poor performance this solution algorithm was abandoned and the utility function upgraded to be like that of the nearest neighbor algorithm Section 5.4. I reran the ratnest algorithm several times, each with an optimization / change in the algorithm operators.

A graph of the collect data for this set of genetic parameters is as shown in Figure 7.2.1



7.4 Discussion of Ratnest Algorithm One

In looking at the data for this technique we see that the percent of completed routing traces never reached 100%. It plateaued at ~40% and then the algorithm's evolution limit caused the algorithm to stop executing and report a failure. In this experiment the algorithm stopped executing and declared failure because the evolution exceeded that of the characterization parameter limit set within the character function.

I did rerun this case with the evolution limit set to 9999. Because of the randomness introduced into the algorithms I am unable to simulate the exact evolution as before, but on average each rerun should be very similar. Having reset the total number of evolutions until failure I found no major benefit. The algorithm would progress in a manner similar to when the limit was 350 and 400 evolutions. The algorithm only reached about 45% trace completion, and this was achieved at about 400 evolution cycles. The evolution did eventually plateau at about 75% trace path completion after about 20,000 evolution cycles.

I reran the algorithm several times attempting to adjust the genetic operators such that they would achieve a better trace completion rate but was unsuccessful.

Having performed the experiment several times with various modifications I was left with a fair amount of data. The data that I focused upon was the trace paths after competition within each evolution cycle. By competition here I am referring to the stage at which each trace path bids and attempts to capture neighbors in an attempt to smooth out the path and no longer share grid cells. If the reader refers back to the functional flow diagrams of Section 4.6.4, I captured my data just after the "neighbor evaluation and capture step" of Figure 4.6.4.

7.5 Problem with RATNEST solution technique

Having examined the data from the ratnest routing algorithm I found that there were several negative conditions that I introduced into the decision algorithm. Two of the most severe negative conditions be described as 1) local thrashing and 2) a local versus global optimization contention.

By local versus global optimization contention I am referring to the problem of a decision being made by the genetic algorithm to modify a point on the trace path that appears to help the local region being evaluated, but causes a negative ripple effect on second and third level neighbors. To compound the problem, the local decisions typically did not help to move the trace towards a path that is a "generally" or "long distance" good choice.

Local thrashing is the phenomenon where in one evolution a trace captures a neighbor that eliminates a jog or shared cell within its path. This appears to be good, at least in the short term. The induced thrashing problem arises in one of two situations. The first occurs when in the same evolution cycle a nearby trace captures a neighboring cell that blocks the previous trace from continuing its path. The second case occurs where thrashing is induced in the next evolution cycle when a trace moves to capture a cell that appears to be eliminating a jog in the immediate neighboring region but causes a jog in an outer region.

8.0 Restricted Optimum Neighbor Routing Problem

In Chapter six I presented the nearest neighbor routing algorithm that appeared to work with only mild success. In Chapter seven I presented a significantly different approach, the ratnest routing approach, a technique that did not work at all. I am now going to present my final technique, which I believe was successful.

In the algorithms of Chapter six and seven all of the POPEs were active and competing at all times. In this technique, Restricted Optimum Neighbor, there are only a few select POPEs active at any given point in the evolution cycle. For any given evolution cycle there is typically only one primary POPE and a couple of immediate neighbors active. The purpose here is to concentrate more effort on completing a trace path than moving onto the next trace path to be routed. Trace paths being evolved are denoted by being listed upon the active list. Trace paths suspended, awaiting to enter into the evolution process, are denoted as being upon the pending list.

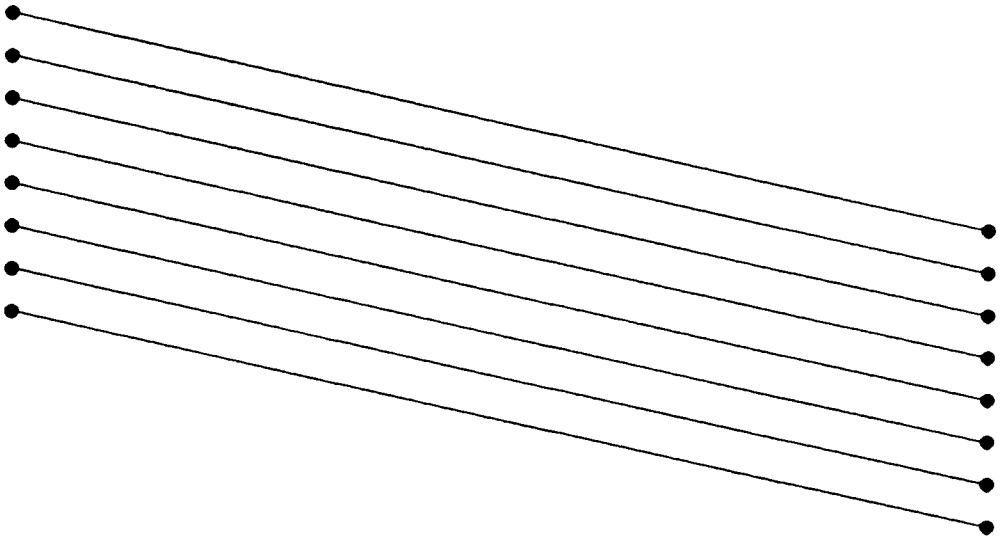
8.1 Characteristic Information of Restricted Optimum Neighbor Algorithm

Having inspected the manner in which the previous two algorithms operated, I incorporated some changes to the fundamental operation of this algorithm. These changes were:

- The ability to mark traces as priority traces. A trace marked as a priority trace will be routed before other traces are entered into the evolution cycle.

- The ability to mark traces as being clustered. This was a way of signifying a series of traces that might be a set of bus paths or address lines. A unique characteristic of these traces is that they all start from approximately the same position, e.g. in a row along one of the axis. Secondly they all terminate

A rat nest drawing of a set of bus lines



This cluster of trace paths can be associated as a group and the algorithm will attempt to route them simultaneously. The desired result here is that the actual trace paths will be synchronized.

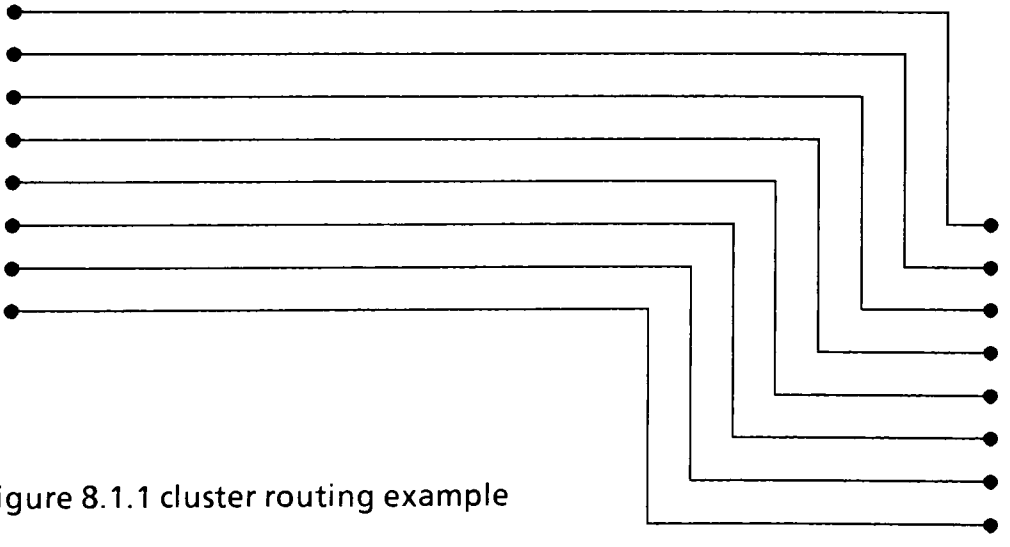


Figure 8.1.1 cluster routing example

in approximately the same position along a row or column at some ending point. See Figure 8.1.1

- This implementation also utilized signal flow Graph data to help prioritize the order of the trace path pending list and relative PWB cell values for given regions.

8.2 Examples and Description of Prioritization

In the netlist specification the user can utilize the term "priority" in front of a trace path definition. Please refer back to Chapter six for other example netlist files. In the netlist the user would specify priority in front of any of their connect statements. Please refer to the sample netlist below in Figure 8.2.1

```
; a circuit for calculating a parity bit for a 16-bit word (an xor tree)
dimension (29,37)

; chip definition -- quadruple 2-input xor gates
chip type = ttl7486 pins = 14 horizontal = 2 vertical = 6
    vcc = 14
    gnd = 7
    a1 = 1
    b1 = 2
    y1 = 3
    a2 = 4
    b2 = 5
    y2 = 6
    y3 = 8
    a3 = 9
    b3 = 10
    y4 = 11
    a4 = 12
    b4 = 13

; power and ground are supplied here
hole (3,20)
hole (3,25)

; the 16-bit input word
hole (26,5)
hole (26,7)
hole (26,9)
hole (26,11)
hole (26,13)
```

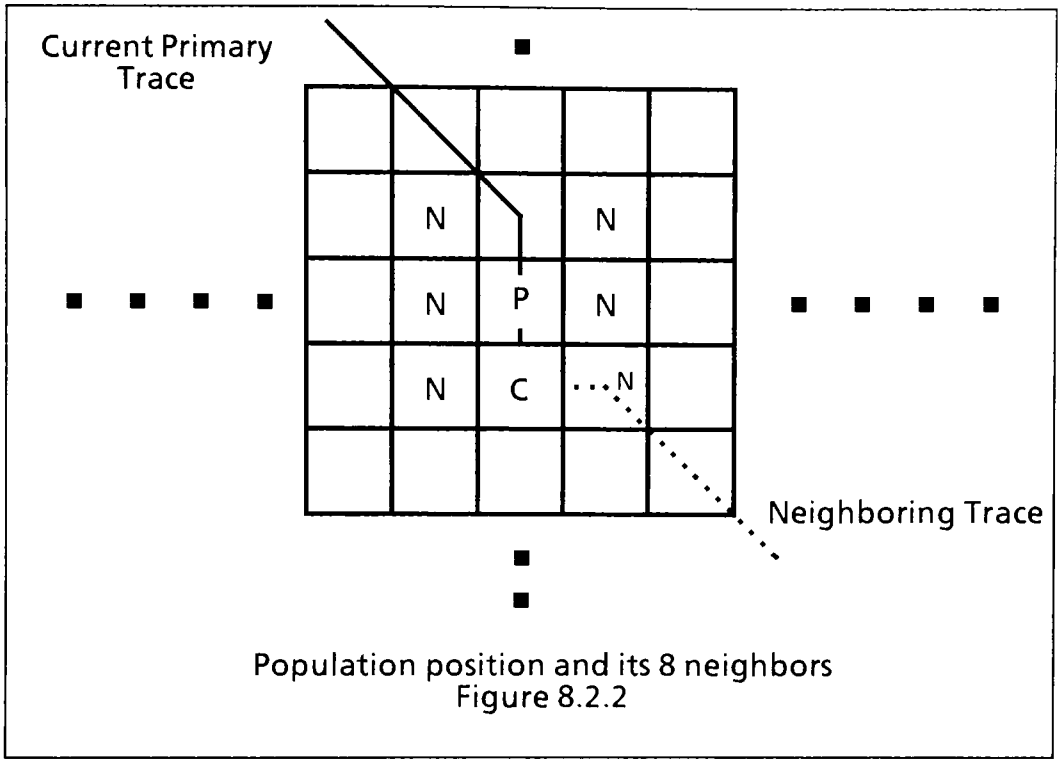
```
hole (26,15)
hole (26,17)
hole (26,19)
hole (26,21)
hole (26,23)
hole (26,25)
hole (26,27)
hole (26,29)
hole (26,31)
hole (26,33)
hole (26,35)

; the output (parity) bit
hole (3,11)

; four instances of the above chip
chipat (6,5) name = xor0 type = ttl7486 orientation = normal
chipat (6,21) name = xor1 type = ttl7486 orientation = normal
chipat (16,5) name = xor2 type = ttl7486 orientation = normal
chipat (16,21) name = xor3 type = ttl7486 orientation = normal

; connect power and ground
priority 1 connect (3,20) and xor0.vcc


; condense 16 bits into 8 bits
connect (26,5) and xor2.a1
connect (26,7) and xor2.b1
connect (26,9) and xor2.a2
connect (26,11) and xor2.b2
connect (26,13) and xor2.a3
connect (26,15) and xor2.b3
connect (26,17) and xor2.a4
connect (26,19) and xor2.b4
connect (26,21) and xor3.a1
connect (26,23) and xor3.b1
connect (26,25) and xor3.a2
connect (26,27) and xor3.b2
connect (26,29) and xor3.a3
connect (26,31) and xor3.b3
connect (26,33) and xor3.a4


; condense 8 bits into 4 bits
connect xor2.y1 and xor1.a1
connect xor2.y2 and xor1.b1
connect xor2.y3 and xor1.a2
connect xor2.y4 and xor1.b2
connect xor3.y1 and xor1.a3
connect xor3.y2 and xor1.b3
connect xor3.y3 and xor1.a4
connect xor3.y4 and xor1.b4

; condense 4 bits into 2 bits
```

```
connect xor1.y1 and xor0.a1
connect xor1.y2 and xor0.b1
connect xor1.y3 and xor0.a2


; condense 2 bits into 1 bit
connect xor0.y1 and xor0.a3
connect xor0.y2 and xor0.b3

; connect the output (parity) bit
priority 3 connect xor0.y3 and (3,11)
```

In the example Figure 8.2.1 I utilize the priority option for the power and ground connections. I group the power connections into priority class 1 and the ground connections into priority class 2. At the bottom of the example file I list the output bit as priority group 3. In this case where there is only one of them, all I am trying to signify is that this one should be routed before the rest of the internal traces.

As mentioned earlier this algorithm primarily has only one trace path being routed at any given time. As the primary trace path is evaluating its neighbors to determine where to route itself, it is possible that a trace path in a neighboring cell may become active. The way a primary trace path's neighbor becomes active is if the neighboring trace path is currently terminated in one of the primary trace path's neighbor cells, and the neighbor trace path desires to move into one of the primary trace paths neighboring cells. Please refer to the series of Figures below 8.2.2 through 8.2.9

In Figure 8.2.2 I show the primary trace and its occupied cells. Also shown in Figure 8.2.2 is the neighbor trace and its occupied cells. In the drawing there is a neighbor labeled C, which is the cell of contention. Both traces, primary and neighbor, wish to occupy this cell. The way that the algorithm resolves this problem is to activate the neighbor trace for this evolution cycle and allow it to compete for the contention cell. After the evolution cycle is complete the neighbor



Population position and its 8 neighbors
Figure 8.2.2

cell is deactivated, put back onto the pending list and the primary trace resumes evolution by it self.

8.3 Extended mutation function

I have programmed the algorithm to extend the mutation function such that the active trace being routed may be switched with one of the traces on the pending list. The way in which this swapping process can occur is one of:

- A neighboring trace that has become active, as described above, and has an estimated completion distance that is less than a threshold found in the character function. If the primary trace's estimated completion distance is also less than the threshold it is possible for the primary trace to remain active rather than be swapped onto the pending que.

- It is possible for a primary trace to be placed upon the pending que based upon sheer random probability. If this is the case, then one trace from the pending queue is selected at random and placed upon the active queue.

- The third extension to the mutation function is that traces of the same blood line will crossover at random points along their connection path. There are two conditions one of which must be satisfied in order for the related traces to be able to cross over in this manner.

  One is: The two traces have a board cell in common. This is the point at which the traces will be crossed.

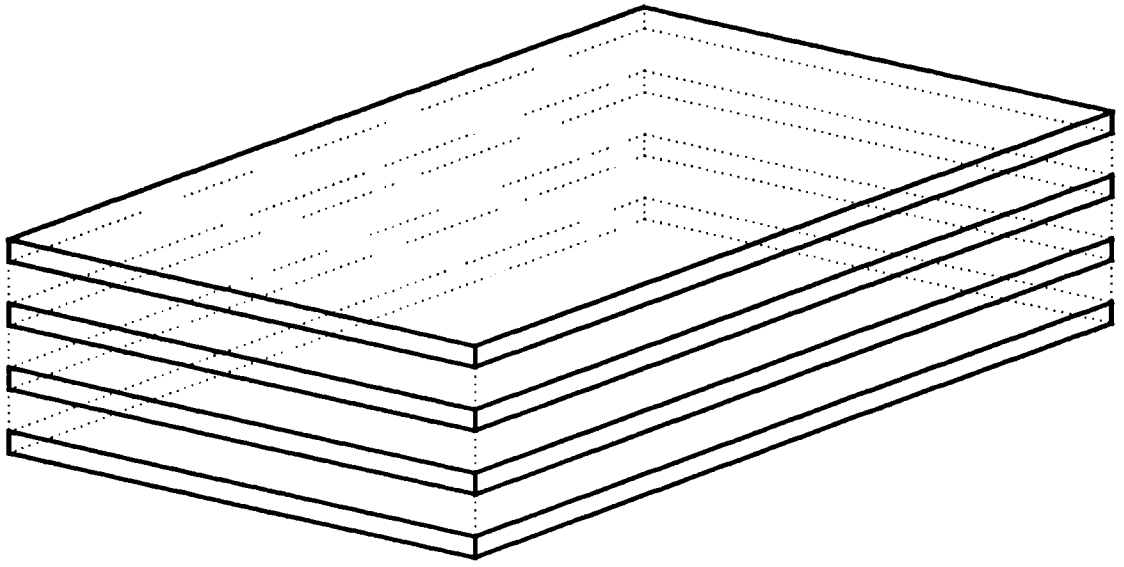
  Two is: The two traces are occupying board cells that are adjacent neighbors to one another. Please refer to Chapter 4 for a detailed description of the neighbor concept.

8.4 Four Layer Board

For the experiments in the previous two Chapters I utilized a single layer board in which all traces were routed upon one side of the board, the top. This last experiment utilized a four layer board. I will utilize the top and bottom sides for traces. There will also be two layers sandwiched into the middle of the board. These two middle layers will be one for power and one for ground. Figure 8.4.1 is an illustration of a four layer board.

By configuring the PWB in this manner I will be better able to handle congested areas where many traces were heavily competing for a cell. This configuration also leads to a lower signal to noise ratio. The two inner layers (power and ground) act a shielding between the two outer layers of traces.

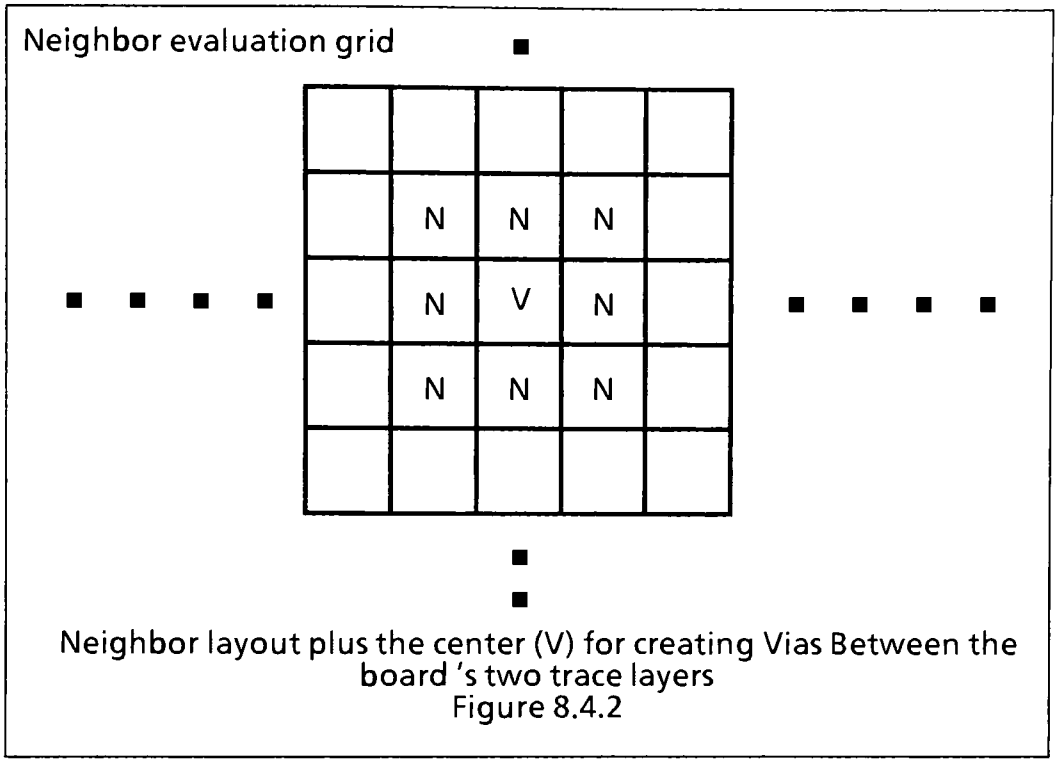
Figure 8.4.1
Four layers of the PWB



- Layer One is for Trace paths and user connections
- Layer Two is for ground (± 0V) connections
- Layer Three is for power (+ 5V) connections
- Layer Four is for Trace path and trace connections only

Please note that for this system all -5V connections need to be placed on layer One or Four and routed as a normal signal trace. Please note that it is possible to add another layer for the -5V into the system.

The way in which I enabled the algorithm to evaluate and Via / Channel between layers One and Four, the two trace layers shown in Figure 8.4.1, is through the center cell of the 3x3 neighbor evaluation grid, Figure 8.4.2. In the prior algorithms the center cell was considered the current position of the trace being



Neighbor layout plus the center (V) for creating Vias Between the board 's two trace layers
Figure 8.4.2

routed and nothing more. In this algorithm the center cell is the way in which a trace can via to the other layer and continue routing.

8.5 Genetic Operators and Utility Function for the Restricted Neighbor Algorithm

All of the operators for this algorithm are the same as the ones defined in Chapters four and five. Even though I have changed the fundamental operation of this algorithm as compared to the algorithms of Chapters six and seven, I have maintained the operators and their functional definitions.

The utility function for this algorithm is exactly a defined in Section 6.1. I have also utilized the character function from Section 6.2. My intent is to try and keep as many variables and operations equivalent across the algorithms being investigated.

8.6 Restricted Neighbor Algorithm Results of the PWB from Chapters six and Seven

In Figure 8.2.1 above is a sample of the PWB board definition submitted to the Restricted Neighbor algorithm. This board is the same board that was submitted to the algorithms of Chapter six and seven. For this test case I did not utilize the priority options since they were not available for the algorithms of Chapter six and seven. Table 8.6.1 found in the appendix is the table of output from the genetic algorithm. Figure 8.6.2A through 8.6.2D are graph of the results of the routing. These results can be compared with the results of the algorithms investigated in Chapters Six and Seven because I utilized the exact same input netlist for purposes of comparison. The output format for the algorithms of Chapter 8 is different because of the fundamental way in which the algorithm works to find a solution is different from that of Chapters six and seven. For this algorithm I show histograms of the the percent of board searched against the trace being routed. Figures 8.6.2A through 8.6.2D are examples of this. Figure 8.6.4 is the completed trace diagram. Figure 8.6.5 is the PWB trace routing diagram for the top layer of the circuit board. Figure 8.6.6 is the PWB trace routing diagram for the bottom layer of the circuit board. I refer the reader back to Section 8.2 for a discussion of the circuit board trace and power layers.

As can be seen from the results this new method is highly successful. Each trace has been routed yet requiring a very small amount of the board to be searched. I am now going to generate a more complex routing diagram to be feed to the algorithm for analysis.

8.7 Example of 8.6 utilizing the Priority and Cluster option

For this example I am going to utilize a slightly

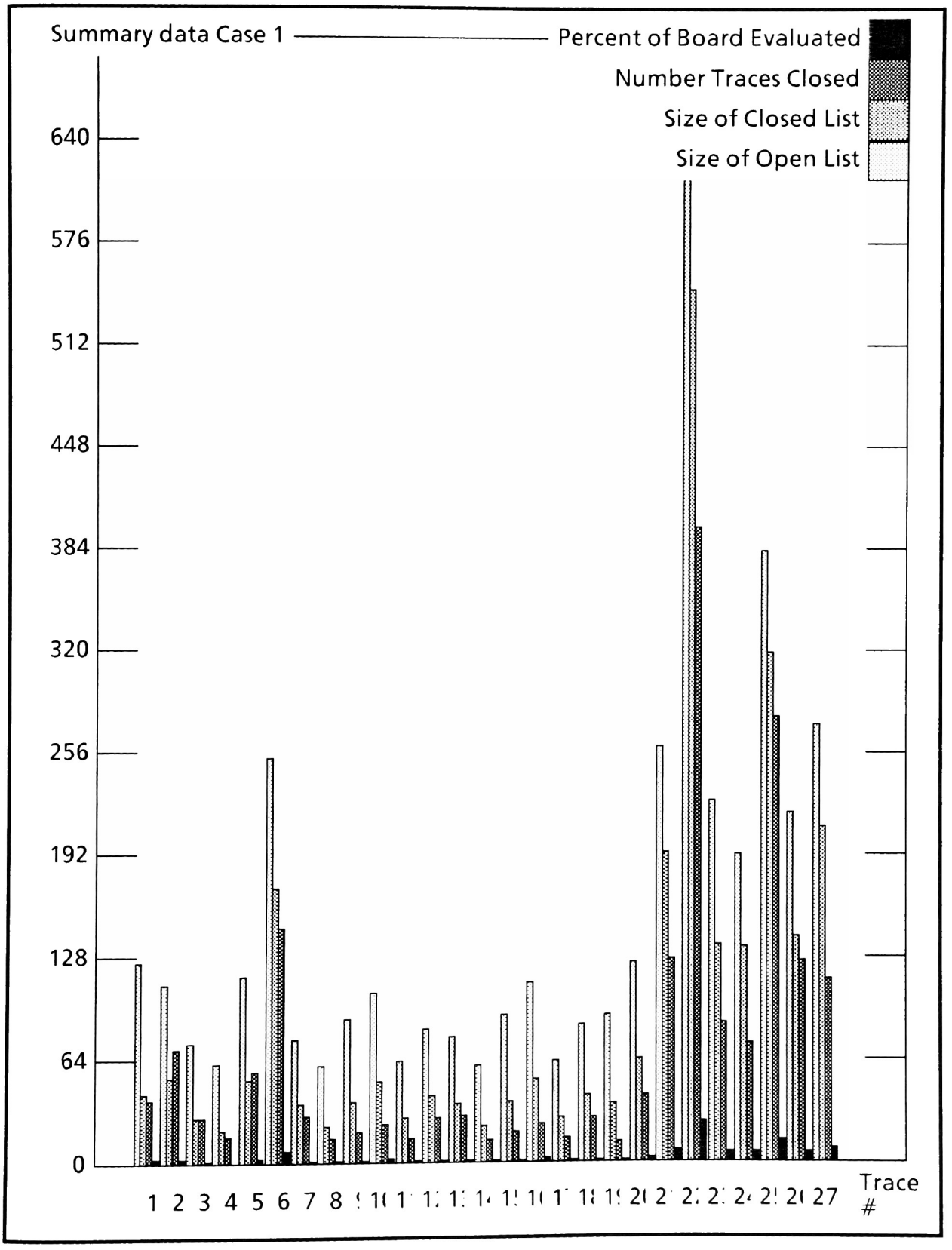
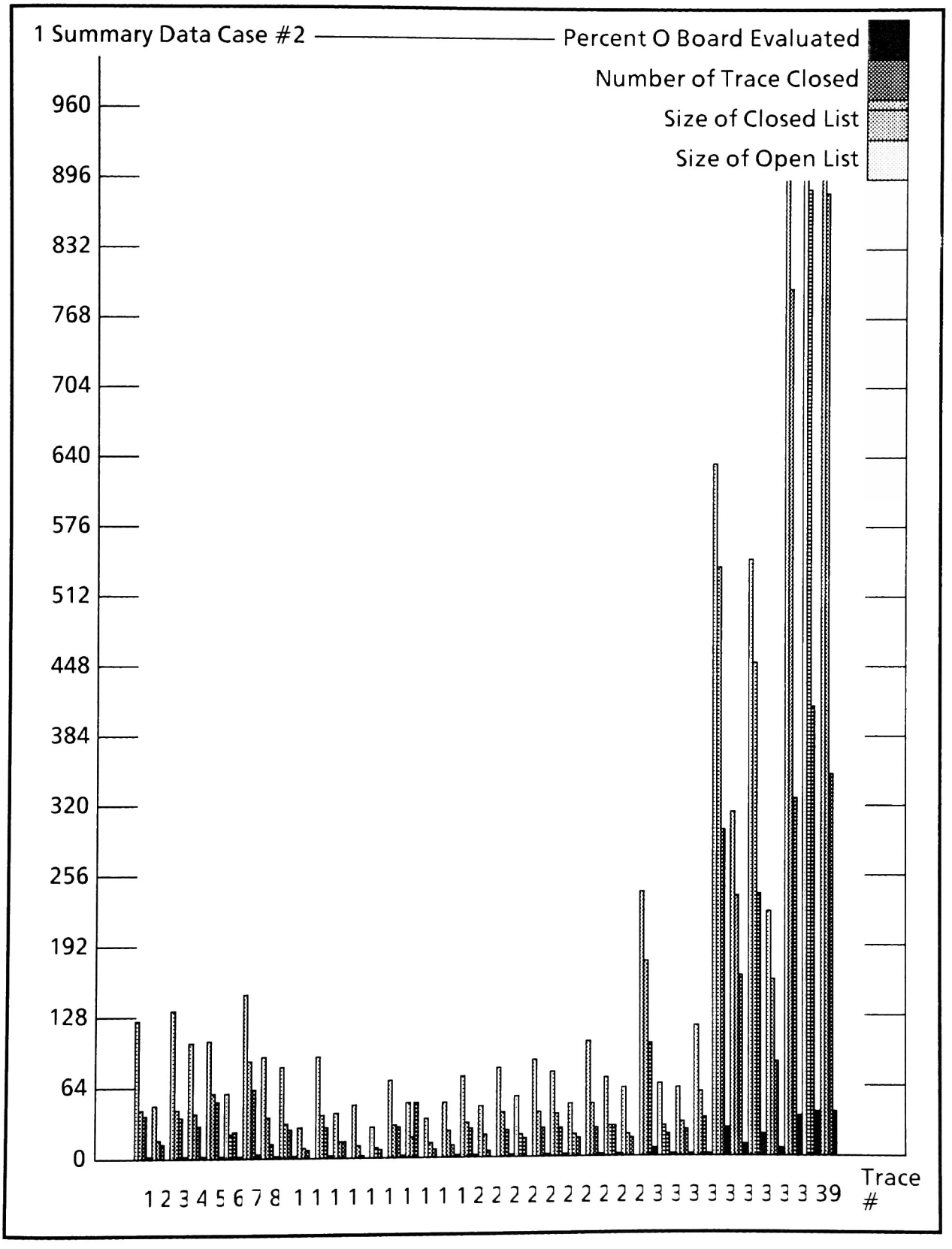

Summary data Case 1
Percent of Board Evaluated
Number Traces Closed
Size of Closed List
Size of Open List
640
576
512
448
384
320
256
192
128
64
0
1 2 3 4 5 6 7 8
Trace
#

Figure 8.6.1 is the netlist that saw submitted to the genetic algorithm for routing. Figure 8.6.2 is the final output data statistics of the routing algorithm. Figure 8.7.3 is the histogram plot of the data from the data table. Figure 8.7.4 is the circuit diagram for the entire routed system. Both the top and bottom trace layers have been merged into one plane for viewing. Figure 8.7.5 is the routed system showing only the top layer of the PWB board. If the reader refers back to Section 8.2 Figure 8.2.2 the top layer is layer one of the diagram. Figure 8.7.6 is the bottom layer of the PWB.

Figure 8.7.1 The netlist for Section 8.7 example

```
; a circuit for calculating a parity bit for a 16-bit word (an xor tree)
dimension (29,37)

; chip definition -- quadruple 2-input xor gates
chip type = ttl7486 pins = 14 horizontal = 2 vertical = 6
    vcc = 14
    gnd = 7
    a1 = 1
    b1 = 2
    y1 = 3
    a2 = 4
    b2 = 5
    y2 = 6
    y3 = 8
    a3 = 9
    b3 = 10
    y4 = 11
    a4 = 12
    b4 = 13

; power and ground are supplied here
hole (3,20)
hole (3,25)

; the 16-bit input word
hole (26,5)
hole (26,7)
hole (26,9)
hole (26,11)
hole (26,13)
hole (26,15)
hole (26,17)
hole (26,19)
hole (26,21)
```


1 Summary Data Case #2
Percent O Board Evaluated
Number of Trace Closed
Size of Closed List
Size of Open List
960
896
832
768
704
640
576
512
448
384
320
256
192
128
64
0
1 2 3 4 5 6 7 8 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 39
Trace #

```
hole (26,23)
hole (26,25)
hole (26,27)
hole (26,29)
hole (26,31)
hole (26,33)
hole (26,35)

; the output (parity) bit
hole (3,11)

; four instances of the above chip
chipat (6,5) name = xor0 type = ttl7486 orientation = normal
chipat (6,21) name = xor1 type = ttl7486 orientation = normal
chipat (16,5) name = xor2 type = ttl7486 orientation = normal
chipat (16,21) name = xor3 type = ttl7486 orientation = normal

; connect power and ground
priority 1 connect (3,20) and xor0.vcc
priority 1 connect (3,20) and xor0.vcc
priority 1 connect (3,20) and xor0.vcc
priority 1 connect (3,20) and xor0.vcc
priority 2 connect (3,25) and xor0.gnd
priority 2 connect (3,25) and xor0.gnd
priority 2 connect (3,25) and xor0.gnd
priority 2 connect (3,25) and xor0.gnd


; condense 16 bits into 8 bits
connect (26,5) and xor2.a1
connect (26,7) and xor2.b1
connect (26,9) and xor2.a2
connect (26,11) and xor2.b2
connect (26,13) and xor2.a3
connect (26,15) and xor2.b3
connect (26,17) and xor2.a4
connect (26,19) and xor2.b4
connect (26,21) and xor3.a1
connect (26,23) and xor3.b1
connect (26,25) and xor3.a2
connect (26,27) and xor3.b2
connect (26,29) and xor3.a3
connect (26,31) and xor3.b3
connect (26,33) and xor3.a4
connect (26,35) and xor3.b4


; condense 8 bits into 4 bits
connect xor2.y1 and xor1.a1
connect xor2.y2 and xor1.b1
connect xor2.y3 and xor1.a2
connect xor2.y4 and xor1.b2
connect xor3.y1 and xor1.a3
connect xor3.y2 and xor1.b3
```

```
connect xor3.y3 and xor1.a4
connect xor3.y4 and xor1.b4

; condense 4 bits into 2 bits
connect xor1.y1 and xor0.a1
connect xor1.y2 and xor0.b1
connect xor1.y3 and xor0.a2
connect xor1.y4 and xor0.b2


; condense 2 bits into 1 bit
connect xor0.y1 and xor0.a3
connect xor0.y2 and xor0.b3

; connect the output (parity) bit
priority 3 connect xor0.y3 and (3,11)
```

End of Figure 8.7.1

8.8 Example of Two 16 Bit Parity Checker Circuits

In this example I have simply replicated the circuit that was fed into the algorithm in the example of Section 8.6. I am going to test with a more complex circuit because as seen by the results of the example in Section 8.6 the circuit is far too simple for the new algorithm. The new algorithm allows for two layers to be utilized for the PWB and therefore it is possible to supply more complex circuits for the algorithm to route.

If the reader examines the net list back in Figure 8.2.1 and the netlist supplied below, they will see that I have simply copied the parity circuit a second time. There are effectively two parallel circuits that are utilizing the same power, ground, and input connects. This system should be fairly rigorous to route, due to the overlapping nature of the signals.

Figure 8.8.1 below is the netlist. Figure 8.8.2 is the table of results from the routing algorithm. Figure 8.8.3 is the histogram showing the Graphical

representation of the data from the table 8.8.2. Figure 8.8.4 is a print of the entire circuit. Figure 8.8.5 is a diagram of the top layer of the PWB and Figure 8.8.6 is a diagram of the bottom layer of the PWB.

Figure 8.8.1 Netlist for circuit of Section 8.8

```
; a circuit for calculating a parity bit for a 16-bit word (an xor tree)
dimension (100,100)

; chip definition -- quadruple 2-input xor gates
chip type = ttl7486 pins = 14 horizontal = 2 vertical = 6
    vcc = 14
    gnd = 7
    a1 = 1
    b1 = 2
    y1 = 3
    a2 = 4
    b2 = 5
    y2 = 6
    y3 = 8
    a3 = 9
    b3 = 10
    y4 = 11
    a4 = 12
    b4 = 13

; power and ground are supplied here
hole (3,20)
hole (3,25)

; the 16-bit input word
hole (26,5)
hole (26,7)
hole (26,9)
hole (26,11)
hole (26,13)
hole (26,15)
hole (26,17)
hole (26,19)
hole (26,21)
hole (26,23)
hole (26,25)
hole (26,27)
hole (26,29)
hole (26,31)
hole (26,33)
hole (26,35)

; the output (parity) bit
hole (3,11)
```

```
; four instances of the above chip
chipat (6,5) name = xor0 type = ttl7486 orientation = normal
chipat (6,21) name = xor1 type = ttl7486 orientation = normal
chipat (16,5) name = xor2 type = ttl7486 orientation = normal
chipat (16,21) name = xor3 type = ttl7486 orientation = normal

chipat (36,35) name = xor4 type = ttl7486 orientation = normal
chipat (36,51) name = xor5 type = ttl7486 orientation = normal
chipat (46,35) name = xor6 type = ttl7486 orientation = normal
chipat (46,51) name = xor7 type = ttl7486 orientation = normal

; connect power and ground to all chips
priority 1 connect (3,20) and xor0.vcc
priority 1 connect (3,20) and xor1.vcc
priority 1 connect (3,20) and xor2.vcc
priority 1 connect (3,20) and xor3.vcc
priority 2 connect (3,25) and xor0.gnd
priority 2 connect (3,25) and xor1.gnd
priority 2 connect (3,25) and xor2.gnd
priority 2 connect (3,25) and xor3.gnd

; connect power and ground to all chips
priority 1 connect (3,20) and xor4.vcc
priority 1 connect (3,20) and xor5.vcc
priority 1 connect (3,20) and xor6.vcc
priority 1 connect (3,20) and xor7.vcc
priority 2 connect (3,25) and xor4.gnd
priority 2 connect (3,25) and xor5.gnd
priority 2 connect (3,25) and xor6.gnd
priority 2 connect (3,25) and xor7.gnd

; condense 16 bits into 8 bits
connect (26,5) and xor2.a1
connect (26,7) and xor2.b1
connect (26,9) and xor2.a2
connect (26,11) and xor2.b2
connect (26,13) and xor2.a3
connect (26,15) and xor2.b3
connect (26,17) and xor2.a4
connect (26,19) and xor2.b4
connect (26,21) and xor3.a1
connect (26,23) and xor3.b1
connect (26,25) and xor3.a2
connect (26,27) and xor3.b2
connect (26,29) and xor3.a3
connect (26,31) and xor3.b3
connect (26,33) and xor3.a4
connect (26,35) and xor3.b4

; condense 16 bits into 8 bits
connect (26,5) and xor6.a1
connect (26,7) and xor6.b1
connect (26,9) and xor6.a2
```

```
connect (26,11) and xor6.b2
connect (26,13) and xor6.a3
connect (26,15) and xor6.b3
connect (26,17) and xor6.a4
connect (26,19) and xor6.b4
connect (26,21) and xor7.a1
connect (26,23) and xor7.b1
connect (26,25) and xor7.a2
connect (26,27) and xor7.b2
connect (26,29) and xor7.a3
connect (26,31) and xor7.b3
connect (26,33) and xor7.a4
connect (26,35) and xor7.b4


; condense 8 bits into 4 bits
connect xor2.y1 and xor1.a1
connect xor2.y2 and xor1.b1
connect xor2.y3 and xor1.a2
connect xor2.y4 and xor1.b2
connect xor3.y1 and xor1.a3
connect xor3.y2 and xor1.b3
connect xor3.y3 and xor1.a4
connect xor3.y4 and xor1.b4

; condense 8 bits into 4 bits
connect xor6.y1 and xor5.a1
connect xor6.y2 and xor5.b1
connect xor6.y3 and xor5.a2
connect xor6.y4 and xor5.b2
connect xor7.y1 and xor5.a3
connect xor7.y2 and xor5.b3
connect xor7.y3 and xor5.a4
connect xor7.y4 and xor5.b4

; condense 4 bits into 2 bits
connect xor1.y1 and xor0.a1
connect xor1.y2 and xor0.b1
connect xor1.y3 and xor0.a2
connect xor1.y4 and xor0.b2

; condense 4 bits into 2 bits
connect xor5.y1 and xor4.a1
connect xor5.y2 and xor4.b1
connect xor5.y3 and xor4.a2
connect xor5.y4 and xor4.b2

; condense 2 bits into 1 bit
connect xor0.y1 and xor0.a3
connect xor0.y2 and xor0.b3

; condense 2 bits into 1 bit
connect xor4.y1 and xor4.a3
connect xor4.y2 and xor4.b3
```

```
; connect the output (parity) bit
priority 3 connect xor0.y3 and (3,11)

; connect the output (parity) bit
priority 4 connect xor4.y3 and (3,11)
```

End of Figure 8.8.1 Netlist listing

9.0 Conclusions

The experiments conducted were performed to gain a better understanding of how genetic algorithms could be applied to solving large search space problems. What I intend to do in this chapter is to draw conclusions from the experiments as well as propose follow-on investigations.

9.1 Conclusions and Remarks for the Nearest Neighbor routing Algorithm CPT 6

This first attempt to solve the major investigation of this thesis, PWB routing, was only mildly successful. My solution technique was to make all of the traces being routed active at all times. I believe that my implementation did not attempt to correlate between the traces properly, and, therefore, I introduced too much internal competition for board cells. In my opinion the algorithm did not properly search the solution space; the algorithm exploited it rather than exploring it.

If the reader refers back to Chapter 5, where I present the fundamental genetic operators utilized for my subsequent experiments, he will find that I did attempt to utilize schema characteristics of the problem. For example, if the reader refers back to Section 4.4 where mutation is presented, I restrict the type of mutation performed on population entries. This is to reduce the number of invalid entries created during evolution. I make the decisions based upon a priori knowledge of the problem and my solution representation.

The algorithm also attempts to use a statistical characterization function to determine how the evolving population is progressing. Information from the character function is utilized by the genetic operators at every evolution cycle.

This is similar to realtime feedback control systems, where the current state of the operation is monitored and utilized to direct the next operation.

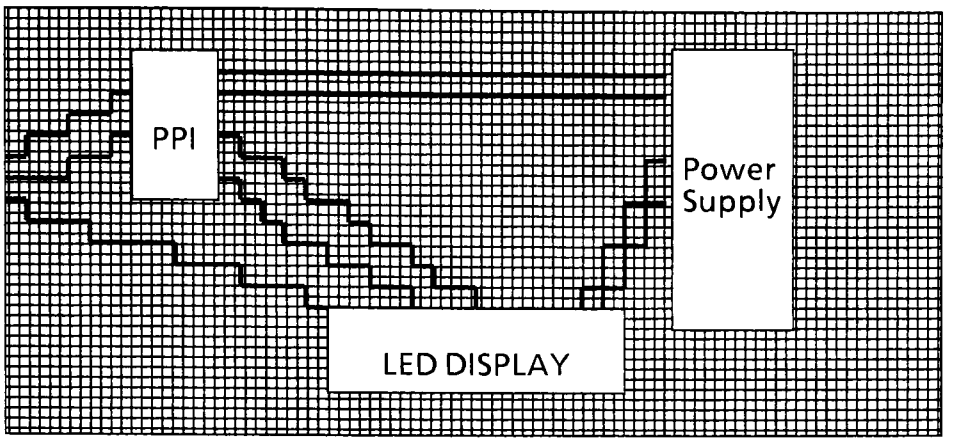
Even though the algorithm did produce solutions for the cases tested, it did not perform very well over all in attempting to generate a solution.

9.2 Conclusions and Remarks for the ratnest Algorithm CPT 7

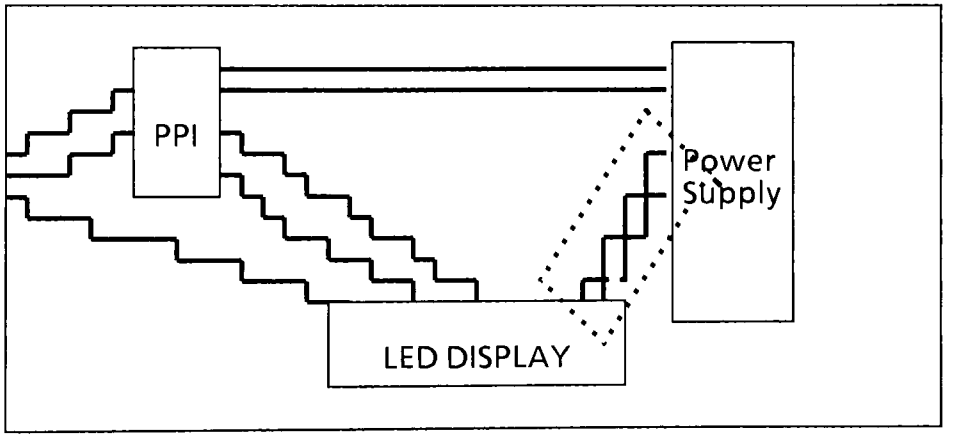
This solution algorithm was not successful at all. It almost never reached an acceptable solution set for the netlists that were presented to it. The algorithm presented in Chapter 6 worked better than this one.

The core concept of this algorithm is that all of the trace paths to be routed were connected, then quantized and used as the initial core population. This is the complete opposite approach to the earlier solution algorithm where traces were started at length 0 and grown to find their destination. the Ratnest algorithm started with traces fully connected and tried to massage them until they met a set of validation criteria.

The primary reason for failure of this algorithm was the fact that the traces started out as fully connected paths. This restricted the the areas of the PWB that the algorithm would search in order to find a solution. Figure 9.4.1 is a sample initial rat nest that would be fed into the algorithm. Figure 9.4.2, the dashed box, indicates the primary areas that the algorithm would search in order to find a solution for the set of trace paths shown . The algorithm would search other areas of the PWB but the other areas would be explored very infrequently, hence poor search space exploration and poor algorithm performance.



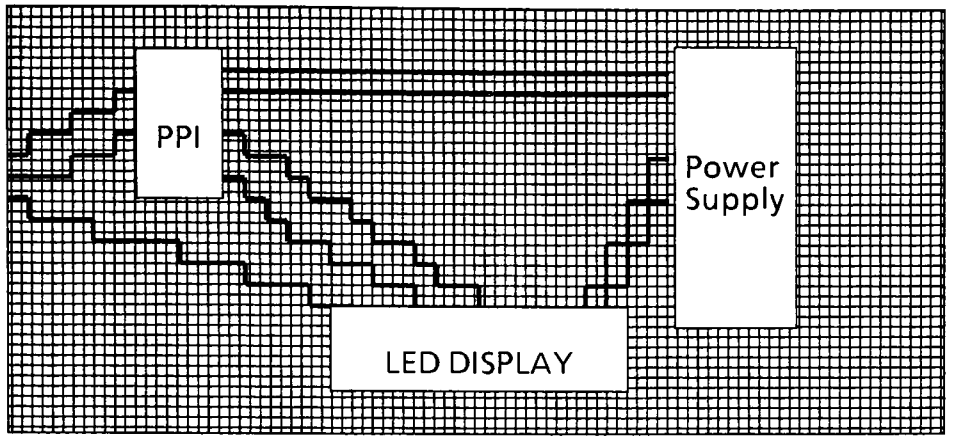
Conditioned ratnest for simple circuit
Figure 9.2.1



Conditioned ratnest for simple circuit
Figure 9.2.2

9.3 Conclusions and Remarks for the Optimum Neighbor Algorithm CPT 8

Of the three routing algorithms tested, this algorithm yielded the best results. The basic concept of this algorithm is that it starts each trace off at length zero



Conditioned ratnest for simple circuit
Figure 9.2.1

and grows the trace towards its destination. An enhancement to this algorithm was to allow the user to enter a priority level and a group tag to each of the traces entered into the netlist. The user would manually enter the traces into the ratnest and give them a cluster number and a priority number. The priority number is used to sort the list and determine which traces will be routed first. The cluster number allows the user to identify groups of traces that should be routed together (analogous to bus routings, ...).

Along with the trace grouping I modified the algorithm such that only one or a very few traces are being routed by the algorithm at any one time. This enabled the algorithm to focus more of its evaluations upon finding a routing path for fewer traces at any given time. The empirical results are that the algorithm performs more efficiently than the prior two. I make this statement based upon the fact that the trace lengths are generally not much longer that a linear trace path between the two trace end points.

9.4 Points of interest beyond these experiments

There are many extrapolations that are of interest beyond the scope of this thesis. For example: back in Section 9.4 it would be interesting to modify the algorithm to better explore other areas of the PWB rather than those near the ratnest traces cells. Such an adjustment might make the algorithm successful and produce efficient solutions.

Another area of exploration might be to introduce the concept of back tracking, as in PROLOG, into all of the algorithms investigated. The ability to back track might prove beneficial. The thought here is that as cells are freed up due to traces being removed from the evolving population, some of the currently evolving traces might either find better, more efficient routing paths, or we might even see a higher trace completion ratio.

Another experiment that would be of interest would be to increase the number of traces allowed active for the optimum nearest neighbor algorithm of Chapter 8. By increasing the active trace count, one could possibly determine when the efficiency peaks, relative to the algorithm's ability to coordinate inter-trace / cell relationships.

Another twist on the above investigation would be to vary the mix of traces that are allowed to be active during the evolution process. What I mean here is that one could investigate if better solutions of more efficient algorithms are found when one allows traces of only one blood line to be active, if one allows only traces from a cluster group to be active, or if one allows an arbitrary mixture of traces to be made active at any give evolution cycle. My thought here are that one might find the algorithm is able to handle many traces simultaneously as long as they

are competing for different areas of the PWB, or if they are all of the same group number.

9.5 Overall conclusions

I conclude that the overall experiment was a success. I base this statement on the fact that the final algorithm developed (Modified Nearest Neighbor) yielded fairly optimal PWB routing solutions when comparing the linear distance of each trace versus the number of board cells required to route the trace. Another perspective by which I judged the algorithm to be successful is that in most of the cases tested, the algorithm routed all of the traces; it was only in the last (most complex) test case that the algorithm failed to route 4 out of the total 57 traces to be routed.

For the design of this experiment I went back to the basic problem statement, that being the requirement to route mildly complex PWB circuits. In reviewing the problem characteristics I found:

1) the problem has no one single solution
2) some solutions are more optimal than others
3) Optimality is primarily judged by the trace lengths and Jogs / trace

I decided to design a solution based on genetic algorithm fundamentals. The first challenge of the solution algorithm was how to represent the problem. I decided not to take the classical genetic algorithm approach where each population entry represented one entire solution. I adapted the classic genetic representation such that the population represented one PWB solution board and that individual population entries represented each of the PWB traces to be routed.

I selected this representation in order to reduce the overhead of having multiple replicated boards that the algorithm would be required to manage. My representation greatly reduced the amount of data that the algorithm was required to process, hence the algorithm was able to expend extra cycles making complex evaluations on the individual population entries while evolving them towards a solution.

Another modification to the classical genetic algorithm representation was the fact that rather than having traces fully connected by illegitimate paths trying to converge to a legitimate trace path, I had the trace paths start out as only the path starting position. The algorithm would evolve each trace path (population entry) by capturing one of its nearest neighbors and progressing forward towards its end point. The ramification of this is that each trace path was primarily routing itself toward completion by pursuing local optima at each evolution cycle. There was a factor of pursuing globally optimum solutions as part of the trace routing criterion (e.g. minimize the overall trace length) but each trace's primary decision criteria were based upon local trace information.

In developing my solution algorithms I designed some modified problem representations relative to classic genetic algorithm problem representations. Finally the last major modification to my genetic solution algorithm for the modified nearest neighbor algorithm of Chapter 8 was that for most of the evolution of a solution there was only one trace active at any given time. Additionally in most cases, except were the proper mutation conditions occurred, this trace was maintained as the active trace until a routing path was found. One primary ramification of this is that the solution can now be greatly affected by the order in which the trace paths were attempted to be routed.

Now that the trace path routing order can so greatly affect the solution, I felt it important to enable the user to enter a routine priority order. I also designed into the algorithm the ability to presort the trace path to be routed by one of several mechanisms, one being general trace distance, another being if the trace is a member of a group / cluster, the third being the traces activity level within the circuit (refer back to the fuzzy cognitive machine investigation).

9.6 Applicability to larger scale problems

I believe that this solution technique will scale up reasonably to larger problems. For example, the solution algorithm lends itself to parallelism in order to accelerate the solution time. In order to parallelize the solution algorithm the implementor at a minimum needs only to manage the board space across all of the fully independent processors. This can be done easily by placing the board itself into a shared memory region. If this is done, then the problem can scale all the way up to one processor per trace to be routed. Another paradigm that can be utilized to parallelize the implementation yet hold the board space as a shared entity would be to use the AI blackboard paradigm. Each processor could write to and read from the black board which housed the PWB board. Each access would be a request as to the condition of the neighboring cells of some trace end point or the request to capture a board cell for a active trace path.

A major algorithm enhancement that should be explored if this algorithm is to be commercialized is how to couple it to a circuit simulation algorithm and a placement algorithm. Some important data items that can be learned from the simulation algorithm are the critical trace paths, those that are most active. These critical traces can be routed with a higher priority level. The coupling of the routing algorithm to a placement algorithm and enabling feed back based

upon intermediate routing results enables the algorithms to maneuver parts placement during the routing process that will minimize the number of trace crossovers, jogs, and inter board vias.

Finally the last modification to the routing algorithm would be to design it to allow for upwards of 6 to 10 board layers to be investigated rather than the 4 designed into the algorithm. By enabling additional board layers, the implementor has increased the possible solution space many orders of magnitude. This will result in more optimal trace routing paths and fewer traces not completing their routing paths for more complex PWBs. There is not just the simple matter of adding more layers to the solution algorithm. The designer also should design into the algorithm additional intelligence to route traces upon certain layers based upon precalculated criteria rather than randomly.

Finally, I believe that if a designer were to add the above functionality / intelligence to the routing algorithm they would be able to return to the Nearest Neighbor algorithm of Chapter 6 and find that it produces solution as optimal if not more optimal than that of the algorithm in Chapter 8. I conclude this based upon the additional solution space added to the solution algorithm and the increased intelligence of the routing decision criteria.

Chapter 10 Equations listed by number

Chapter 2

Equation # 1 Chapter 2 Section 2.2 Page 14
Measure of efficiency

$$EFF = \sum_{i=1}^{n} F_i(ES, CS) \quad EQN\#1$$

Chapter 2 Section 2.5 Equation # 2 Page 18
Standard Deviation for an Entire Population

$$\sigma = \left[\frac{(X-\mu)^2}{N} \right]^{-2} \quad EQN\#2$$

Chapter 2 Section 2.5 Equation # 3 Page 19
Standard Deviation for a Sub-Sample of a Population

$$s = \left[\frac{n \sum_{i=1}^{i=n} X^2 - \left(\sum_{i=1}^{i=n} X \right)^2}{n(n-1)} \right]^{-2} \quad EQN\#3$$

Chapter 2 Section 2.5 Equation # 4 Page 19
Skewness of the population

$$g_1 = \left[\frac{n^2 \sum_{i=1}^{i=N} X^3 - 3N \sum_{i=1}^{i=N} X^2 \sum_{i=1}^{i=N} X + 2\left(\sum_{i=1}^{i=N} X \right)^3}{s^3} \right] \quad EQN\#4$$

Chapter 2 Section 2.5 Equation # 5 Page 19
Kurtosis of the population

$$g_2 = \left[\frac{\left(\right)}{s^4} \right] \quad EQN\#5$$

Chapter 2 Section 2.5 Equation # 6 Page 19

Test of the means of two different populations

$$z = t_{\infty} = \frac{\overline{\overline{(X_1 - X_2) - (\mu_1 - \mu_2)}}}{\left[\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}\right]^{-2}} \quad EQN\#6$$

Chapter 2 Section 2.6 Equation # 7 Page 21

Linear function applied to matrix F

$$Y(m_1, m_2) = \sum_{n_1 = 1}^{n_1 = N_1} \sum_{n_2 = 1}^{n_2 = N_2} F(n_1, n_2)\ O(n_1, n_2; m_1, m_2) \quad .EQN\#7$$

Chapter 2 Section 2.6 Equation # 8 Page 22

Matrix Vector transform

$$\mathbf{f} = \sum_{n = 1}^{n = N_2} \mathbf{N}_n\ \mathbf{F}\ \mathbf{V}_n \quad EQN\#8$$

Chapter 2 Section 2.6 Equation # 9 Page 22

Vector Matrix transform

$$\mathbf{F} = \sum_{n = 1}^{n = N_2} (\mathbf{N}_n)^T\ \mathbf{f}\ (\mathbf{V}_n)^T \quad EQN\#9$$

Chapter 3 Section 3.2 Equation # 10 Page 38
Mean Population Size estimator function

$$MPS(BS, ETS) = \left(\frac{BS * ln(\frac{2048}{ETS}) * ln(2^{BS})}{ln(BS)^2} \right) \quad : eqn\,10$$

Chapter 3 Section 3.4 Equation # 11 Page 42
Chess Board generation equation

$$BOARD(\{\Delta\}, \{\tau\}, \{F\}) = \{ Vec(8, F) : (Vec(8, F) \cap \tau)\ ' * (\Delta \in Vec(8, F)) \} \quad : eqn\,11$$

Chapter 3 Section 3.4 Equation # 12 Page 42
Individual chess board vector generation function

$$Vec(N, F) = \bigcup_{i=0}^{i=N-1} F[Rand(seed) * Rank(F)] : eqn\,12$$

Chapter 3 Section 3.4 Equation # 13 Page 43
Chess board population matrix function

$$\left\{ \{POP\} : \left[\bigcup_{m=1}^{m=MPS()} BOARD() \right] \bigcup \left[\bigcup_{m=1}^{m=\phi} Vec() \right] \right\} \quad : eqn\,13$$

Chapter 3 Section 3.5 Equation # 14 Page 44
Chess board replication function

$$REP() = \frac{NQC(POPE)^{ln(SQRT(BS))}}{3} \quad : eqn\,14$$

Chapter 3 Section 3.9 Equation # 15 Page 47
Number of parents to add back to evolving population

$$NPTA() = \frac{MPS()}{ln(BS)^2} + \frac{Rand(BS)}{10} Rand(BS) * 2 * ln(BS)^2 - DPPU \quad : eqn\,15$$

Chapter 3 Section 3.10 Equation # 16 Page 49
Resample population size function

$$RPS() = MPS() + \quad : eqn\ 16$$

Chapter 3 Section 3.12 Equation # 17 Page 51
Average utility function

$$AUF() = \frac{\sum_{i=1}^{i=N} NQC(POP_i)}{N} \quad : eqn\ 17$$

Chapter 4 Section 4.7 Equation # 18 Page 68

Replication Operator:

$$\left\{\{Replicated\ Population\}_a\right\} = \sum_{m=POPE_1}^{m=POPE_n} Replicate(POPE_m) \quad EQN\,18$$

Chapter 4 Section 4.7 Equation # 19 Page 69

Crossover Operator:

$$\left\{\{Crossover\ Population\}_b\right\} = \sum_{m=1}^{m=Number\_to\_cross(POPE_n)} Crossover(\{Replicated\ Population\}_a)\ eqn\,19$$

Chapter 4 Section 4.7 Equation # 20 Page 71

Entire possible search space

$$Population\ Set\{Z\} = \{A\} \cup \{B\} \cup \{C\} \cup \{D\} \quad EQN\,20$$

Chapter 4 Section 4.7 Equation # 21 Page 71

Population set of entire possible search space

$$Population\ Set\{Z\} = \{A\} \cup \{B\} \cup \{C\} \cup \{D\} = Unfiltered\ Algorithm\ Search\ Space \quad EQN\,21$$

Chapter 4 Section 4.7 Equation # 22 Page 71

Filtered search space for population evaluation

$$Filtered\ Algorith\ Search\ Space\ \{F\} = \{Z\} \cap \{\overline{D}\} \quad EQN\,22$$

Chapter 4 Section 4.7 Equation # 23 Page 72

Mutation Operator:

$$\left\{\{Mutated\ Population\}_c\right\} = \sum_{m=POPE_1}^{m=\{POPE_n\}b} Mutate(POPE_m) \quad EQN\,23$$

Chapter 4 Section 4.7 Equation # 24 Page 72

Resample Operator:

$$\left\{\{Resampled\ Population\}_d\right\} = \sum_{m=POPE_1}^{m=POPE_n} Resample(\{POPE_m\}_c) \quad EQN\,24$$

Chapter 4 Section 4.7 Equation # 25 Page 74

Shuffle Operator:

$$\left\{\{Shuffeled\ Population\}\right\} = \sum_{m=POPE_1}^{m=N} Shuffel(\{POPE_m\}) \quad EQN\,25$$

Chapter 5 Section 5.1 Equation # 26 Page 94
Annealing Temperature

$$Anneal\,Temp = \frac{Average\,Estimated\,Remaining\,Trace\,Distance}{Average\,Population\,Utility} \quad EQN\,26$$

Chapter 5 Section 5.2 Equation # 27 Page 95
Routing algorithm utility function

$$U_i = \sum_{m=1}^{m=i} A_i * F_m(X_m) \quad EQN\,27$$

Chapter 5 Section 5.3 Equation # 28 Page 96
Routing algorithm replication function

$$REP() = \frac{\left(UTIL(POPE)^{ln(SQRT(BS))} \right)^{-2}}{ln(BS)} \quad : eqn\,28$$

Chapter 5 Section 5.4 Equation # 29 Page 97
The MPSA() function is defined as (Mean Population Size):

$$MPSA(\{\alpha\},\{\beta\},\{\zeta\}) = \left(\sum_{m=1}^{m=RANK(\alpha)} \beta_m \times \alpha_m + (Rand(1.0) \times \alpha_m \right) \quad : eqn\,29$$

Chapter 5 Section 5.4 Equation # 30 Page 97
Beta Multiplication factor for Mean Population Size Algorithm

$$\beta_m = \frac{1}{ln(\alpha_n)} \quad EQN\,30$$

Chapter 5 Section 5.4 Equation # 31 Page 98
The MPSB() function is defined as:

$$MPSB(BS, ETS) = \left(\frac{BS * ln(\frac{2048}{ETS}) * ln(2^{BS})}{ln(BS)^2} \right) \quad : eqn\,31$$

Chapter 5 Section 5.4 Equation # 32 Page 98
Mean Population Size function

$$MPS(MPSA(), MPSB()) = \left(\frac{MPSA() + MPSB()}{2} \right) \quad : eqn\,32$$

Chapter 5 Section 5.5 Equation # 33 Page 98
Core population replication factor

$$\sum_{i=1}^{i=CPS} \left[\overline{RVEC(i)} = REP(POPE_i) \right] \quad EQN\,33$$

Chapter 5 Section 5.5 Equation # 34 Page 99
Total Replication count

$$RTOT = \sum_{i=1}^{i=CPS} \overline{RVEC(i)} \quad EQN\,34$$

Chapter 5 Section 5.5 Equation # 35 Page 99
Replication scale factor

$$RSF = \frac{MPS}{RTOT} \quad EQN\,35$$

Chapter 5 Section 5.5 Equation # 36 Page 100
Core Populatin generation function

$$INIT\_POP = \bigcup_{i=1}^{i=CPS} \left[\bigcup_{j=1}^{j=RVEC(i)} COREPOP(i) \right] \quad EQN\,36$$

Chapter 5 Section 5.8 Equation # 37 Page 104
Neighbor identification function

$$Neighbors(X, Y) = \sum_{m=X-1}^{m=X+1} \sum_{n=Y-1}^{n=Y+1} Coordinate(M, N) \therefore m \neq x \,\&\, n \neq y \quad EQN\,37$$

Appendix of Miscellaneous Figures

Data comparison of hybrid mutaion function
Vs standard mutation function
Figure 3.3.3B

Sample set Number	Standard Mutation Number of Queens Correct	hybrid Mutation Number of Queens Correct
1	80	80
2	120	200
3	120	160
4	200	200
5	160	200
6	200	240
7	200	280
8	240	280
9	160	320
10	200	360
11	280	360
12	200	360
13	240	320
14	320	480
15	320	480

Data comparison of hybrid mutaion function
Vs standard mutation function
Figure 3.3.3B

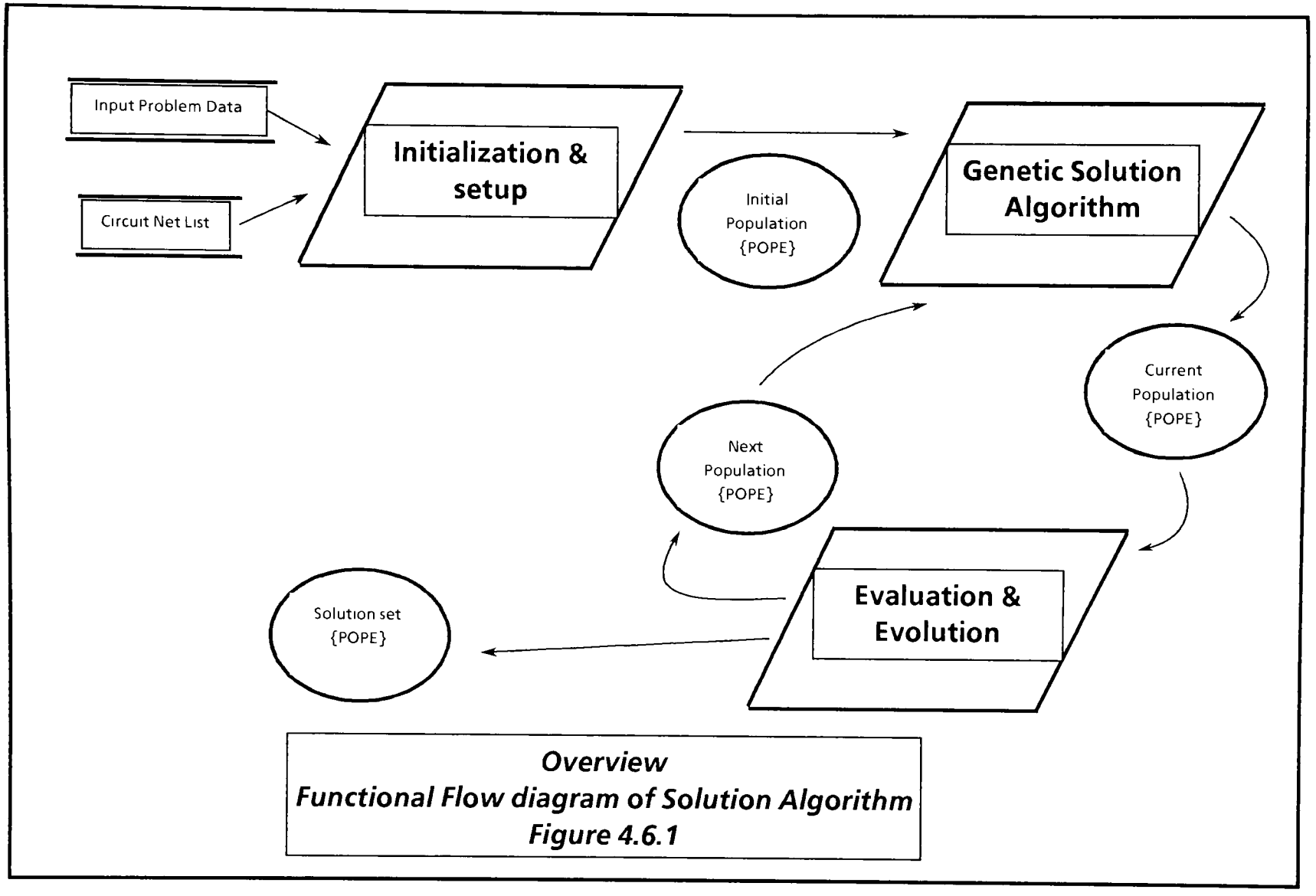
Sample set Number	Standard Mutation Number of Queens Correct	hybrid Mutation Number of Queens Correct
16	240	480
17	360	480
18	360	480
19	440	480
20	400	480
21	400	480
22	440	480
23	480	480

Comparison of hybrid corssover Vs standard crossover Re: Average Number of queens correct Total = 12
Figure 3.3.4B

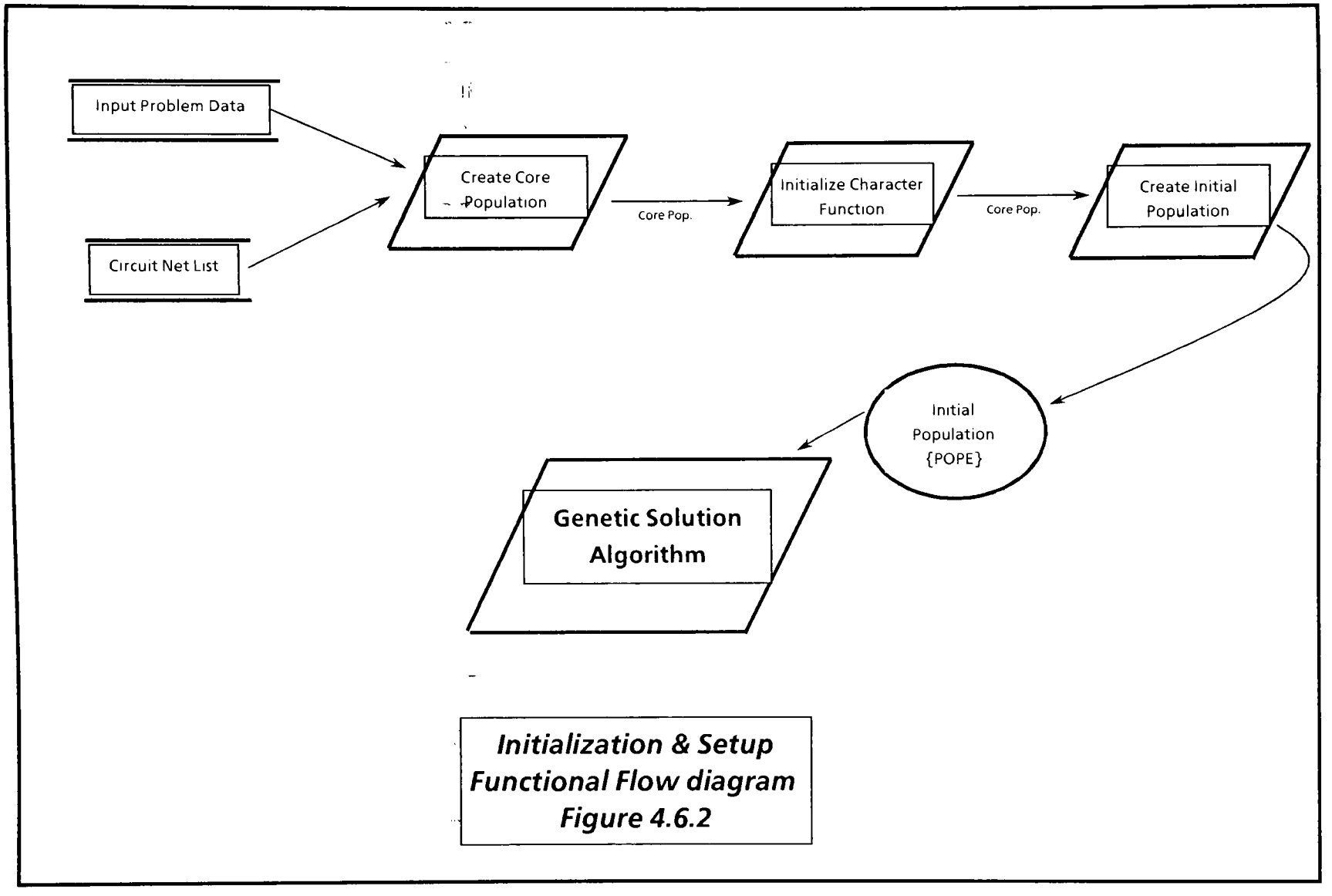
Generation Number	Standard Crossover Number of Queens Correct	Hybrid Crossover Number of Queens Correct
1	2	2
2	3	5
3	3	4
4	5	5
5	4	5
6	5	6
7	5	7
8	6	7
9	4	8
10	5	9
11	7	9
12	5	9
13	6	8
14	8	12
15	8	12
16	6	12
17	9	12
18	9	12
19	11	12
20	10	12
21	10	12

Comparison of hybrid corssover Vs standard crossover Re: Average Number of queens correct Total = 12
Figure 3.3.4B

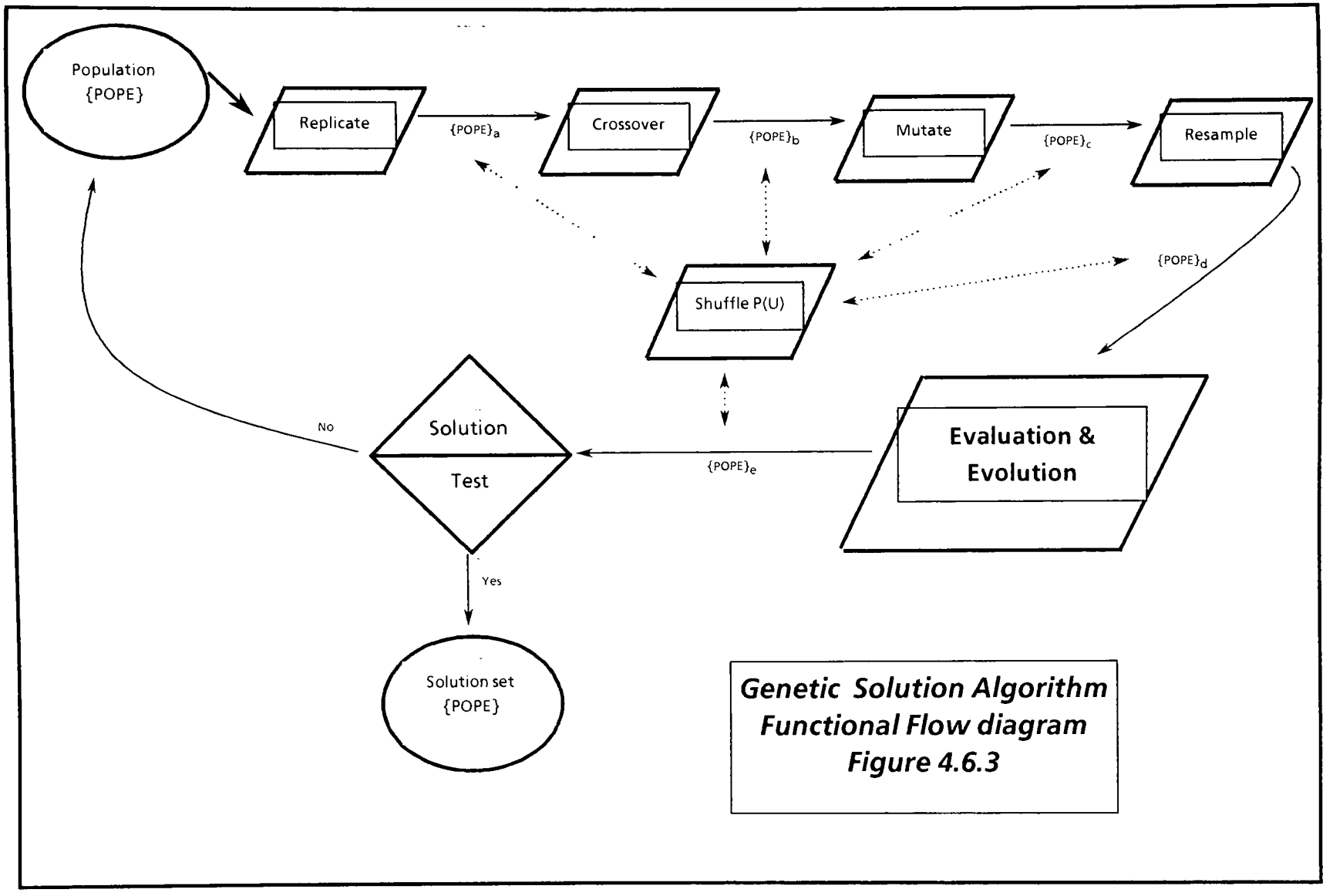
Generation Number	Standard Crossover Number of Queens Correct	Hybrid Crossover Number of Queens Correct
22	11	12
23	12	12



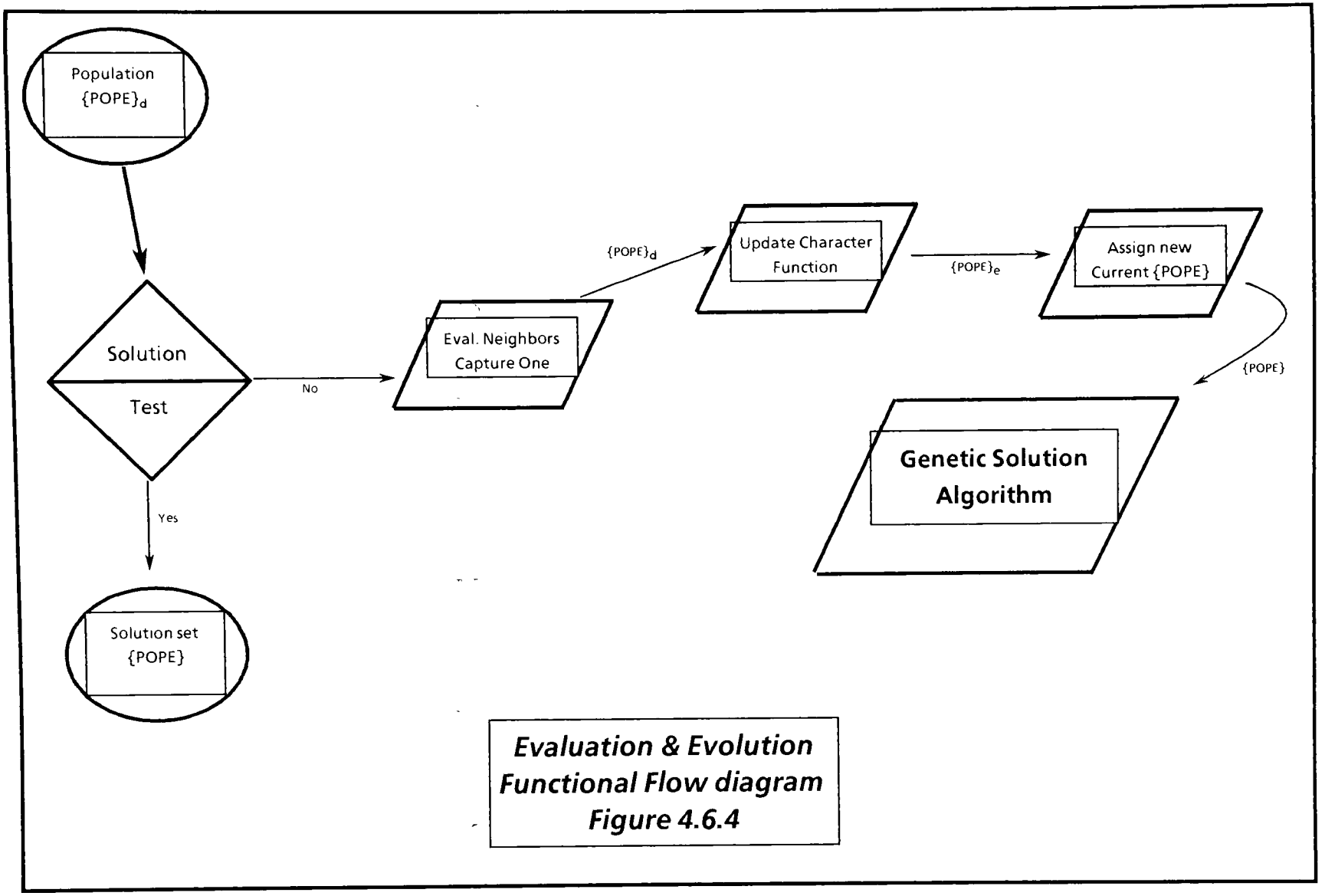
Overview
Functional Flow diagram of Solution Algorithm
Figure 4.6.1



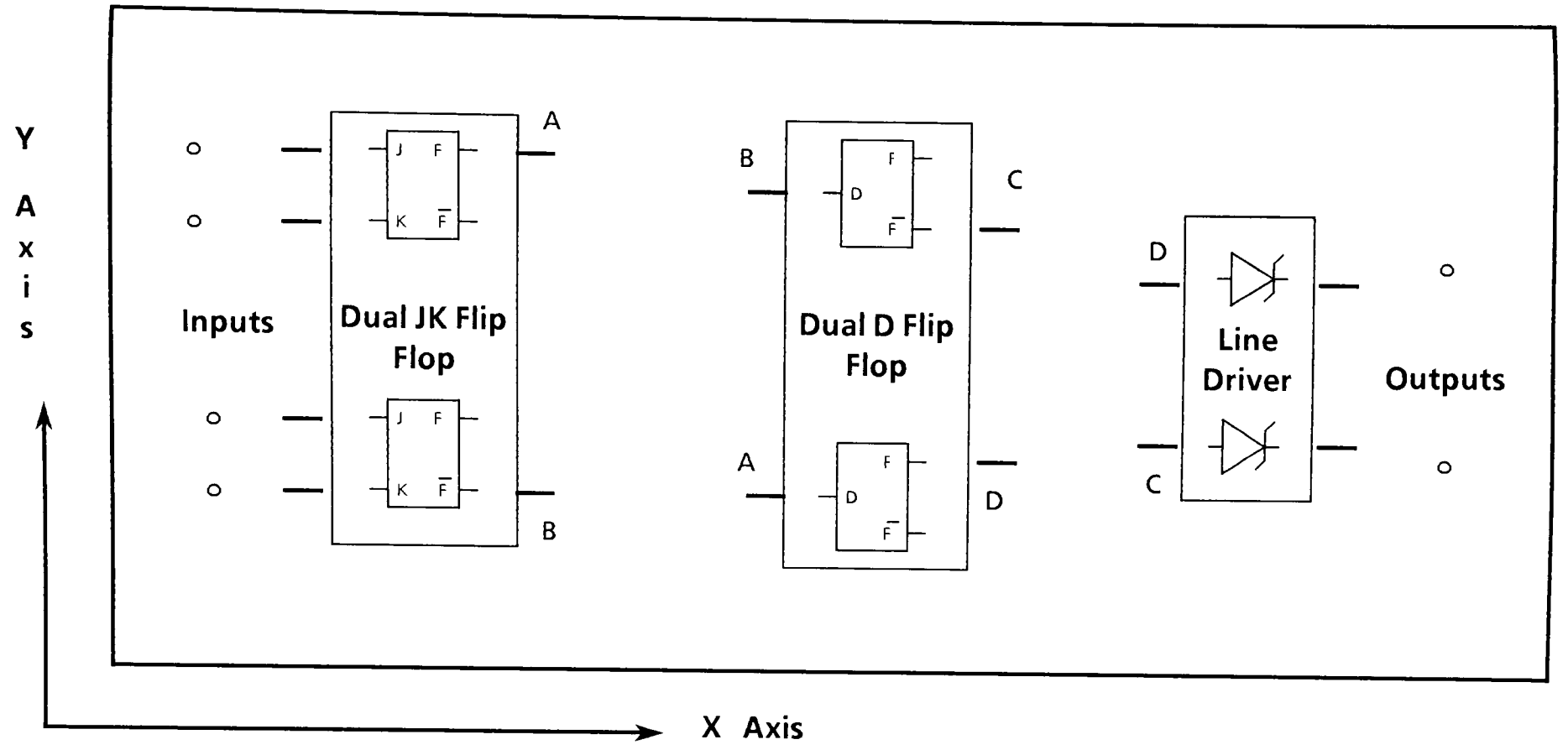
Initialization & Setup Functional Flow diagram Figure 4.6.2



Genetic Solution Algorithm
Functional Flow diagram
Figure 4.6.3



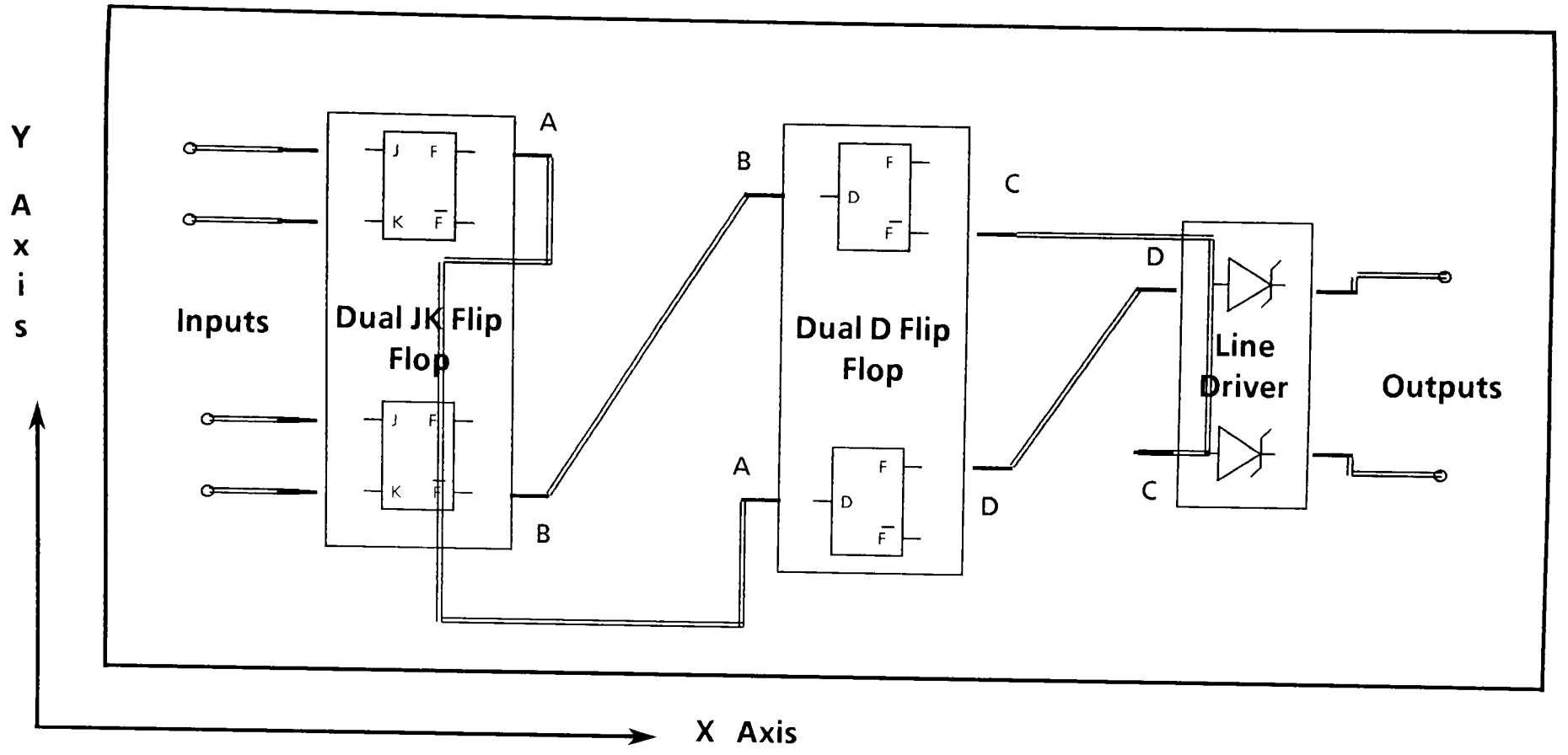
Evaluation & Evolution
Functional Flow diagram
Figure 4.6.4



M x N cell PWB board

Board layout for a sample circuit

Figure 4.1.B



M x N cell PWB board

Board layout for a sample circuit

Figure 4.1.C

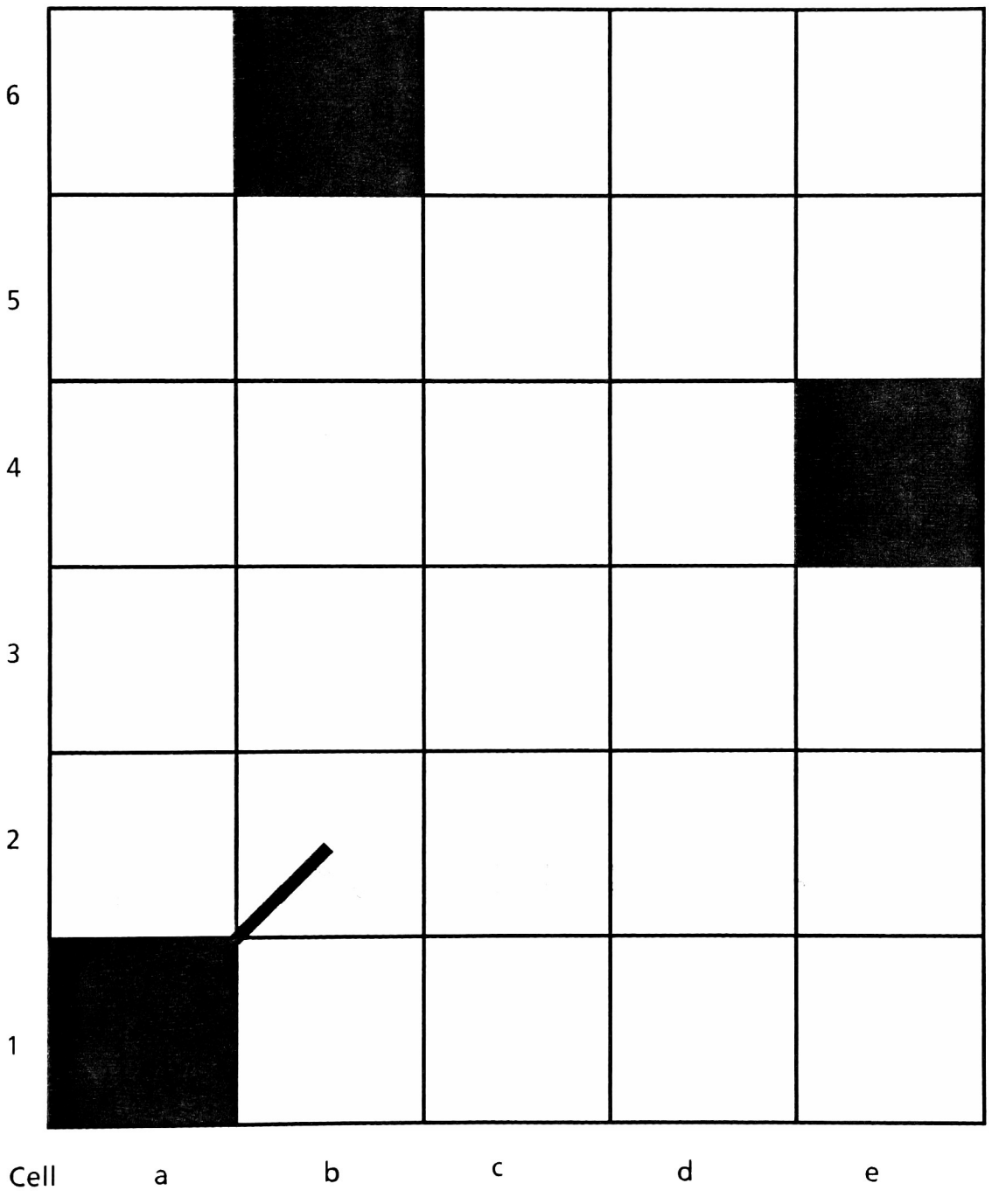


Figure 4.9.6
We have added the Schema block G

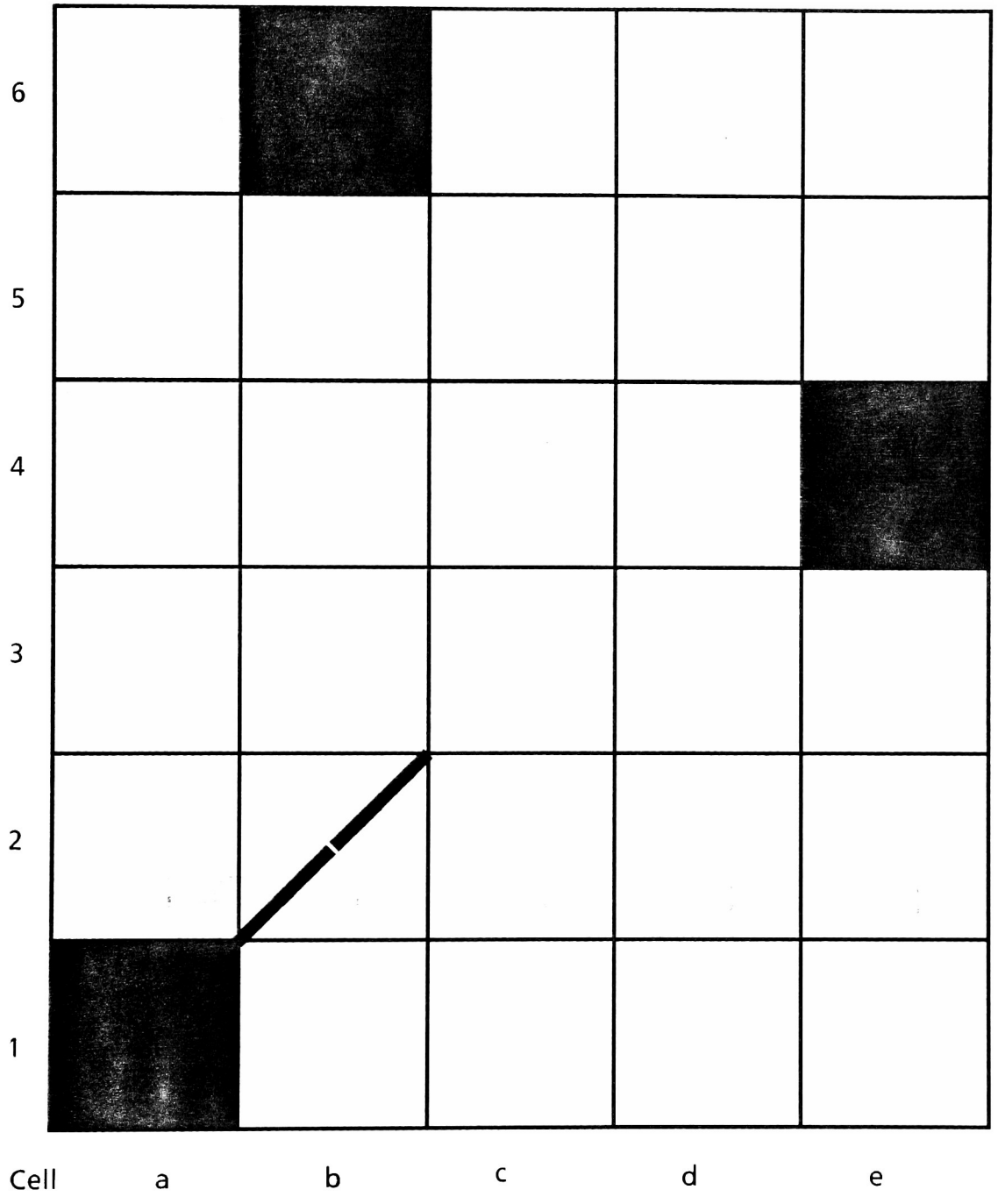


Figure 4.9.7
We have added the Schema block B

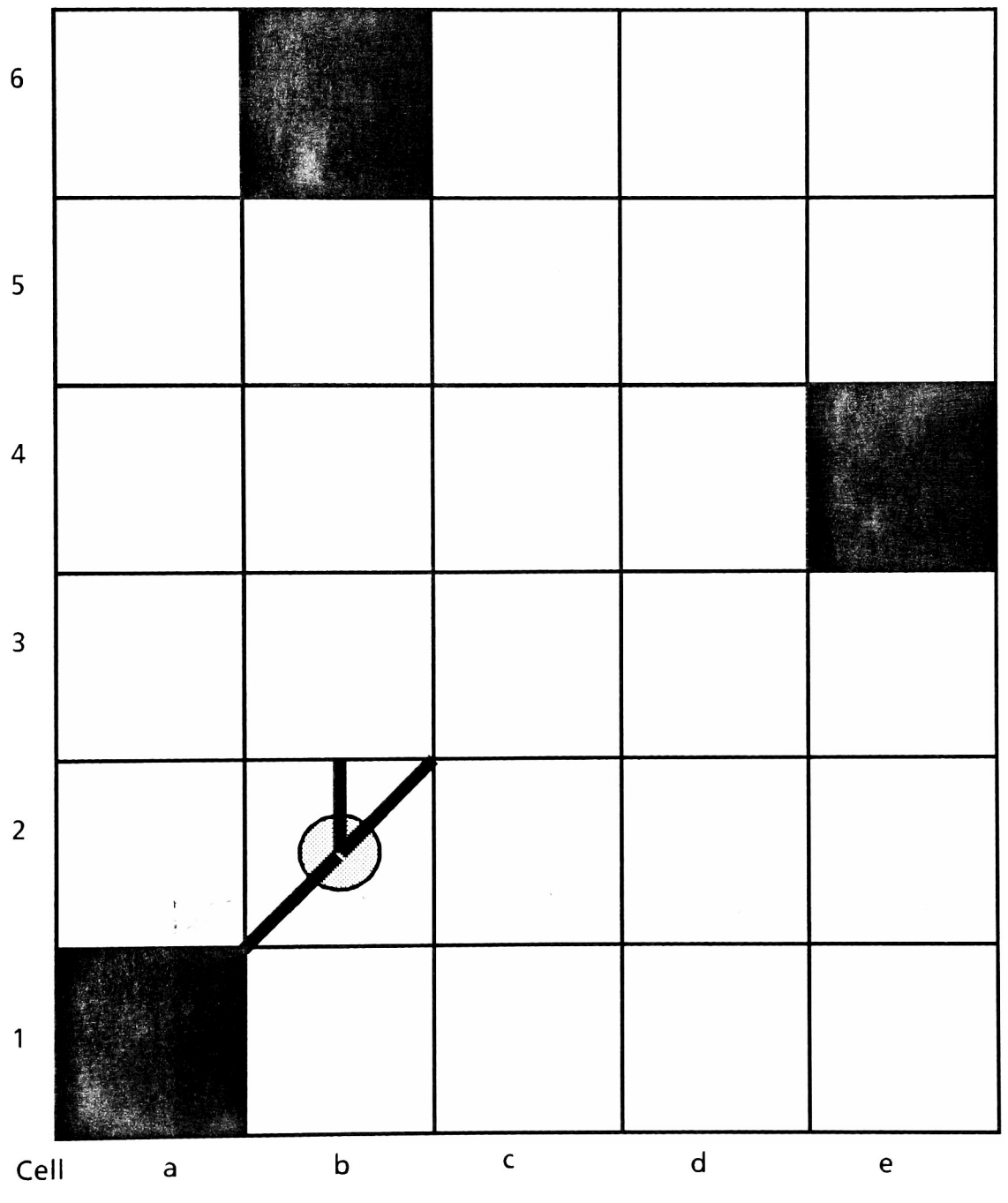


Figure 4.9.8
We have added the Schema block A
This is one complete block construction

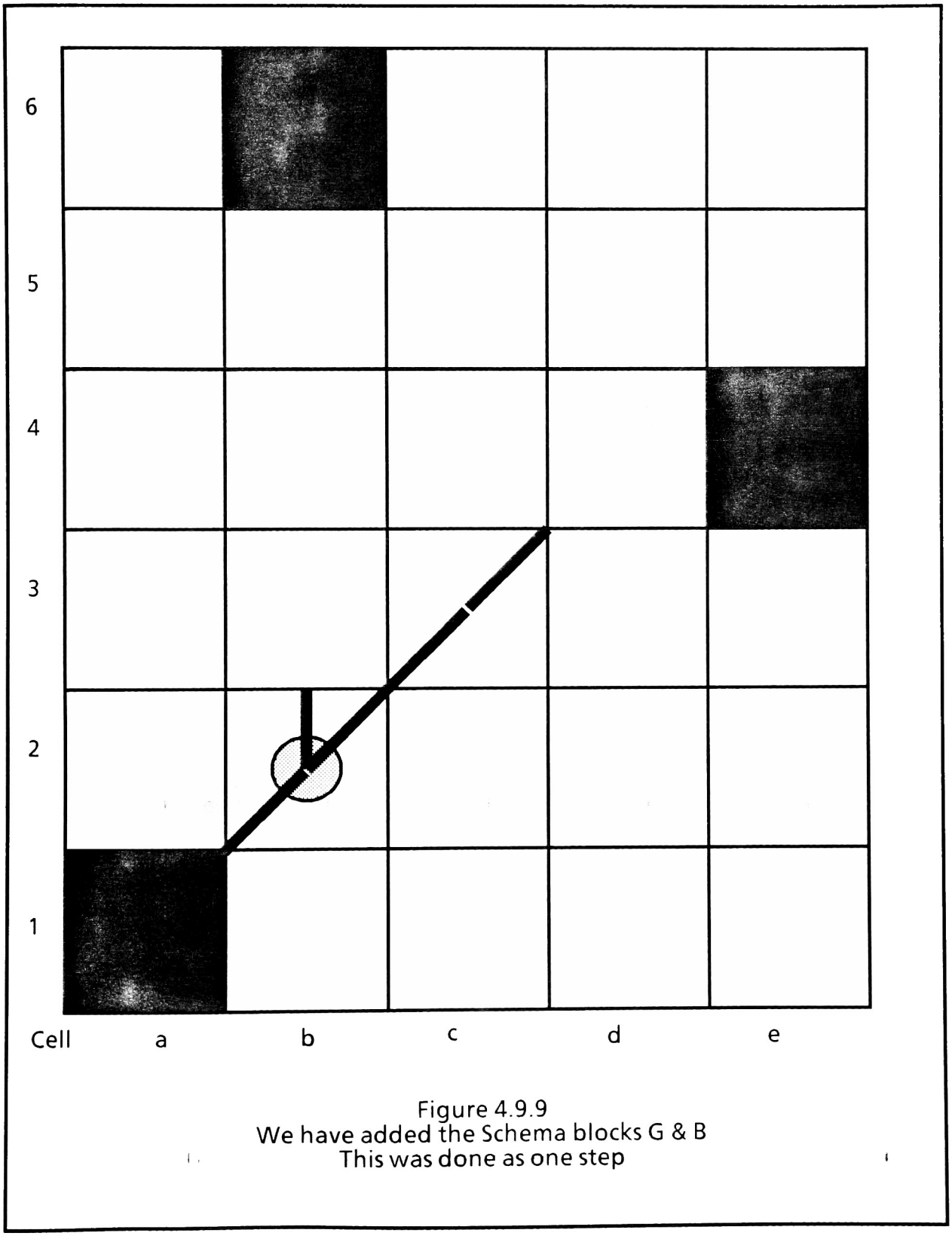


Figure 4.9.9
We have added the Schema blocks G & B
This was done as one step

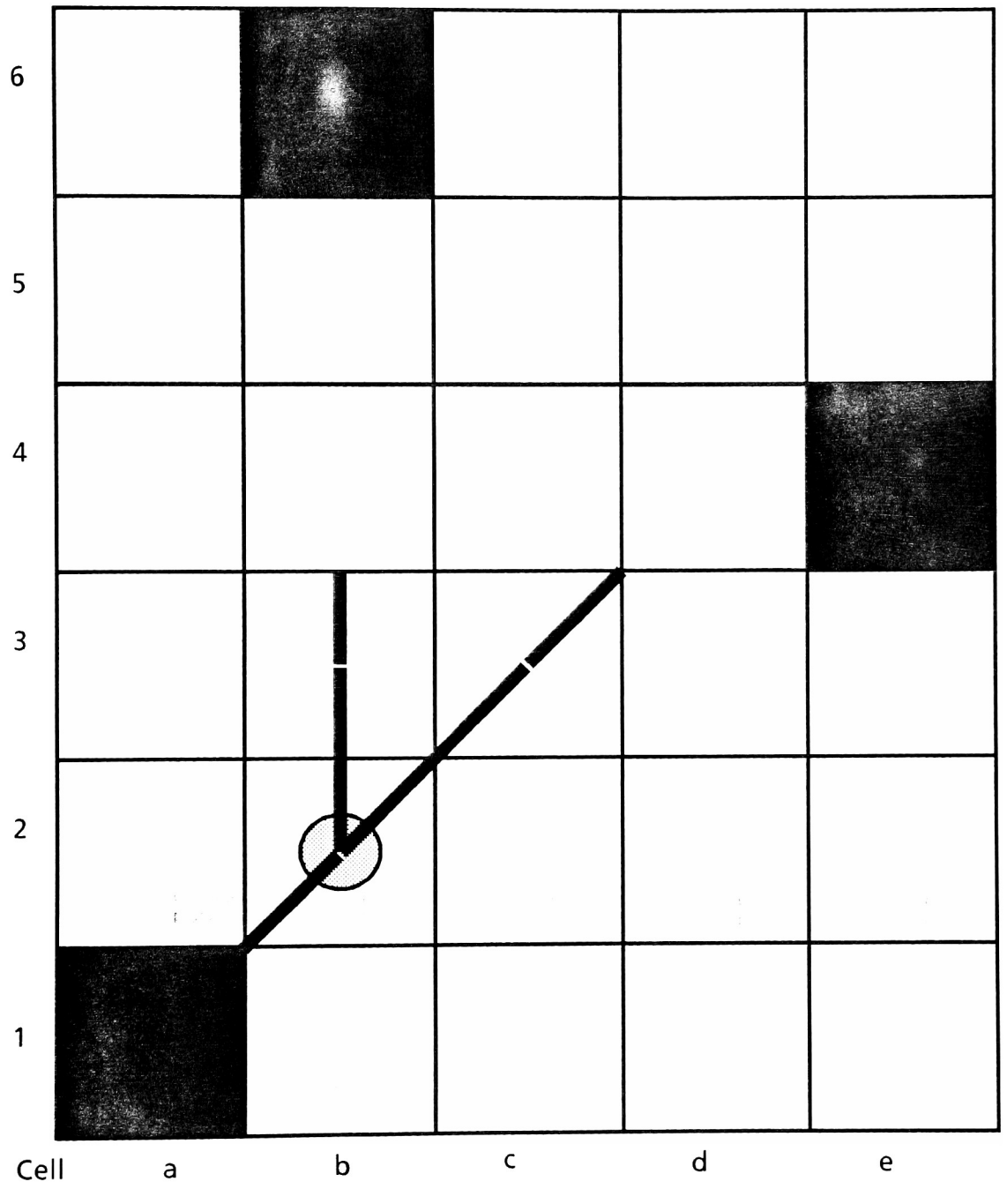


Figure 4.9.10
We have added the Schema blocks A & C
This was done as one step

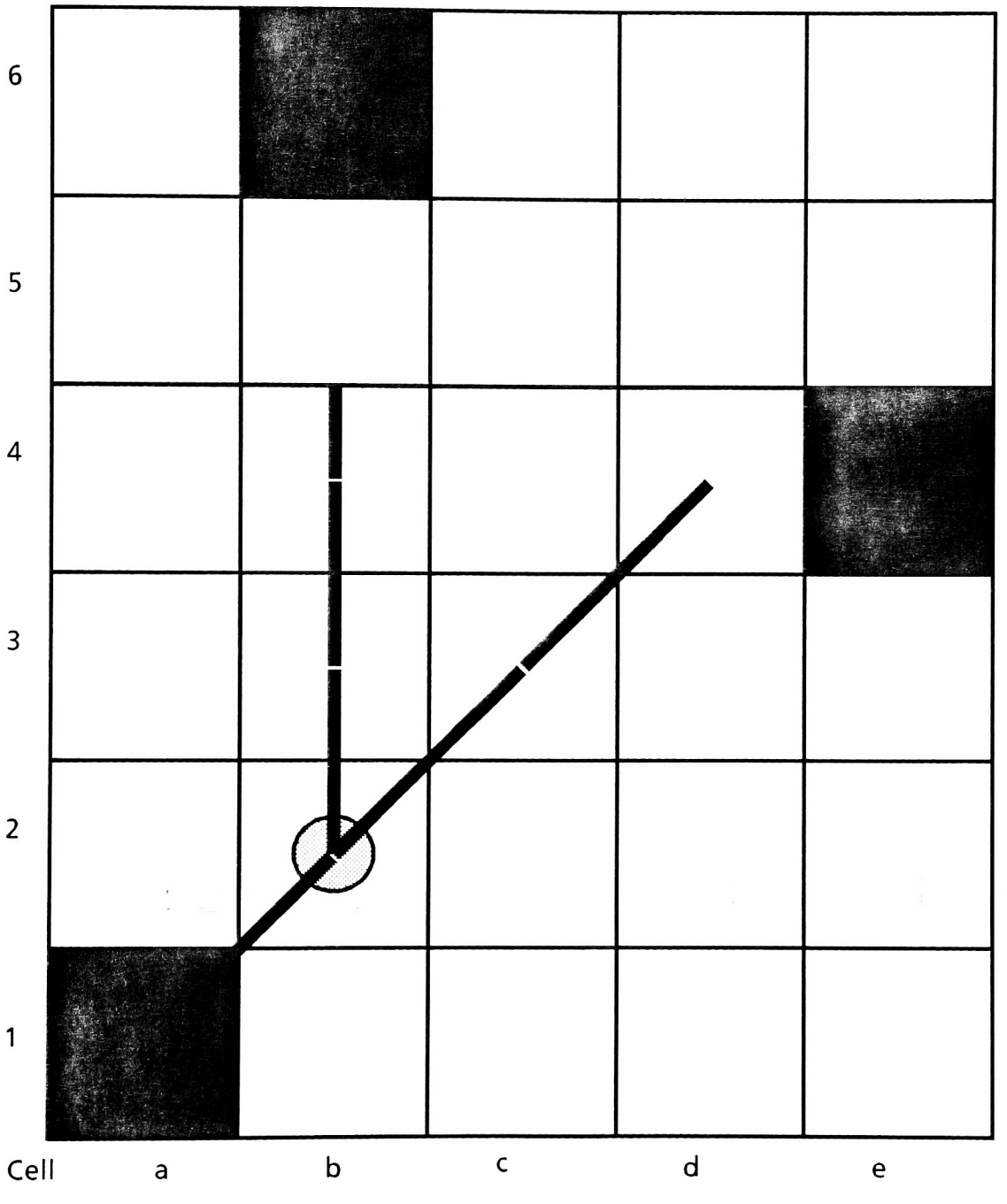


Figure 4.9.11
We have added the Schema blocks A & C
And also G to advance both traces
This was done as two steps (two trace paths)

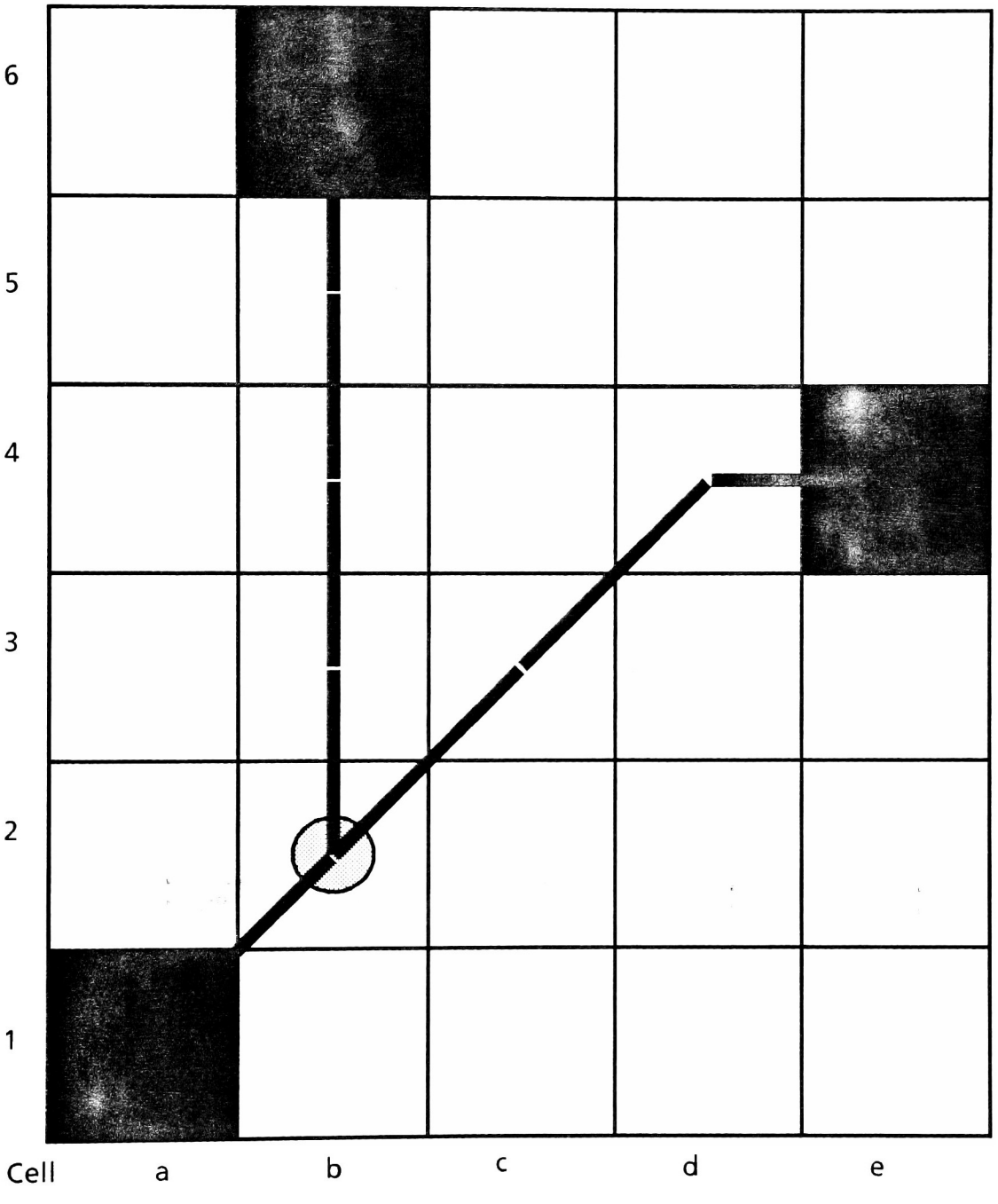


Figure 4.9.12

We have added the Schema blocks A & C And also G to advance both traces. This was done as two steps (two trace paths). The result is that we have connected all three blocks.

Table 6.3 Optimum Neighbor Solution Data

Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
10	2.3	-0.4	-0.9	0
20	2.5	-0.4	-0.8	0
30	1.8	-0.2	-0.5	0
40	3.6	-0.1	0.2	0
50	2.5	0.2	0.5	0
60	4.6	0.3	0.1	0
70	4.2	0.3	0.2	0
80	5.1	0.6	-0.3	0
90	6.3	-0.4	0.2	0
100	5.8	-0.2	0.8	2.5
110	6.2	0.1	0.4	12.8
120	6.7	0.3	-0.3	15.3
130	7.4	0.7	-0.8	25.6
140	10.5	0.5	0.2	46.1
150	11.7	0.2	0.3	46.1
160	11.9	-0.4	-0.8	58.9
170	13.8	0.3	0.5	58.9
180	14.3	0.6	-0.8	61.5
190	15.7	0.3	0.1	69.2
200	12.3	0.1	0.2	74.3
210	15.9	-0.1	0.2	82.
220	16.3	0.7	-0.8	82.
230	17.7	0.5	-0.1	87 1
240	17.3	-0.1	0.2	94.8
250	18.5	0.8	0.2	94.8

Table 6.3 Optimum Neighbor Solution Data

Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
258	20.8	0.9	0.6	100.0

Table 6.4 Algorithm Results Data with Growth Modification

Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
10	2.2	0.2	0.5	0
20	2.6	0.2	0.2	0
30	3.2	-0.6	0.6	0
40	3.9	-0.5	0.8	0
50	4.1	-0.2	0.5	2.5
60	4.5	0.9	-0.4	7.6
70	5.2	0.5	-0.3	10.2
80	7.6	0.7	-0.4	17.9
90	9.1	-0.3	0.5	17.9
100	8.7	0.6	-0.5	25.6
110	10.3	0.1	0.9	28.2
120	14.5	0.3	-0.1	38.4
130	15.2	0.8	0.5	46.1
140	13.6	0.5	-0.3	55.0
150	14.9	0.6	-0.1	55.0
160	15.4	-0.2	-0.2	56.4
170	14.7	-0.5	0.8	66.6
180	17.7	0.6	0.3	66.6
190	17.4	0.1	0.4	66.6
200	19.6	0.6	-0.3	84.6
210	21.1	0.2	-0.4	89.7
220	22.3	-0.4	0.6	92.3
230	21.5	0.1	0.3	97.4
234	26.3	0.0	0.1	100.0

Table 6.5 Optimum Neighbor Results Data with Reduced Shuffel Operator

Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
10	3.6	0.2	0.5	2.5
20	3.2	0.2	0.2	5.1
30	3.8	-0.6	-0.3	10.2
40	4.6	0.1	-0.2	12.8
50	4.9	-0.2	0.5	20.5
60	5.8	0.5	0.6	28.2
70	5.5	0.5	0.6	30.7
80	7.6	0.7	0.1	35.8
90	7.7	0.3	0.2	41.0
100	8.3	0.1	-0.1	43.5
110	11.2	0.1	-0.3	56.4
120	15.6	0.3	0.5	58.9
130	10.2	-0.2	0.5	61.5
140	16.9	-0.1	0.8	66.6
150	15.9	-0.6	0.7	69.2
160	14.3	-0.4	0.3	74.3
170	16.5	-0.1	-0.2	79.4
180	16.8	0.3	-0.3	82.0
190	16.4	0.5	0.4	87 1
200	18.2	0.5	-0.3	92.3
210	18.6	0.1	0.2	94.8
220	20.3	0.8	-0.3	97.4
222	25.2	0.9	-0.8	100

Table 7.2.1 RatNest Algorithm Data Test Case 1

Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
10	2.3	0.5	0.4	0
20	2.5	0.5	0.9	0
30	1.8	0.8	-0.2	0
40	3.6	-0.3	0.2	0
50	2.5	0.7	-0.8	0
60	4.6	-0.2	-0.3	0
70	4.2	0.3	-0.6	0
80	5.1	0.6	-0.3	0
90	6.3	0.6	0.5	0
100	5.8	0.8	0.3	2.5
110	6.2	0.8	-0.2	2.5
120	6.7	-0.3	0.7	2.5
130	5.9	-0.1	0.3	5.0
140	9.9	-0.9	0.2	5.0
150	3.3	-0.4	-0.3	5.0
160	7.8	0.7	0.4	10.2
170	4.0	-0.3	0.4	10.2
180	11.3	0.2	-0.1	10.2
190	8.7	0.5	-0.8	12.8
200	11.4	0.8	0.2	12.8
210	5.9	-0.3	-0.2	12.8
220	12.2	-0.6	0.5	10.2
230	8.6	0.2	0.3	12.8
240	9.3	-0.6	0.6	15.4
250	12.5	-0.6	0.1	15.4
260	5.8	-0.4	-0.4	15.4

Table 7.2.1 RatNest Algorithm Data Test Case 1

Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
270	14.8	-0.3	-0.3	20.5
280	15.1	0.2	-0.1	28.2
290	14.9	0.5	-0.1	30.7
300	16.7	0.6	0.3	30.7
310	17 4	0.7	0.2	33.3
320	16.9	0.1	-0.5	41.0
330	15.2	-0.4	0.2	43.5
340	15.9	0.1	0.5	43.5

Table 7.2.2 Ratnest Algorithm Solution Data

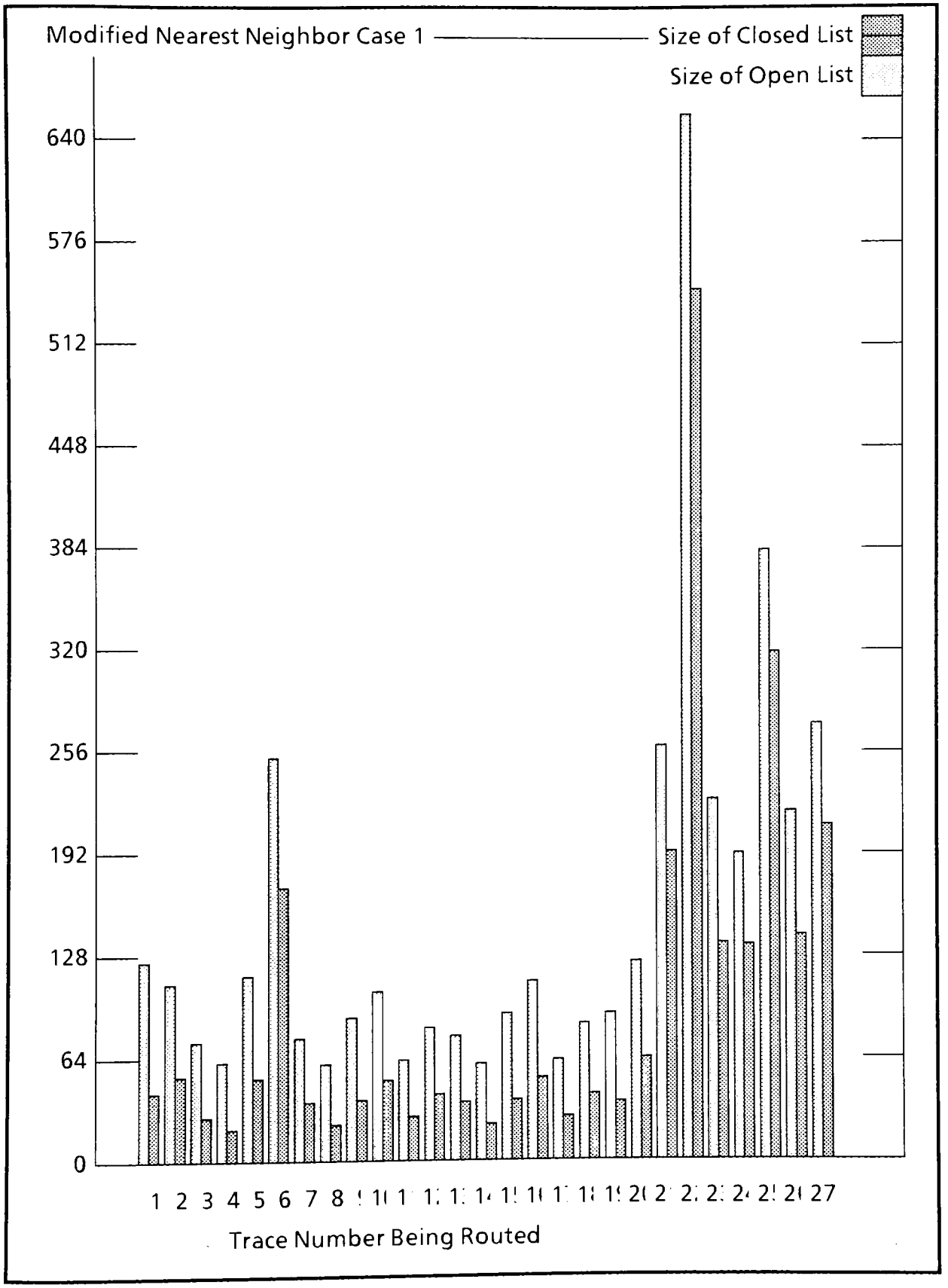
Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
10	2.9	.02	0.3	2.5
20	2.5	-0.2	0.4	2.5
30	3.0	0.3	0.4	2.5
40	3.9	.08	0.9	5.0
50	4.4	0.4	0.3	5.0
60	4.6	-0.9	0.1	8.3
70	3.3	-0.6	-0.2	10.2
80	5.9	-.02	.01	10.2
90	7.6	0.1	0.3	12.8
100	6.6	0.7	0.5	12.8
110	6.8	-.06	0.7	15.4
120	6.8	0.4	-0.7	15.4
130	7.7	-0.6	0.7	15.4
140	8.8	0.1	.01	17.6
150	10.2	-0.2	-0.8	17.6
160	6.6	-0.6	-0.2	17.6
170	12.8	-0.9	-0.5	17.6
180	9.4	0.5	-0.6	17.6
190	11.2	-0.3	-0.2	20.5
200	13.6	-0.9	-0.7	20.5
210	14.2	0.6	0.8	20.5
220	10.9	0.4	-0.9	22.4
230	12.9	-0.6	-0.4	22.4
240	15.7	0.5	0.9	26.8
250	16.4	-0.6	0.1	26.8
260	12.6	-0.4	-0.4	26.8

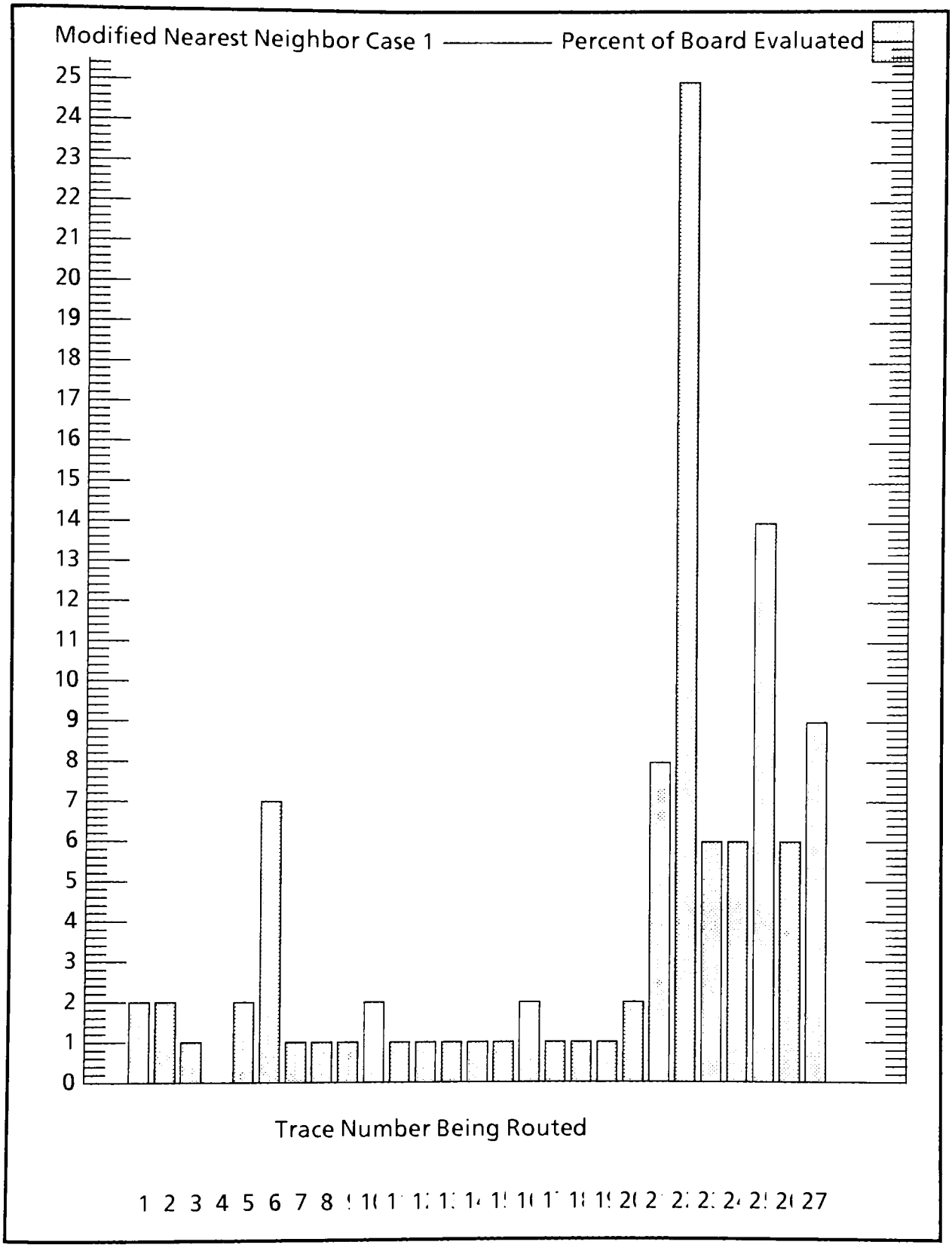
Table 7.2.2 Ratnest Algorithm Solution Data

Dependent unit: Evolutions X10	Average Population Utility	Population Skewness	Population Kurtosis	Percent of Traces Routed
270	17.6	0.6	0.7	28.2
280	14.2	0.2	-0.1	28.2
290	14.9	-0.5	-0.9	30.7
300	16.7	0.6	0.8	30.7
310	17.4	-0.1	-0.3	33.3
320	16.9	-0.1	0.1	33.3
330	15.2	-0.4	0.2	33.3
340	15.9	0.1	0.5	35.8
350	16.0	0.2	0.2	35.8
360	14.8	0.3	0.1	35.8
370	14.2	0.6	0.4	38.4
380	17.5	0.1	-0.2	38.4
390	18.8	-0.4	-0.3	41.0
400	17.4	0.2	0.6	41.0

Table 8.6.1 Restricted Nearest Neighbor Results

Trace Number	Size of Open List	Size of Closed List	Number Traces Closed	Percent of Board Evaluated
1	124	43	39	2
2	110	53	70	2
3	74	28	28	1
4	61	20	16	0
5	115	51	57	2
6	252	171	145	7
7	77	37	29	1
8	60	23	15	1
9	89	38	19	1
10	105	50	24	2
11	63	28	15	1
12	83	42	27	1
13	78	37	29	1
14	60	23	14	1
15	91	38	19	1
16	112	51	24	2
17	63	28	15	1
18	85	42	27	1
19	92	36	12	1
20	124	64	41	2
21	260	193	127	8
22	656	547	398	25
23	226	135	86	6
24	192	134	74	6
25	383	319	279	14
26	218	141	125	6
27	273	209	114	9


Modified Nearest Neighbor Case 1
Size of Closed List
Size of Open List
640
576
512
448
384
320
256
192
128
64
0
1 2 3 4 5 6 7 8
Trace Number Being Routed


Modified Nearest Neighbor Case 1 ——— Percent of Board Evaluated
25
24
23
22
21
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
Trace Number Being Routed
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

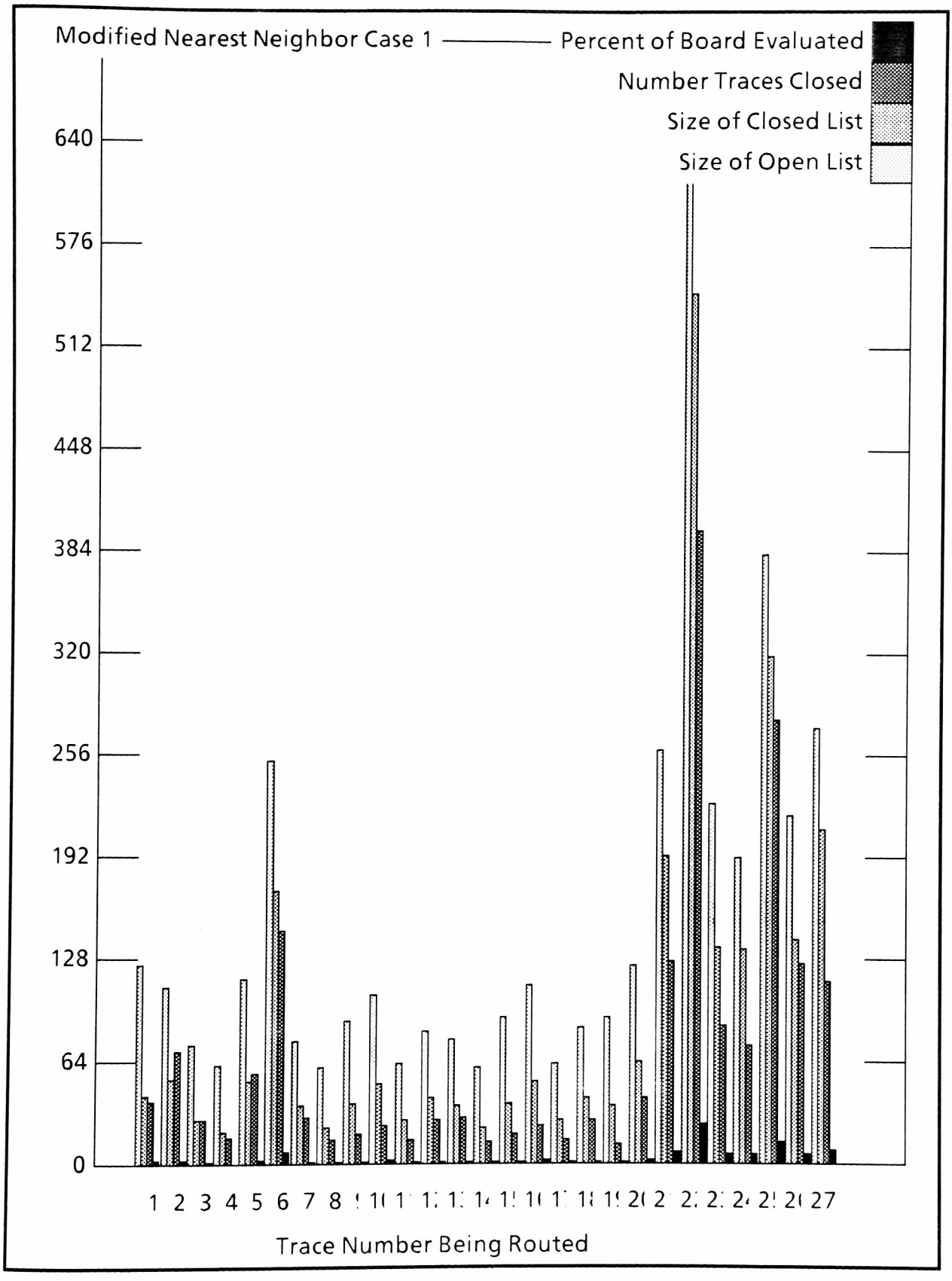
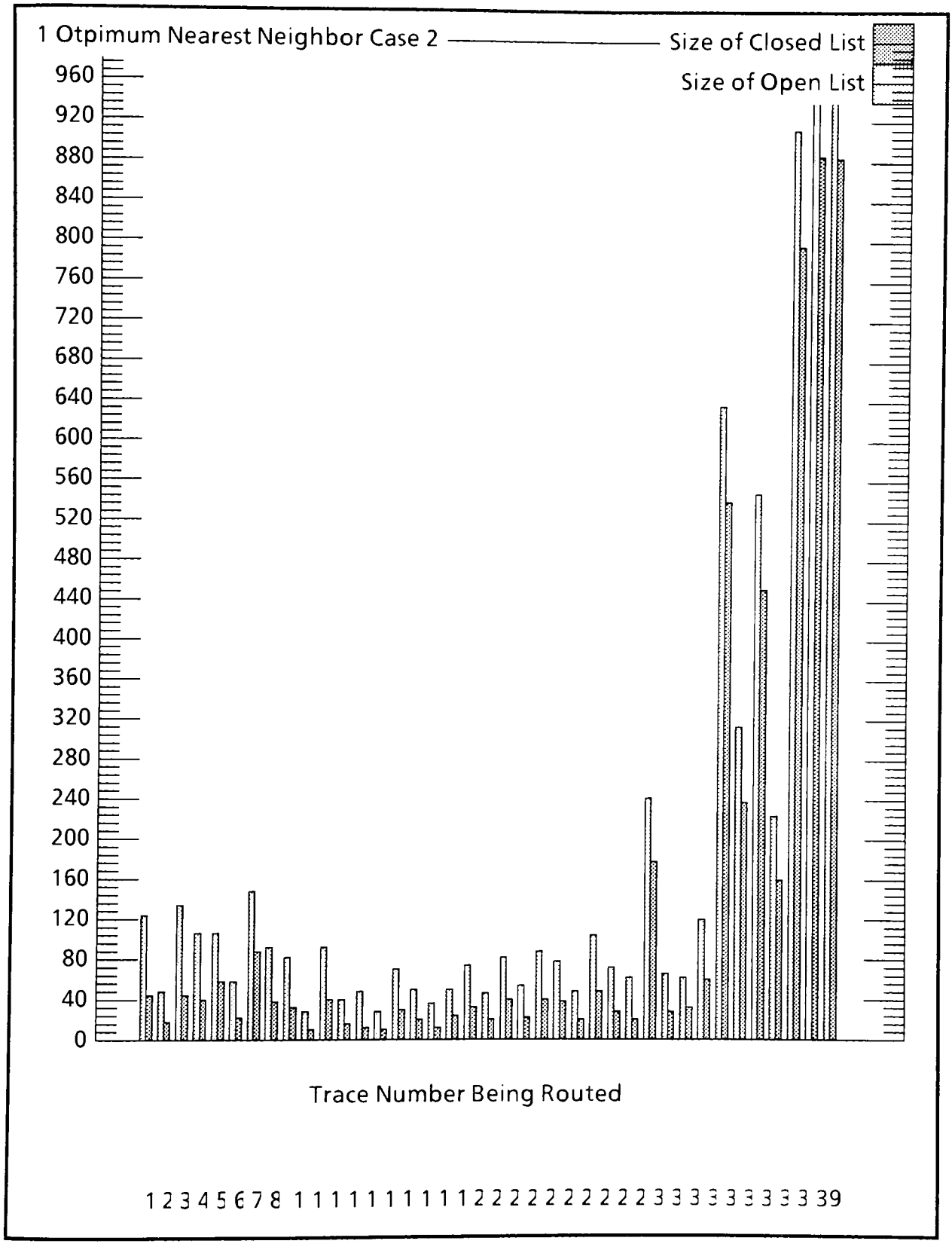

Modified Nearest Neighbor Case 1
Percent of Board Evaluated
Number Traces Closed
Size of Closed List
Size of Open List
640
576
512
448
384
320
256
192
128
64
0
1 2 3 4 5 6 7 8
Trace Number Being Routed

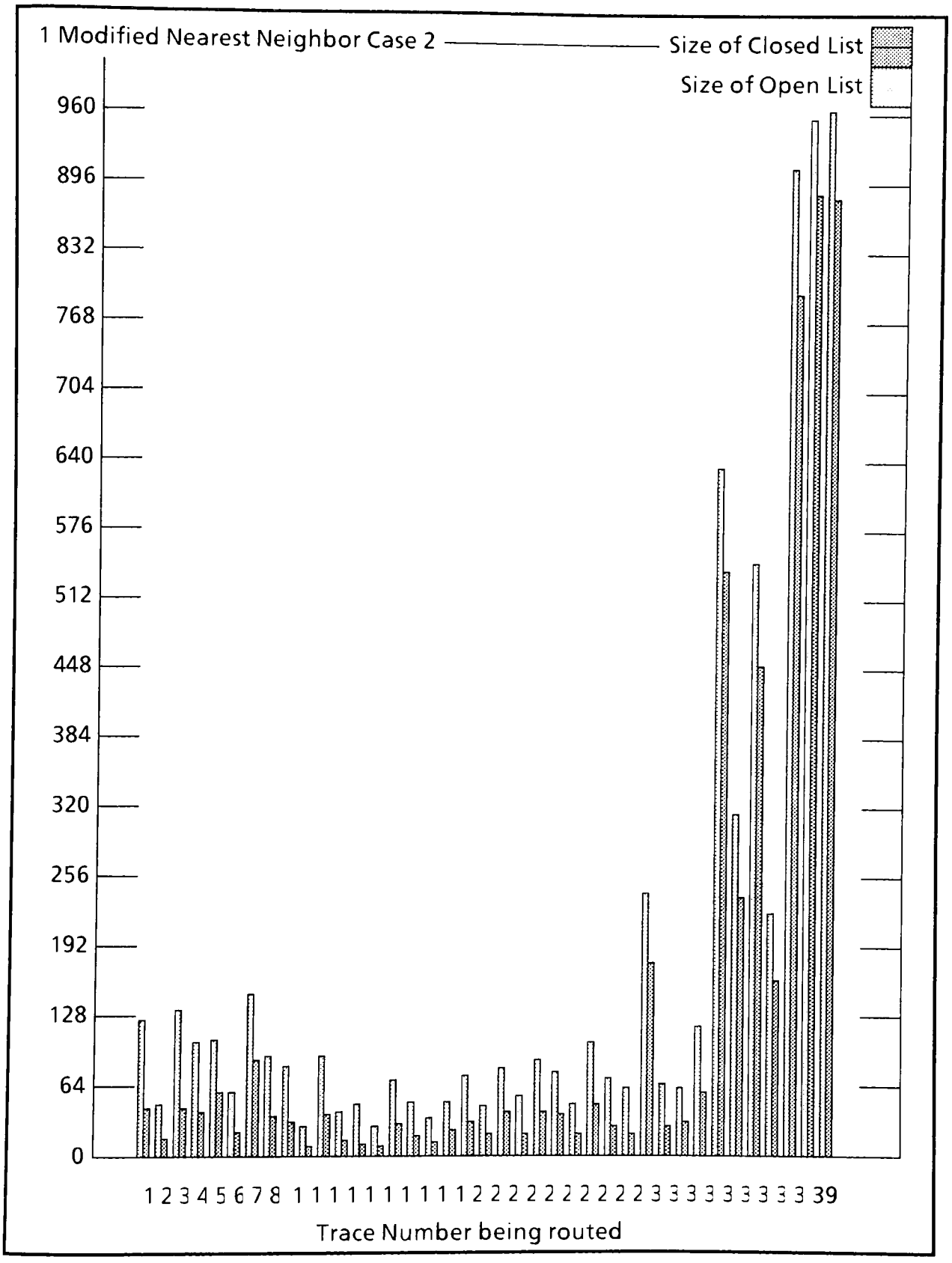
Table 8.7.1

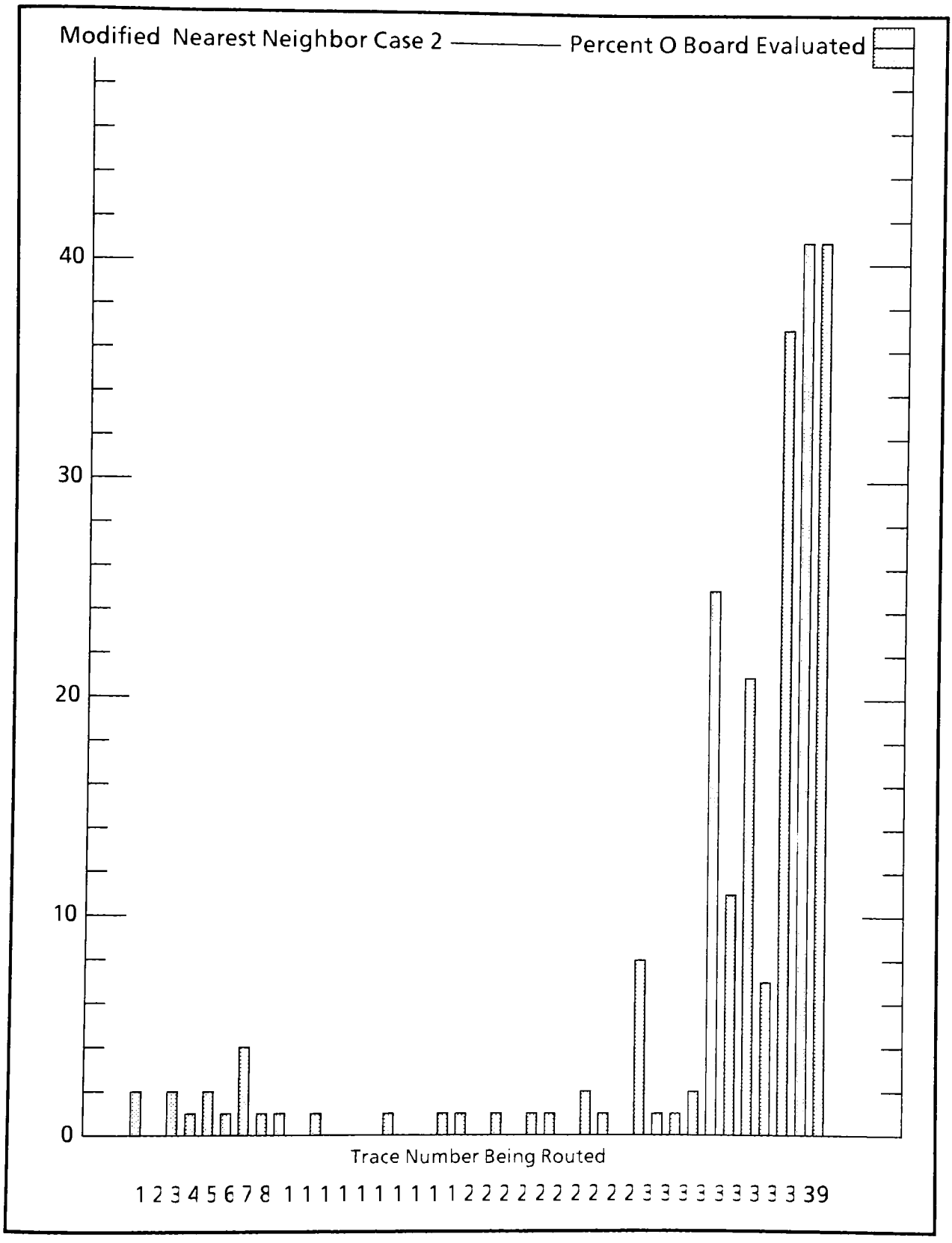
Trace Number	Size of Open List	Size of Closed List	Number of Trace Closed	Percent Of Board Evaluated
1	124	43	39	2
2	48	17	13	0
3	133	44	37	2
4	105	40	29	1
5	106	58	52	2
6	58	22	24	1
7	148	87	62	4
8	92	37	12	1
9	82	31	26	1
10	28	9	8	0
11	91	39	27	1
12	40	15	14	0
13	47	11	1	0
14	28	9	8	0
15	70	30	28	1
16	50	19	50	0
17	35	12	8	0
18	49	24	11	1
19	73	31	25	1
20	45	20	5	0
21	81	40	23	1
22	54	21	17	0
23	88	40	25	1
24	77	38	25	1
25	48	20	16	0
26	104	48	26	2
27	72	28	28	1
28	62	20	16	0
29	241	177	102	8
30	65	28	20	1

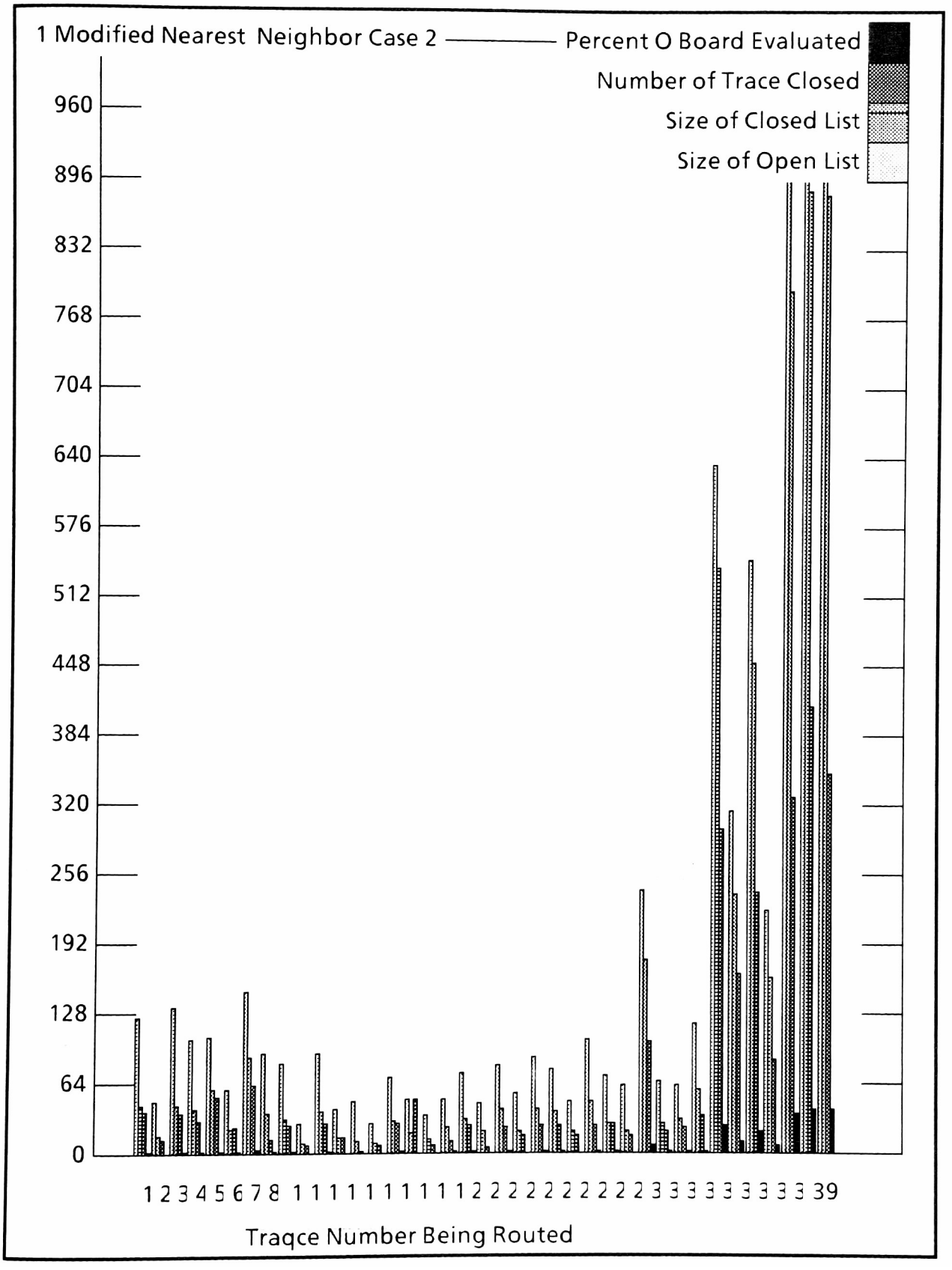
Table 8.7.1

Trace Number	Size of Open List	Size of Closed List	Number of Trace Closed	Percent Of Board Evaluated
31	62	31	23	1
32	119	59	35	2
33	635	539	298	25
34	314	238	164	11
35	547	451	240	21
36	223	160	86	7
37	911	795	327	37
38	957	886	411	41
39	964	884	349	41


1 Otpimum Nearest Neighbor Case 2
Size of Closed List
Size of Open List
960
920
880
840
800
760
720
680
640
600
560
520
480
440
400
360
320
280
240
200
160
120
80
40
0
Trace Number Being Routed
1 2 3 4 5 6 7 8 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 39


1 Modified Nearest Neighbor Case 2
Size of Closed List
Size of Open List
960
896
832
768
704
640
576
512
448
384
320
256
192
128
64
0
1 2 3 4 5 6 7 8 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 39
Trace Number being routed


Modified Nearest Neighbor Case 2
Percent O Board Evaluated
40
30
20
10
0
Trace Number Being Routed
1 2 3 4 5 6 7 8 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 39


1 Modified Nearest Neighbor Case 2
Percent O Board Evaluated
Number of Trace Closed
Size of Closed List
Size of Open List
960
896
832
768
704
640
576
512
448
384
320
256
192
128
64
0
1 2 3 4 5 6 7 8 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 39
Traqce Number Being Routed

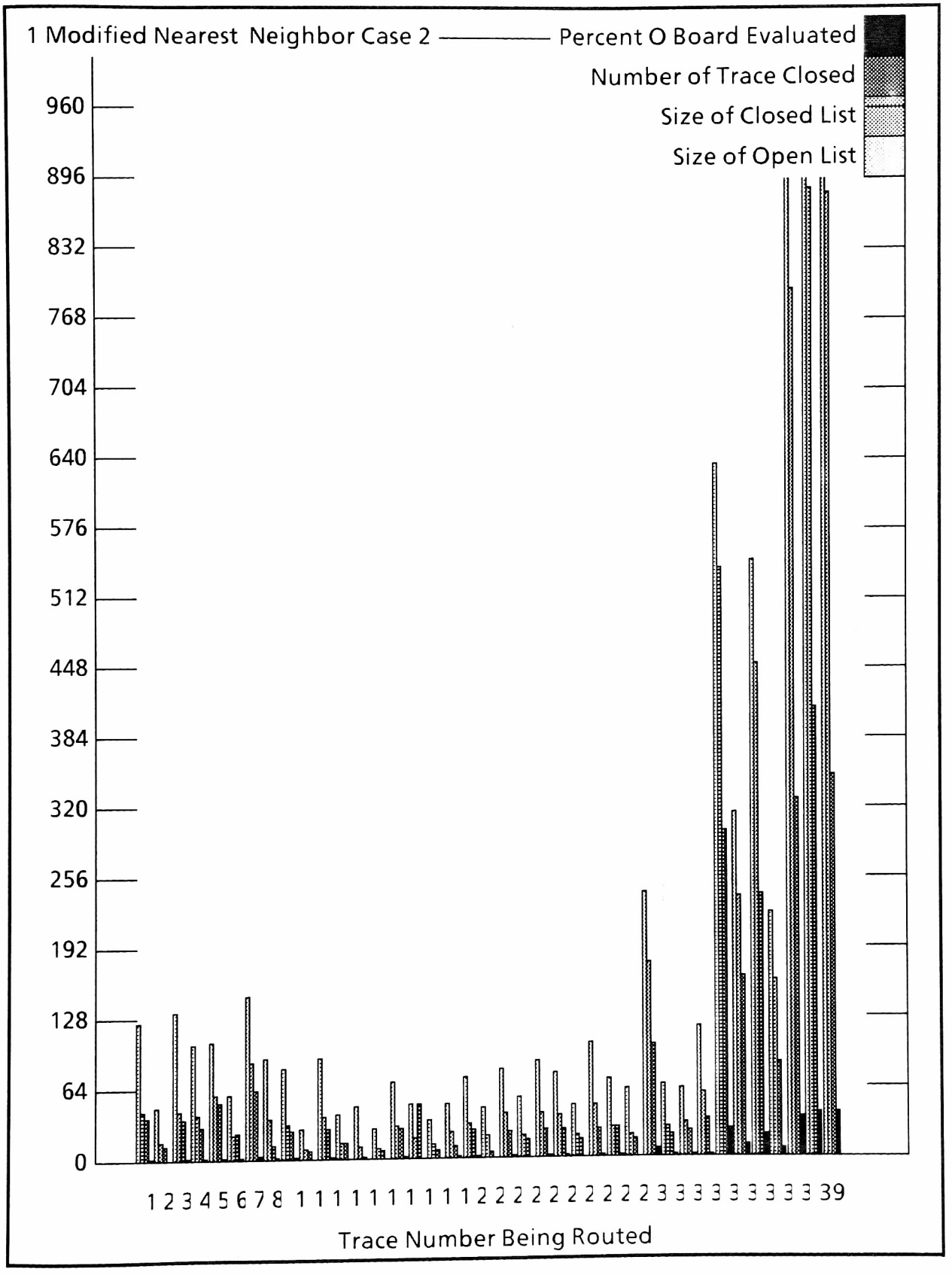
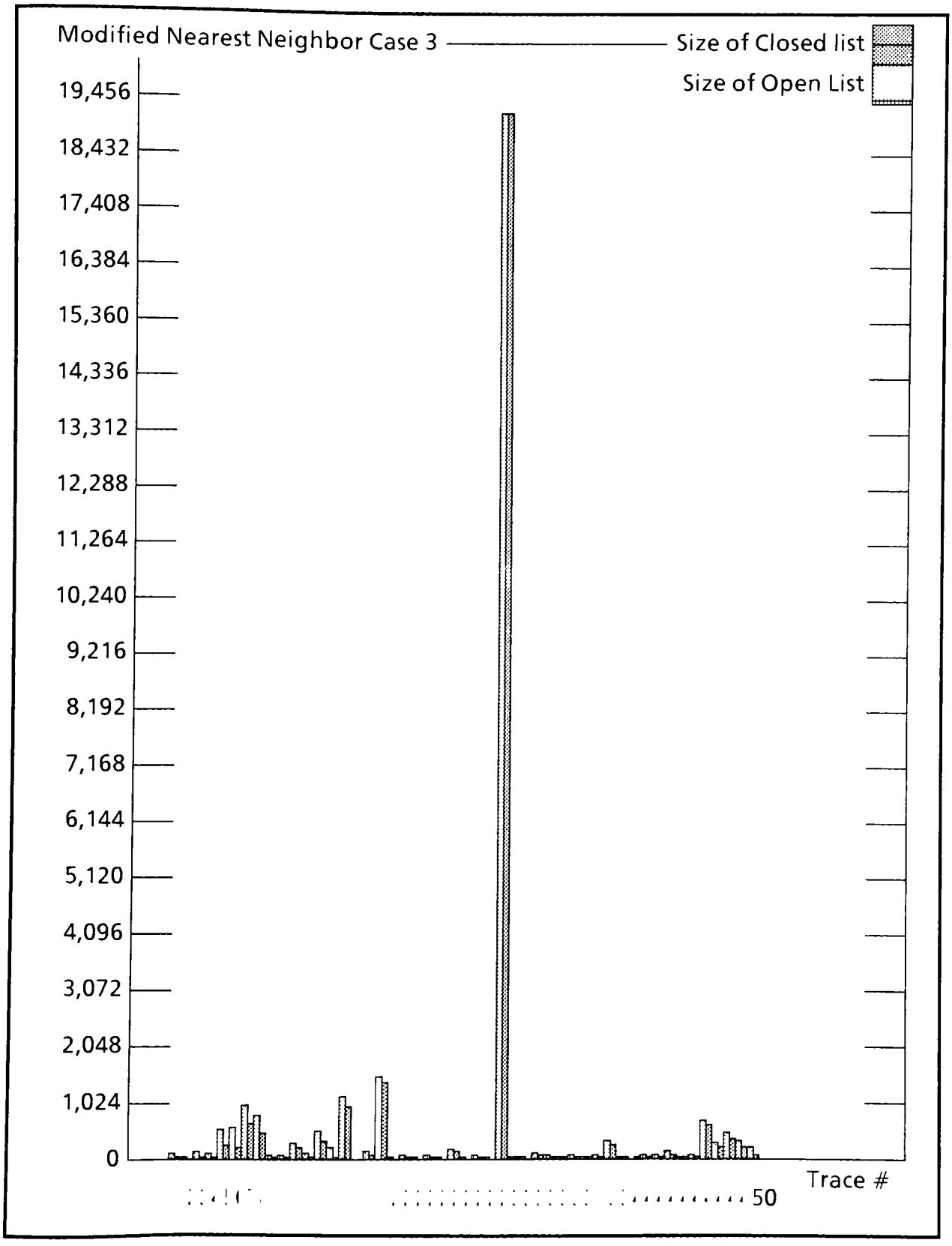

1 Modified Nearest Neighbor Case 2
Percent O Board Evaluated
Number of Trace Closed
Size of Closed List
Size of Open List
960
896
832
768
704
640
576
512
448
384
320
256
192
128
64
0
1 2 3 4 5 6 7 8 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 39
Trace Number Being Routed

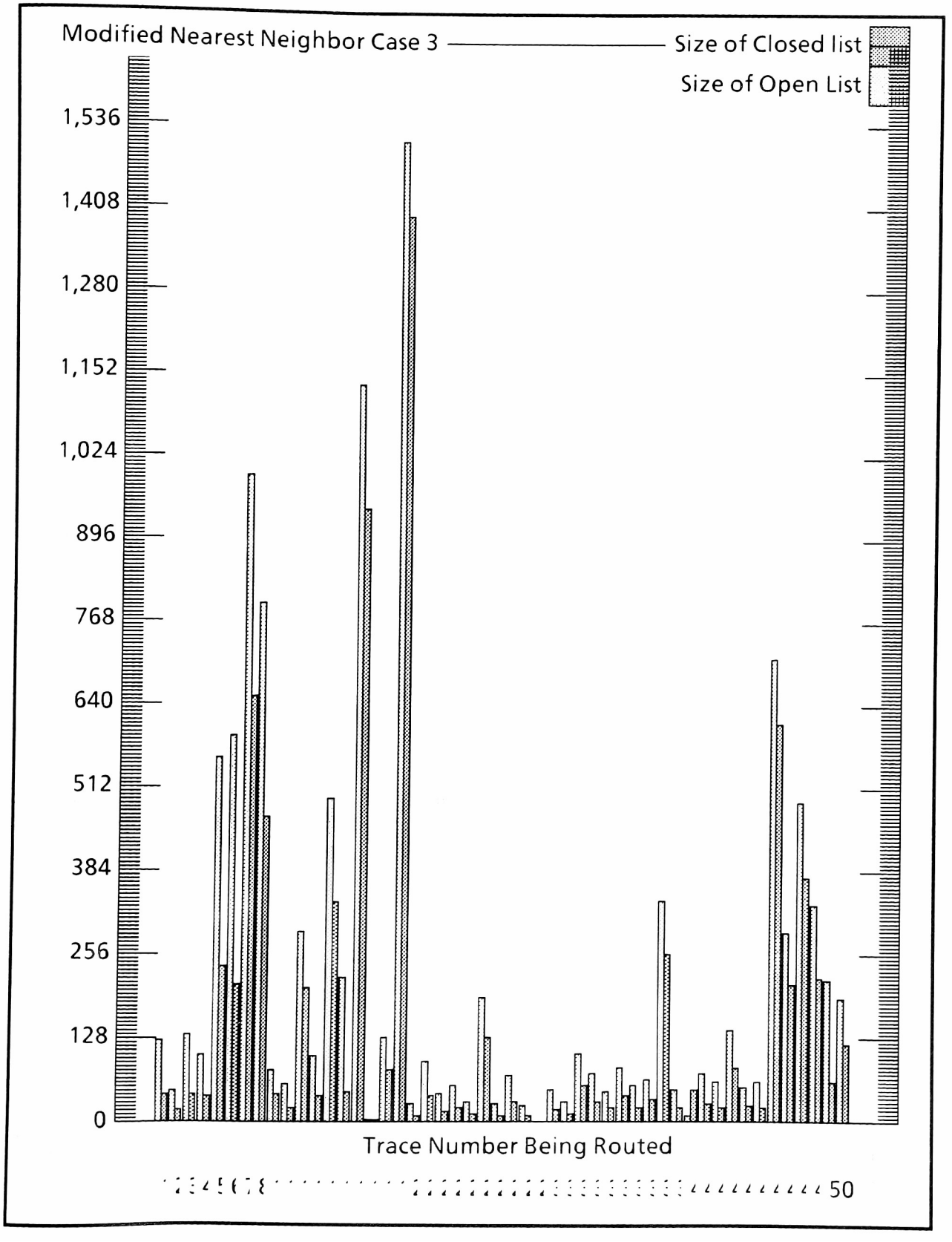
Table 8.8.2

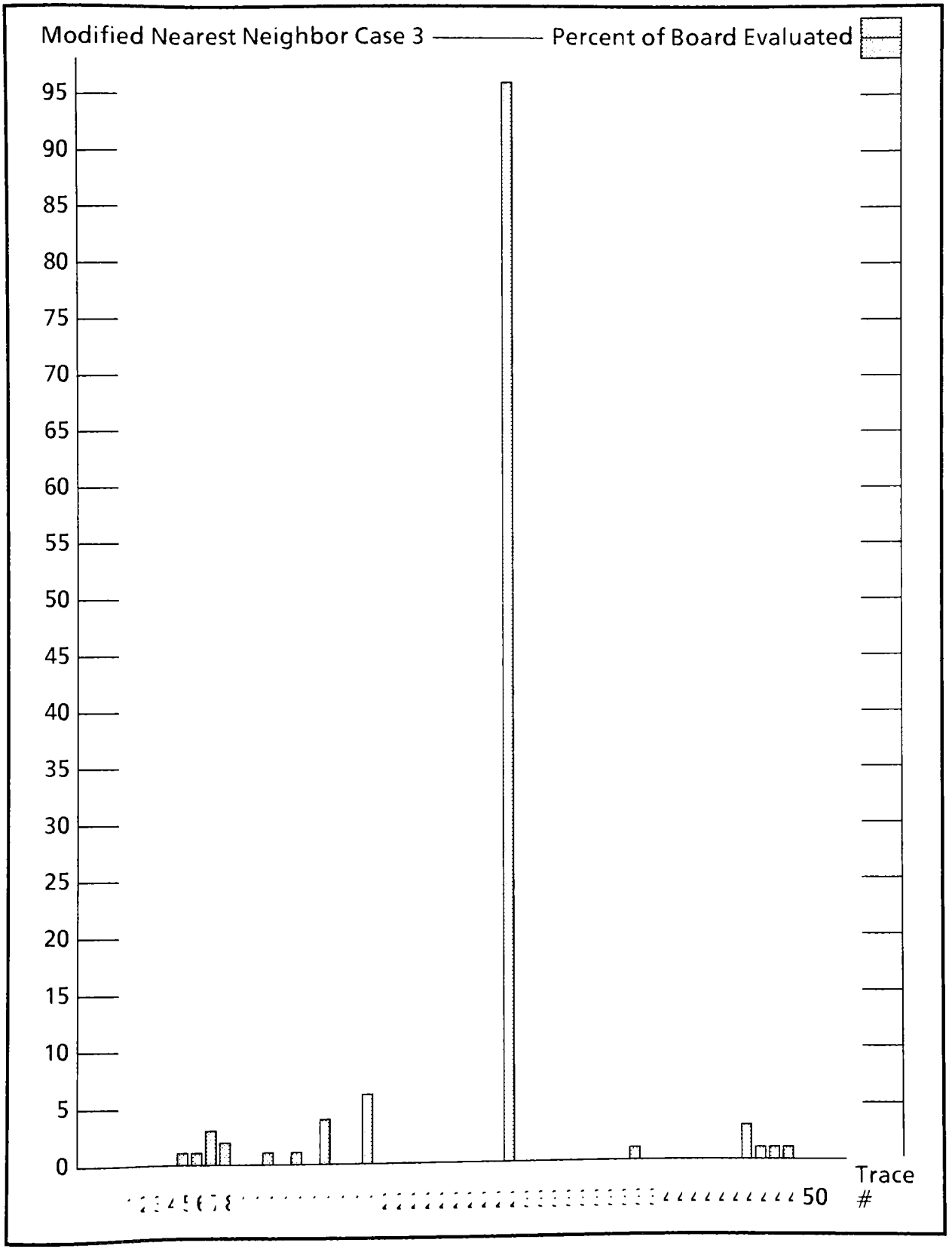
Trace Number	Size of Open List	Size of Closed list	Number of Closed Traces	Percent of Board Evaluated
1	124	43	39	0
2	48	17	13	0
3	133	44	37	0
4	105	40	29	0
5	559	238	253	1
6	591	211	133	1
7	994	653	535	3
8	794	465	240	2
9	80	43	31	0
10	58	22	24	0
11	288	203	87	1
12	100	39	33	0
13	495	334	194	1
14	220	45	0	0
15	1133	943	461	4
16	2	2	0	0
17	128	80	29	0
18	1511	1396	1212	6
19	28	9	8	0
20	91	39	27	0
21	42	15	16	0
22	56	22	21	0
23	31	12	8	0
24	190	128	84	0
25	28	9	8	0
26	71	30	28	0

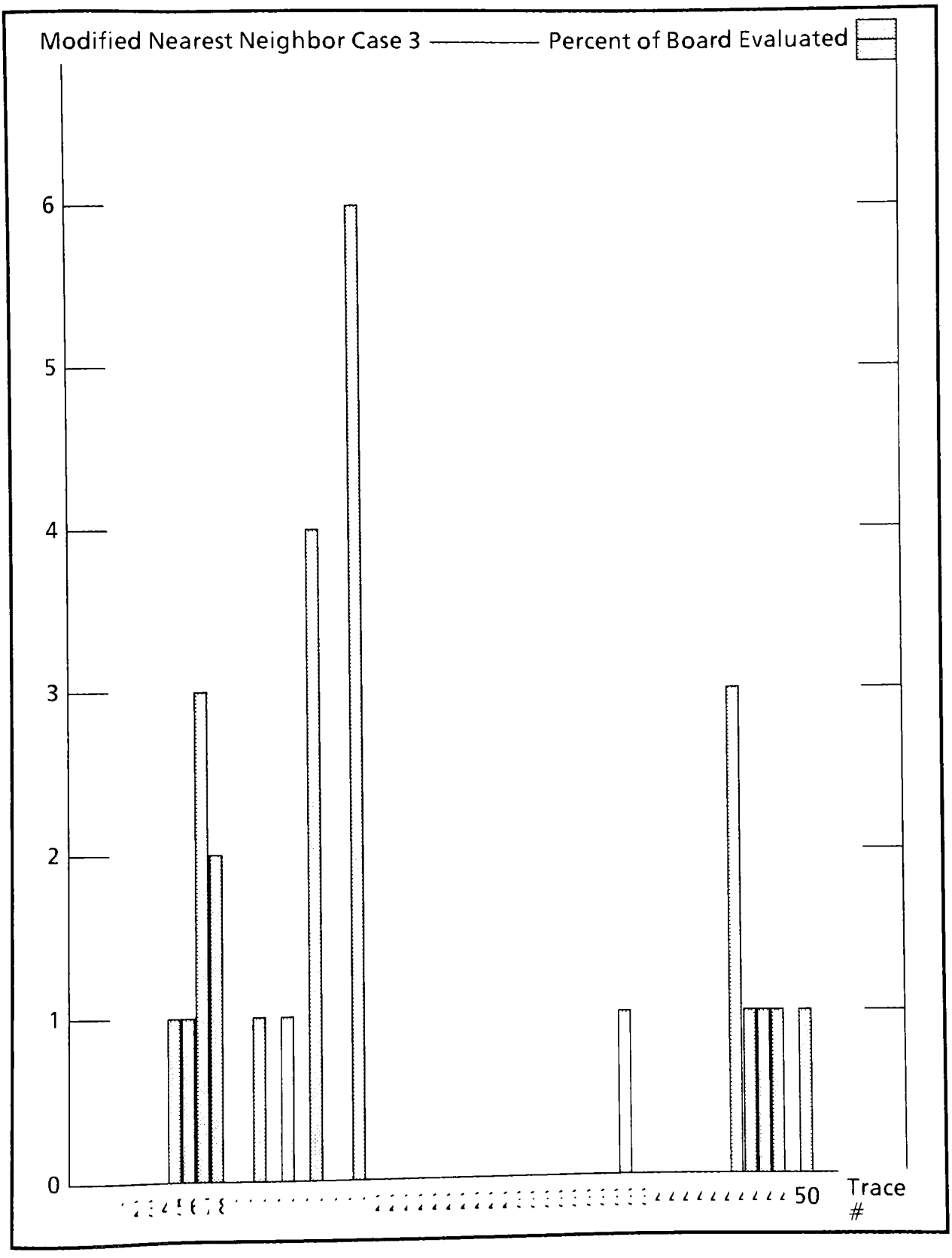
Table 8.8.2

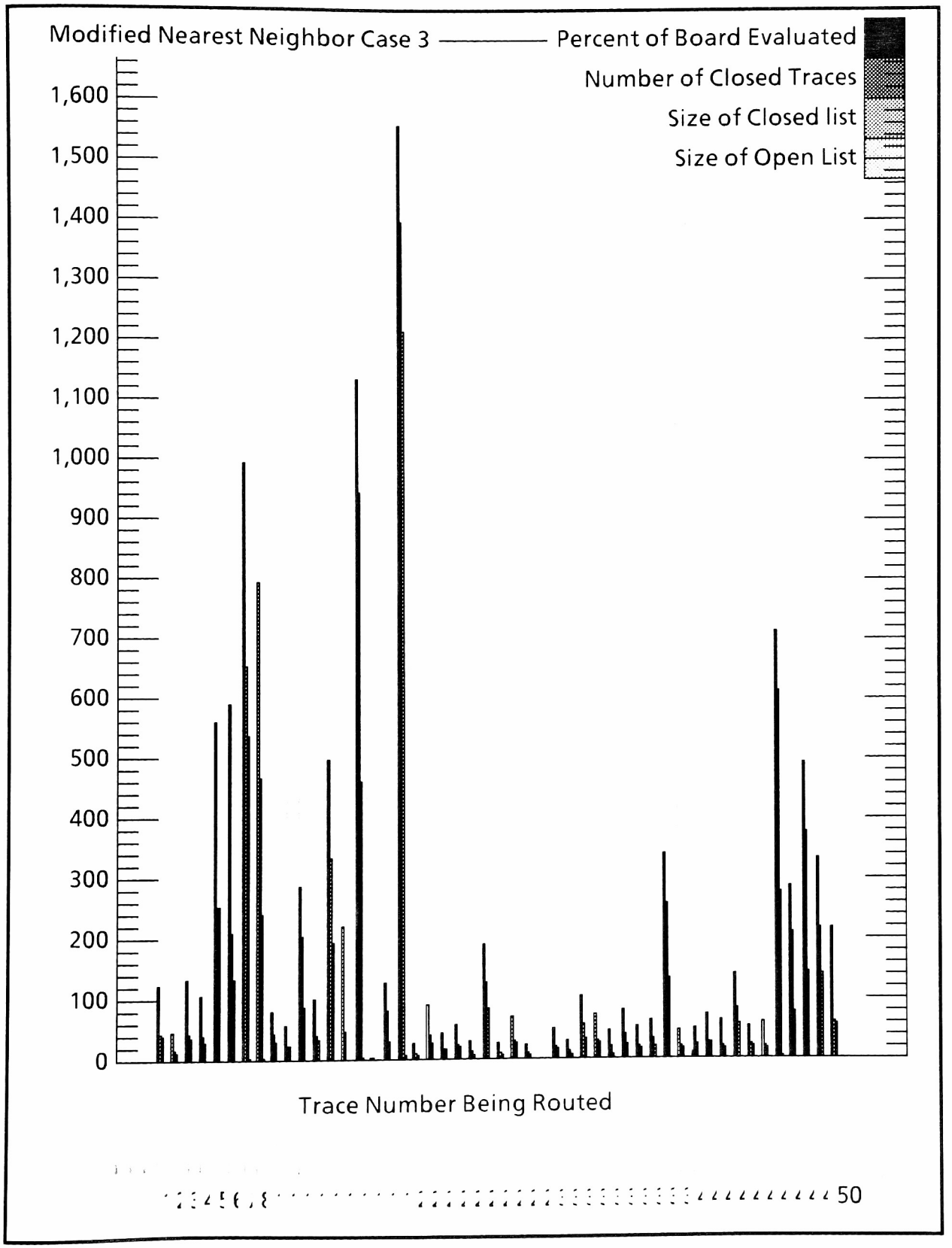
Trace Number	Size of Open List	Size of Closed list	Number of Closed Traces	Percent of Board Evaluated
27	24	9	6	0
28	19218	19218	10625	96
29	49	19	15	0
30	29	12	8	0
31	104	56	34	0
32	73	31	25	0
33	45	20	5	0
34	81	40	23	0
35	54	21	17	0
36	64	33	19	0
37	339	256	133	1
38	48	20	16	0
39	10	49	22	0
40	74	28	28	0
41	62	20	16	0
42	139	82	55	0
43	52	23	20	0
44	61	20	16	0
45	712	614	278	3
46	288	209	76	1
47	492	375	142	1
48	332	218	139	1
49	216	60	57	0
50				

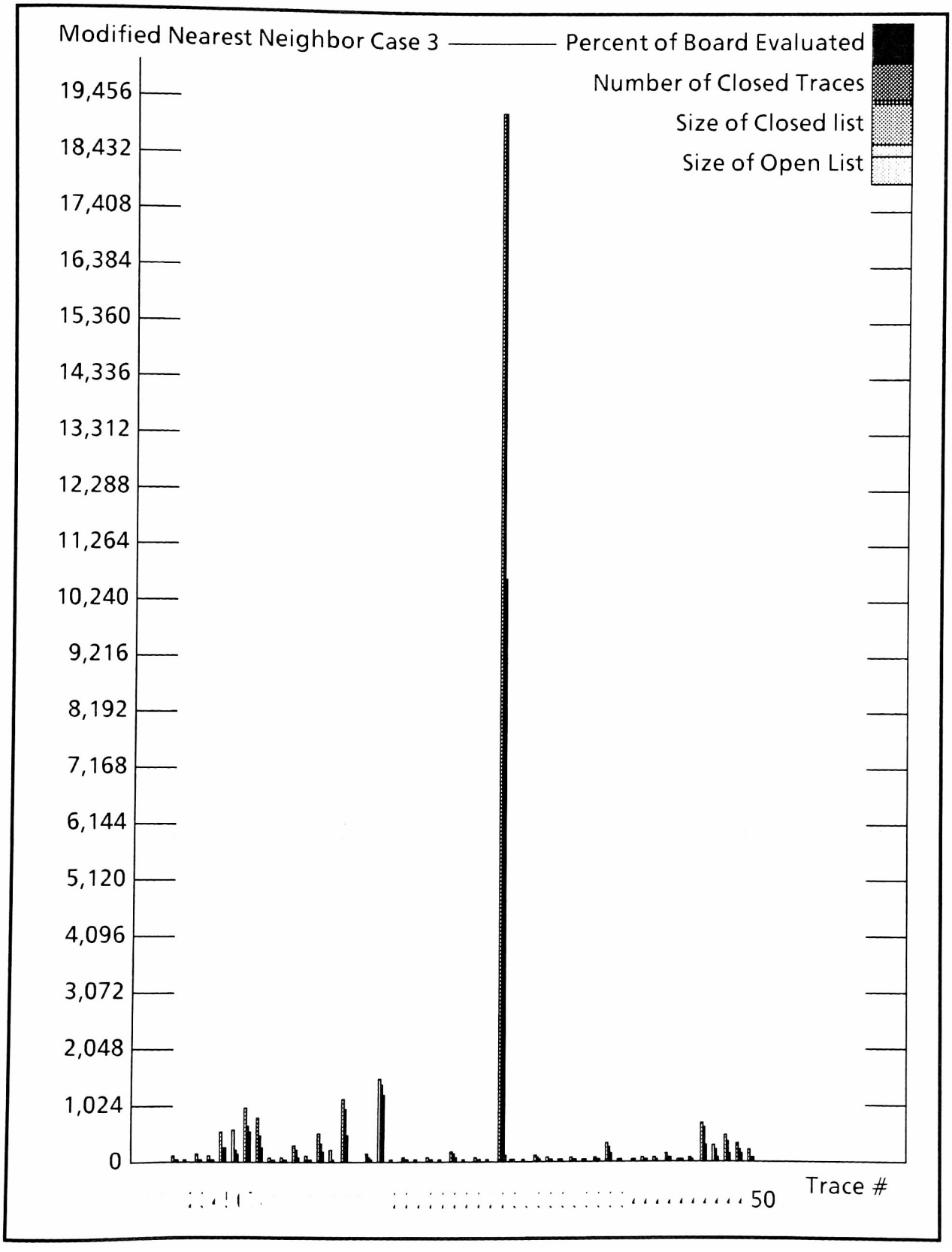

Modified Nearest Neighbor Case 3
Size of Closed list
Size of Open List
19,456
18,432
17,408
16,384
15,360
14,336
13,312
12,288
11,264
10,240
9,216
8,192
7,168
6,144
5,120
4,096
3,072
2,048
1,024
0
Trace #
50


Modified Nearest Neighbor Case 3
Size of Closed list
Size of Open List
1,536
1,408
1,280
1,152
1,024
896
768
640
512
384
256
128
0
Trace Number Being Routed
50


Modified Nearest Neighbor Case 3
Percent of Board Evaluated
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
50
Trace #


Modified Nearest Neighbor Case 3
Percent of Board Evaluated
6
5
4
3
2
1
0
50
Trace #


Modified Nearest Neighbor Case 3
Percent of Board Evaluated
Number of Closed Traces
Size of Closed list
Size of Open List
1,600
1,500
1,400
1,300
1,200
1,100
1,000
900
800
700
600
500
400
300
200
100
0
Trace Number Being Routed
50


Modified Nearest Neighbor Case 3
Percent of Board Evaluated
Number of Closed Traces
Size of Closed list
Size of Open List
19,456
18,432
17,408
16,384
15,360
14,336
13,312
12,288
11,264
10,240
9,216
8,192
7,168
6,144
5,120
4,096
3,072
2,048
1,024
0
50
Trace #

Chapter 12

References

Chapter 1

1. SIAM Series #3, Symposium on applied probability and Monte Carlo Methods, 1967

2. Binder, Kurt, Monte Carlo methods in statistical physics, 1/1/79, QC 174.85.m64 M66

3. Gorden, M., D., Adaptive subject indexing in document retrieval. (PHD disertation at University of Michigan), Dissertation abstracts international, 45(2), 611B

4. Booker, L., B., Improving search in genetic algorithms, L. Davis book on Genetic algorithms and simulated annealing, p 61-74, London Press.

5. Dejong, k., A., An alysis of the behacior of a class of genetic adaptive systems, Dissertation abstracts international 36(10), 5140B.

6. Holland, J., H., Adaptation in natural and artificial systems, University of Michigan Press (1975)

7. Goldberg, D., E., & Lingle, R., Alleles, Loci and the traveling salesman problem, Proceedings of an internatinal conference on genetic algorithms and their appoications pps154-159.

8. Goldberg, D., E., & Thomas, A., L., Genetic Algorithms: a bibliography (1962-1986), TCGA report #86001, University of Alabama.

Chapter 2

9. Hammersley, J. m. & Handscomb, D. C. Monte Carlo Methods, 1965, QA.273.H224

10. Studies In Applied Mathmatics, #3 Symnposium on applied probability amd Monte Carlo Methods, 1967, QA.1.S863

11. Binder, K. Et. Al, Monte Carlo methods in statistical physics, 1979, QC.174.85.M64

12. Styblinski, M. A. & Meyer, B. D., Fuzzy Cognitive Maps, Signal Flow Graphs and Qualatitive Circuit Analysis, Proc. IEEE Conf on Neural Networks, 6/87

13. Kosko, B., "Fuzzy Cognitive Maps", International Journal of Man-Machine Studies, Volum 24, pps 65-75, 1/1986.

14. Davis, L. & SteenStrup, M. (1987). Genetic Algorithms and simulated annealing: An overview in.

15. Glossary and tables for statistical quality control. Published American society for quality control 1973.

16. William K. Pratt, Digital Image Processing, Wiley-Interscience, 1978.

Chapter 3

17. H.S.Stone, J.M.Stone, Efficient Search Techniques - An emperical study of the N-Queens problem, IBM J. Res. Development., pp464-474, vol.31, no.4, 1987

18. Goldberg, D., E., Optimal initial poplation size for binary-coded genetic algorithms (TCGA report #85001).

19. C.L. Bridger, D.E. Goldberg, An Analysis of Reproduction and crossover in a binary coded Genetic algorithm, Proceedings of the Second Internation Conference on Genetic Algorithms, 7/1987

20. Holland, J., H., Genetic Algorithms and the optimal allocations of trials, SIAM journal of Computing, 2(2), 88-105

21. Suh, J., Y., & Gucht, D., V., Incorporating heurstic information information into genetic search, Proceedings of the Swcond International Conference of Genetic Algorithms 7/1987

22. Johnson, K, & Daniell, c., & Burman, J., Feature extraction in the Neocognitron, Proceedings from the confrence on Neural Network

23. Krishnan, G., & Walters, D., Psychologically plausible features for shape recognition in a neural network

24. DeJong, K., A., (1981) Adaptive search procedures for large complex spaces., (technical report #81-2), Uinversity of Pittsburgh

25. Foo, N., Y., & Bosworth, J., L., (1972) Algebraic, geometric, and stochastic aspects of genetic operators, (CR-2099)

26. Grefenstette, J., J., Optimization of control parameters for genetic algorithms, IEEE Transactions on Systems, Man and Cybernetics, SMC-16(1), 122-128

27. Bosworth, J., & Foo, N., & Zeigler, B., P., Comparison of genetic algorithms with conjugate gradient methods (CR-2093) National Aeronautics and space administration

28. Goldberg, D., E., (1987) A note on the disruption due to crossover in a binary coded algorithm, (TCGA report #87001).

29. Wetzel, A., Evaluatin of the effectiveness of genetic algorithms in combinatorial optimization, Unpublished manuscript, University of Pittsburgh (1983).

30. Booker, L., B., Improving performance of genetic algorihtms in classifier systems, Proceedings of an internatinal conference on genetic algorithms and their applications, pp80-92.

Chapter 4

31. Moopenn, A., & Thakoor, A., P., & Duong, T., A Neural network for Euclidean distance minimization< proceedings from

32. Van Den Bout, D., E., & Miller, T., K., A traveling Salesman Object function that works, North Carolina University, Proceeding from ACM

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