TOPOLOGICAL OPTIMISATION OF DOUBLE LAYER GRIDS USING GENETIC ALGORITHM

HOSSEIN EBRAHIMI FARSANGI

**A THESIS SUBMITTED FOR THE DEGREE OF
DOCTOR OF PHILOSOPHY**

**SPACE STRUCTURES RESEARCH CENTRE
CIVIL ENGINEERING
SCHOOL OF ENGINEERING
UNIVERSITY OF SURREY**

NOVEMBER 2002

ABSTRACT

Double layer grids are one of the most commonly used space structures. Normally, these grids have rather dense configurations. In practice, the tendency is to use grids that are obtained by removing a number of elements from a dense grid. This is prompted by the desire to have a grid with a 'lighter looking' configuration. This would also help in allowing the natural lighting through where translucent cladding is used. However, different reduced grids meeting these requirements may be derived from a dense grid. Usually, the most suitable reduced grid is chosen based on experience and engineering judgment.

In this work, the densest configuration in a particular family of double layer grids is called a 'base grid'. The reduced grids derived from the base grid have different topologies. The main objective of this Thesis is to establish a method for comparing these reduced grids to choose the grid with the most suitable topology. To achieve this, the process of genetic algorithm is employed. As the result of applying the genetic technique, a numerical value is obtained for each element of the base grid that indicates the 'degree of importance' of that element. This value is called 'portancy'. A graphical representation of the element portancies, called 'portancy map' is used to provide an overall view of the degree of importance of the elements of the base grid.

The portancy map introduced in this Thesis may be used in two ways. Firstly, using the map a designer may easily decide about the regions from which the elements may be removed such that the loss of the loading capacity of the structure is minimised. Secondly, the grids with different topologies derived from a base grid can be compared with each other using the element portancies. This comparison leads to the choice of the grid whose elements contribute more effectively in carrying the loads.

The method established in this Thesis is employed in relation to a number of double layer grids with different patterns. For each of these double layer grids, the particulars of the corresponding portancy map are discussed. Using the portancy map, the reduced grids derived from the base grid are compared with each other and the grid with the most suitable topology is found.

*To my family,
for their support and encouragement*

تقدیم به همسر من

که با بردباری و محبت خویش امکان انجام این پژوهش را
برای من فراهم نمود.

تقدیم به فرزندانم مهدی، رضا، صدرا و علی

که با ابراز محبت و علاقه بی شائبه، خود موجبات پیشگامی مرا
فراهم آوردند.

حسین آذر ۱۳۸۱

ACKNOWLEDGEMENTS

I wish to express my sincere gratitude to my supervisors Professor H. Nooshin and Dr. P. Disney for all their help, advice and enthusiasm throughout my research studies.

My thanks are due to Professor E. Salajegheh for his useful guidance, while I was doing a part of my research in Iran.

The financial assistance of the Ministry of Science, Research and Technology of Islamic Republic of Iran and the help of the University of Kerman, Iran, in supporting my research studies are also gratefully acknowledged.

Further thanks are due to my dear wife Nasrin for her patience and understanding, without whose unconditional support, this research would not have reached the end. I especially appreciate here for accepting the responsibility of the family, while I was far from home. Also I would like to thank my children Mahdi, Reza, Sadra and Ali who provided me with confidence through their love and kindness.

TABLE OF CONTENTS

ABSTRACT.....2

ACKNOWLEDGEMENTS.....4

CHAPTER 1 INTRODUCTION.....8

1.1 INTRODUCTION.....8

1.2 OPTIMISATION TECHNIQUES.....8

1.3 HISTORY OF GENETIC ALGORITHM.....10

1.4 GENETIC ALGORITHM AND STRUCTURAL OPTIMISATION.....11

1.4.1 Sizing Optimisation.....11

1.4.2 Sizing and Geometrical Optimisation.....12

1.4.3 Sizing and Topology Optimisation with Fixed Geometry.....12

1.4.4 Sizing, Geometrical and Topology Optimisation.....13

1.5 BASE GRID VERSUS GROUND STRUCTURE.....16

CHAPTER 2 GENETIC ALGORITHM.....21

2.1 INTRODUCTION.....21

2.2 ILLUSTRATIVE EXAMPLE.....23

2.3 INITIATION.....24

2.4 PAIRING.....24

2.5 MATING.....25

2.5.1 Encoding.....26

2.5.2 Crossover.....27

2.5.3 Mutation.....28

2.5.4 Decoding.....29

2.6 REPLACEMENT.....31

2.7 TERMINATION.....32

2.8 FURTHER DICUSSION OF GENETIC OPERATORS.....37

2.8.1 Significance of Mutation.....37

2.8.2 Two-point Crossover.....37

2.8.3 Uniform Crossover.....38

2.9 EFFECTS OF THE GENETIC OPERATORS.....38

2.10 GENETIC ALGORITHM AND CONSTRAINED PROBLEMS.....41

2.11 GENETIC ALGORITHM IN STRUCTURAL OPTIMISATION.....46

2.11.1 Sizing Optimal Design.....46

2.11.2 Shape Optimal Design.....46

2.11.3 Topology Optimal Design.....46

2.11.4 Illustrative Example.....46

2.11.5 Genetic Algorithm and Constrained Structural Optimisation.....49

2.11.5.1 Handling of the constraints.....52

2.11.6 Pairing.....58

2.11.7 Mating.....58

2.11.7.1 Encoding.....59

2.11.7.2 Crossover.....62

2.11.7.3 Mutation.....63

2.11.7.4 Decoding.....63

2.11.8 Replacement.....64

2.11.9 Evolution Cycle.....65

2.11.10 Termination.....65

2.11.10.1 Termination in phase one.....65

2.11.10.2 Termination in phase two.....66

2.12 A CHECK FOR THE ACCURACY OF THE DEVELOPED TECHNIQUE.....68

CHAPTER 3 A GENETIC APPROACH FOR TOPOLOGICAL OPTIMISATION OF

DOUBLE LAYER GRIDS.....71

3.1 INTRODUCTION.....71

3.2 ESTABLISHING THE MAIN CONCEPTS.....71

3.3 APPLICATION OF GENETIC ALGORITHM.....81

3.3.1 Initiation.....82

3.3.2 Fitness Function.....84

3.3.3 Pairing.....87

3.3.4 Mating.....87

3.3.4.1 Crossover.....87

3.3.4.2 Mutation.....87

3.3.5 Replacement.....89

3.3.6 Termination.....92

3.4 PORTANCY MAP.....93

3.5 SOME INVESTIGATIONS IN RELATION TO THE PORTANCY MAP.....105

3.5.1 Statistical Investigations.....105

3.5.2 Sensitivity of the Portancy Map to Parameters Used by Genetic Algorithm.....111

3.6 EFFECTS OF THE SUPPORT ARRANGEMENT ON THE PORTANCY MAP.....113

3.7 COMPARING REDUCED GRIDS USING THE PORTANCY MAP.....116

3.7.1 Weight Optimisation of Reduced Grids.....119

3.7.2 Comparing Reduced Grids with Other Support Arrangements.....125

3.8 EFFECTS OF THE LOADING ARRANGEMENT ON THE PORTANCY MAP.....129

3.9 PORTANCY MAP FOR DENSER DOUBLE LAYER GRIDS.....136

3.9.1 Denser Double Layer Grids with Other Support Conditions.....145

CHAPTER 4 DOUBLE LAYER GRIDS WITH OTHER PATTERNS.....151

4.1 INTRODUCTION.....151

4.2 DOUBLE LAYER GRIDS WITH SQUARE ON DIAGONAL PATTERN.....151

4.2.1 Effects of the Support Conditions on the Portancy Map.....158

4.2.2 Denser Double layer Grids with Square on Diagonal Pattern.....164

4.3 A HEXAGONAL DOUBLE LAYER GRID WITH TRIANGLE ON TRIANGLE
PATTERN.....181

4.3.1 Effects of the Support Conditions on the Portancy Map.....188

4.4 A TRIANGULAR DOUBLE LAYER GRID WITH TRIANGLE ON TRIANGLE
PATTERN.....196

4.4.1 Effects of the Support Conditions on the Portancy Map.....203

CHAPTER 5 CONCLUSIONS AND SUGGESTIONS FOR FUTURE WORK.....212

5.1 INTRODUCTION.....212

5.2 OUTLINE OF THE WORK AND CONCLUSIONS.....212

5.3 SUGGESTIONS FOR FUTURE WORK.....215

APPENDIX A RANDOM NUMBERS.....217

A.1 DESIRABLE SPECIFICATIONS FOR A RANDOM ENERATOR.....217

A.2 RANDOM NUMBER GENERATORS.....218

A.2 1 Power Residue Method.....218

A.2 2 Mixed Congruential Method.....219

APPENDIX B DESCRIPTION OF PROVIDED CODE.....221

REFERENCES.....224

CHAPTER 1

Introduction

1.1 INTRODUCTION

In this chapter, at first, a brief description is given in relation to the optimisation techniques dealing with engineering problems. Then, genetic algorithm, the technique in the present work, is introduced. Thereafter, the history of the researches particularly carried out in relation to the optimisation of skeletal structures using genetic algorithm are reviewed. At the end of this chapter the genetic technique developed in this study for obtaining the suitable topologies of double layer grids is briefly outlined

1.2 OPTIMISATION TECHNIQUES

Generally speaking, optimisation is concerned with achieving the best outcome of a given objective while satisfying certain imposed restrictions. Many science and engineering systems involve cost or benefit functions, or in other words, objective functions that should be optimised in order to optimise the performance of the system.

In the context of structural engineering, optimisation techniques are used for creating the most cost effective designs that satisfy the constraints. In this field, optimisation is carried out to determine some set of design variables that maximise or minimise the objective function with

respect to the given load conditions, constraints and prescribed parameters. Prescribed parameters are fixed quantities in the design that are not changed by the optimisation process. Design variables are quantities that can be changed by the optimisation process such that an optimal solution is obtained. Load conditions are one or more sets of mechanical or thermal loads that may be imposed on the structure during its expected service life. Constraints are restrictions imposed on the structure. For example, the stresses and deflections may be limited to allowable values to ensure that the structure has a satisfactory behaviour under the anticipated load conditions.

Different approaches have been developed in dealing with the optimisation problems. These approaches include analytical techniques such as calculus of variations, differential calculus and Lagrange multipliers, and numerical techniques such as linear programming, direct search methods, penalty functions methods, dual methods and optimality criteria methods. More details regarding these approaches can be found in textbooks [1-5]. There are some limitations for each of these analytical and numerical techniques. For example, the analytical techniques are applicable only for simple problems. Also, analytical based optimisation approaches may be entrapped in local optima. The numerical methods are applicable for a broad range of problems. However, these methods also possess limitations. For example, all numerical methods make use of some form of initial trial design from which the optimal solution is reached iteratively by modifying the design in accordance with certain prescribed search directions. Except for the case where the optimisation problem possesses a convex design space, it is not guaranteed that the numerical optimisation process will reach the optimum solution. Another difficulty with numerical optimisation techniques is that the function and constraints must be expressed explicitly in terms of the design variables. This may be possible for some simple structures but for most of the practical structures this is difficult to achieve. Usually, approximation techniques involving Taylor series expansion, which often require gradient information, must be used to achieve an explicit problem formulation. Another problem related to the numerical optimisation techniques is that almost all these approaches can only deal with continuous variables. However, in most practical problems in engineering design, the design variables are discrete values. This is due to the availability of components in standard sizes. Usually, discrete variables are treated as being continuous and after the optimum solution is obtained the variables are discretised by converting them to the nearest discrete values. This approach is taken because optimisation problems involving continuous design variables are generally easier to solve than those with discrete variables. One algorithm

that can incorporate discrete variables directly in the optimisation is the dual method. With this method, however, the computations required in solving discrete optimisation problems are often excessive.

1.3 HISTORY OF GENETIC ALGORITHM

In this study an evolutionary based technique, called ‘genetic algorithm’, is employed. Genetic algorithm is an adaptive method that may be used to solve the optimisation problems. This is based on the genetic processes of biological organisms. That is, it is based on the principles of ‘natural selection’ and ‘survival of the fittest’, stated by Charles Darwin in the Origin of Species [6]. In nature, individuals in a population compete with each other for resources such as food, water and shelter. Also, members of the same species often compete to attract a mate. Those individuals that are most successful in surviving and attracting mates will have a relatively large numbers of offspring. Poorly performing individuals will produce few or even no offspring at all. This means that the genes from the highly adapted, or ‘fit’ individuals will spread to an increasing number of individuals in each successive generation. The combination of good characteristics from different ancestors can sometimes produce ‘super fit’ offspring, whose fitness is greater than that of either parent. In this way, species evolve to become more and more well suited to their environment. The genetic algorithm is a direct analogy of the natural behaviour that combines the concept of artificial survival of the fittest with genetic operators abstracted from nature to form a powerful search mechanism. It works with a population of ‘individuals’, each representing a possible solution to a given problem.

Genetic algorithm is a direct search strategy with a random component and more importantly a ‘learning aspect’ [7]. This algorithm does not have many of the limitations associated with conventional ‘Mathematical Programming’ techniques. The power of genetic algorithm comes from the fact that the technique is robust and can successfully deal with a wide range of problem areas including those which are difficult for other methods to solve. Commencing from a random initial population of designs, the genetic algorithm determines the regions in the design space which yield above average solutions. Restricting the optimisation search to these regions and employing certain genetic operators, the population of designs will tend on average to be more fit than the population of the previous generation. By allowing the genetic algorithm to operate for a successive number of generations, an optimal or near-optimal solution is obtained. Since the genetic algorithm starts its search with a number of different

random designs, it is less sensitive than Mathematical Programming methods to the pitfalls of local optima and non-convexity in the design space. Genetic algorithm operates solely on function evaluation and requires no gradient information. This makes it suitable for situations where the design space is discontinuous or gradient information is not available. The genetic algorithm also is ideal for the problems with discrete variables.

Much of the early research in the area of the genetic algorithm can be attributed to the work of J.H. Holland and his students at the university of Michigan, USA. Holland proposed the use of genetic algorithm as an efficient search mechanism in artificially adaptive systems [8]. Noting that the genetic algorithm is a form of adaptive system, this paper provided the elementary basis for genetic algorithm. In 1975, Holland published a book containing a compilation of the researches conducted by him and his students [9]. This book provided a mathematical foundation for much of the later research.

Significant contributions to the area of the genetic algorithm were also made by D E Goldberg. In his doctoral research [10], he used the genetic algorithm to optimise gas pipeline networks. Goldberg later described in his book [11], the theories and workings of the genetic algorithm. In recent years, genetic algorithm has been applied to a wide variety of disciplines including biology, computer science, engineering, social and physical sciences. More details regarding the theory and applications of the genetic algorithm can be found in textbooks [12-15].

1.4 GENETIC ALGORITHM AND STRUCTURAL OPTIMISATION

Genetic algorithm has been used for solving a variety of structural optimisation problems. The previous researches in relation to the optimisation of skeletal structures may be categorised as follows:

1. Sizing optimisation with fixed geometry and topology
2. Sizing and geometrical optimisation with fixed topology
3. Sizing and topology optimisation with fixed geometry
4. Sizing and geometrical as well as topology optimisation

1.4.1 Sizing Optimisation

As reported in the literature in the area of structural engineering, for the first time the genetic algorithm was employed by Goldberg and Samtani [16], where the genetic algorithm was

used to find the optimal design of a 10-bar truss. By this example, the capability of genetic algorithm in dealing with such optimisation problems was demonstrated. Rajeeve and Krishnamoorthy [17] proposed an algorithm as a modified version of the simple genetic algorithm developed by Goldberg [11]. In their work a new method for incorporating the constraint violations was proposed. The proposed approach was used for optimising a 3-bar truss, a 10-bar truss, a 25 bar space truss and a 160-bar transmission tower. Adeli [18] introduced a quadratic penalty function for transformation of constrained problem to an unconstrained one. A variant penalty function coefficient strategy was employed in Adeli's work. His proposed genetic technique was used for optimising a number of space trusses. Wu and Chow [19] introduced the steady state genetic algorithm in which a small percentage of the population of members needed to be replaced during each generation.

1.4.2 Sizing and Geometrical Optimisation

Jenkins [7] used the genetic algorithm for optimising the weight of a trussed-beam structure. He proposed a penalty function for involving the constraints and also a method for defining the fitness function. In his work both size and geometrical variables were involved. The values of the size variables were chosen from a set of discrete values. Wu and Chow [20] made some modifications to the simple genetic algorithm. They implemented the constraint normalisation and also fitness scaling. This modified genetic algorithm was applied to treat the discrete sizing and continuous geometrical variables simultaneously to find the minimum weight of the truss structures. A 15-bar plane truss and a 25-bar space truss were optimised using the proposed genetic technique. Yang et al [21] applied a genetic approach with tournament selection to optimise a number of trusses incorporating sizing and geometrical variables. In Yang's work a 18-bar cantilever plane truss and a 25-bar tower space truss as well as a 112-element dome subjected to stress constraints were optimised. In these examples the cross-sectional areas and coordinates of some of the nodes were considered as the independent variables of the problem.

1.4.3 Sizing and Topology Optimisation with Fixed Geometry

For discrete structures such as trusses, the topology means not only how nodes are connected to each other, but how many nodes are to be present. The choice of element connectivity as design variable leads to a discontinuous design space. In an evaluation of numerical optimisation methods for topological design, also the issue of size of the problem cannot be ignored. While, traditional non-linear programming methods have been employed

successfully in smaller problems, an increase in the number of design variables is detrimental to the efficiency of these optimisation techniques [22]. The optimal criterion method has been adapted with some success in larger problems [23]. The shortcoming of these techniques make the genetic algorithm an alternative technique for topology optimisation.

One of the most commonly used approaches for topology optimisation of skeletal structures is the ‘ground structure’ approach. This approach was first proposed by Dorn et al [24], where duality was used to formulate the optimal topology problem as one of the linear programming problems. This approach assumes an initial ground structure that contains many joints and connecting elements, namely, all the possible non-overlapping connections between the nodes. Some authors choose any given set of nodal connections for the ground structure [25].

Ohsaki [26] presented a genetic approach for topology optimisation of trusses with stress and displacement constraints. In his work, the nodal cost as well as the element cost was incorporated in the cost function. The cross-sectional area of each element was represented by a binary string. A topological bit was added to the left of each binary string to indicate the absence or presence of an element. A random number was generated to decide for the value of each topological bit in the members of the initial population. An element was to be removed if its corresponding topology bit was ‘0’ or its corresponding cross-sectional area became zero. The proposed genetic approach was used for a 20-bar truss, where the truss was subjected to two loading conditions and stress constraints. Ohsaki concluded that the optimal topologies with nodal cost might be quite different from those without the nodal cost.

1.4.4 Sizing, Geometrical and Topology Optimisation

Grierson and Pak [27] proposed a genetic approach for discrete optimal design of skeletal structural frameworks. In their study, an approximate re-analysis technique was presented for decreasing the computational effort required to evaluate the fitness values. The topological variability was accommodated by allowing the sizing variables to take zero values. That is, if a value of zero was assigned to a size variable, then its corresponding element was eliminated from the framework. In their work sizing, geometrical and topological variables involved and a couple of plane frameworks were optimised.

Hajela and Lee [22] described a genetic algorithm-based strategy for generating optimal structural topologies. This approach may be considered as a derivative of the ground structure

approach. In their work a two-stage optimisation process was introduced. At the first stage, a number of low weight but statically stable topologies were generated through the use of the genetic algorithm, ignoring the structural response constraints (stress, buckling, displacements). The second stage involved a number of resizing exercises with emphasis on the minimal weight and satisfaction of the response constraints. Actually, in this approach the structural topologies generated in stage 1 were used as seeds in stage 2. However, structural element removal or addition was permitted only to the extent that the resulting topology belonged to the subset of the stable topologies identified in stage 1. For stage 2, discrete variations in the cross-sectional areas were considered. The developed approach was used for a case in which a 14-bar truss was considered as the ground structure. In another example, the optimum topology was found for a bridge-type truss with 61 elements for the ground structure. In these examples the cross-sectional areas were treated as discrete variables. In Hajela's study the influence of geometry on the optimum topology was also included. In the examples solved in Hajela's work, element overlapping was permitted during the optimisation process.

In Rajan's work [28] the topology design variables were defined as Boolean design variables and included not only element connectivity, but also the support conditions. A '0' indicated that an element should not be considered during analysis or fitness evaluation. Similarly, the support conditions along a particular degree of freedom at a joint was also represented by a Boolean variable. A '0' was used to indicate that the degree of freedom was unconstrained. Rajan used a penalty approach to penalise the unstable structures and structures violating the constraints.

Rajeeve and Krishnammorthy [29] used a genetic technique for obtaining optimal design solutions simultaneously, considering topological, geometrical and sizing variables. In their proposed method both discrete as well as continuous design variables could be handled. The number of design variables for the optimal solution was unknown, but one should know the upper and lower limits of the number of variables. In this case, the number of the variables was treated as 'control variable' and different values of control variable defined different topologies. Formulation of the genetic model for such a problem resulted in strings of different lengths. In the presented work, a method was introduced for using the genetic algorithm in such a case. The proposed approach was used for obtaining the optimum

topology for a 10-bar cantilever truss. Also, a microwave antenna tower was topologically optimised.

Shetha and Ghabousi [30] proposed a methodology in which the structural designs were free to assume any geometry and topology. That is, the number and positions of nodes and the number and connectivity of elements were free of restrictions. They introduced the concept of physical design space, which was a special physical space within which the generated structures must be fully enclosed. This design space could have any arbitrary shape and might contain internal holes through which no part of the generated structures must pass. The physical design space allowed limits to be imposed on the geometry of generated structure, which was important for functional considerations. The structure could have any number of free nodes and then might have any number of elements with any pattern of nodal connectivity. In the illustrative examples, optimising the weight of the structure was considered as the objective. The element constraints were stress, slenderness ratio, minimum and maximum element length and element symmetry. The nodal constraints considered were nodal displacement and nodal symmetry. The performance of the proposed methodology was demonstrated on two simple examples of single-span plane trusses. The evolved shapes for these structures were in agreement with general engineering practice.

Deb and Gulati [31] proposed a representation scheme that allowed all three optimisations (namely, sizing, geometry and topology) to be used simultaneously. In order to make the solutions practically useful, they introduced a concept of basic and non-basic nodes which emphasized that the important nodes should be included in the optimised solutions. These important nodes were usually the ones which carried load or which supported the truss. Stress, deflection and static stability considerations were also added as constraints to find functionally useful trusses.

The proposed genetic technique assumed a 'ground structure' which was a truss with all possible element connections among all nodes (basic or non-basic). The presence and absence of an element was determined by comparing its cross-sectional area with a user predefined small critical cross-sectional area. Hence, the design variables of the optimisation problem were the cross-sectional areas of the elements present in the truss and the coordinates of all the non-basic nodes. A real-coded genetic algorithm was used. That is, variables were coded in real numbers rather than in binary strings.

1.5 BASE GRID VERSUS GROUND STRUCTURE

As reported in the literature, the ground structure approach has been used for rather small structures. This approach usually leads to the creation of configurations that may not be practically useful. Although, some of the researchers have tried to overcome this shortcoming by implementing some modifications. However, in the present work, the topology optimisation problem is dealt with from another point of view. Namely, a method is established by which only practical topologies are studied. A brief outline of the method is given below.

Consider the double layer grids whose plans are shown in Figs 1.1 to 1.4. In these figures the top layer elements are shown by thick lines and the bottom layer elements as well as the web elements are shown by thin lines. The grids shown in Figs 1.1 to 1.4 belong to a family of double layer grids with a square on square offset pattern. The grid of Fig 1.1 is the most dense grid of this family of double layer grids. In the case of the grids of Figs 1.2 to 1.4, they have been derived from the grid of Fig 1.1 by removing some of the elements. The removed elements are indicated by dotted lines. The grid of Fig 1.1 which is used for generating the other grids of this particular family, is referred to as the ‘base grid’. The base grid can itself be used for an actual structure, but in many practical cases its reduced forms are used.

It is desirable that the importance of each element of the base grid be expressible quantitatively, such that different elements of the base grid may be compared in terms of their importance. In the proposed method, a degree of ‘importance’ is assigned to each element of the base grid. The term ‘portancy’ is used to indicate this degree of importance. To find the portancy values of the elements of the base grid, the genetic algorithm is employed. The resulting portancies are numerical values between zero and one. To have a clearer view of the element portancies, a graphical method is used to indicate the portancies. The resulting graphical representation is called a ‘portancy map’. As an example, the portancy map obtained for the base grid of Fig 1.1 is shown in Fig 1.5. Also, the portancy values of a number of selected elements of the base grid of Fig 1.1 are listed in Table 1.1. The element numbers in Table 1.1 are indicated in Fig 1.1.

The portancy values can be used to compare the reduced grids of Figs 1.2 to 1.4 derived from the base grid. To this end, the summation of the portancies of the removed elements is

calculated for each reduced grid. Then, the reduced grids are compared with each other with respect to these summations. The results may be given as listed in Table 1.2.

Table 1.1 Portancy values for a number of elements of the base grid

Element number	26	50	211	344
Portancy value	0.01	1.00	0.53	0.70

As it is seen from Table 1.2, the reduced grid of Fig 1.2 has the smallest value of summation of portancies of removed elements in comparison with the other reduced grids. Then, it may be concluded that this reduced grid has lost the least number of important elements and, therefore, this reduced grid may be regarded as the most suitable reduced grid.

Table 1.2 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 1.2	5.2
Grid of Fig 1.3	11.8
Grid of Fig 1.4	10.1

Also, an optimisation process is carried out for the control of the reliability of the proposed method. To this end, the minimum weights of the reduced grids are obtained. It turns out that the results based on the weight optimisation, in almost all the cases, are consistent with the results obtained based on the portancy values. In other words, the reduced grid that has the best rank based on the comparison of the summations of the portancies has usually the lightest weight.

Fig 1.1 A base grid

Fig 1.2 A reduced grid

Fig 1.3 Another Reduced grid

Fig 1.4 Another reduced grid

Fig 1.5 Portancy map

CHAPTER 2

Genetic Algorithm

2.1 INTRODUCTION

Genetic algorithm is a numerical search technique, analogous to many of the processes of natural selection in the biological world. In nature, the evolution of populations occurs according to the principles of natural selection and survival of the fittest, as stated by Darwin. Based on these principles, individuals in a population compete with each other. Those that are most fitted to their environment have more chance to survive and will have relatively more offspring in the next generation. On the contrary, individuals having poor performance produce fewer offspring or even die out and produce no offspring at all. This means that the features of the most successful individuals in surviving will spread to an increasing part of the population.

Genetic algorithm works with a population of individuals in which each member of the population represents a possible solution for a given problem. Just like the natural genetics, the population of individuals evolves through mating between members. In what follows, the process of the genetic algorithm is described in some detail. To begin with, consider the function

$$y = f(x)$$

2.1

with the independent variable x being in the range

$$x_1 \leq x \leq x_2$$

2.2

Here, y is the dependent variable of the function and x_1 and x_2 are the lower and upper limits for the variable x , respectively.

Let it be required to find the maximum value of this function. For finding the value of the variable x corresponding to the maximum value of y , one may use a random number based method in which finding the maximum is carried out through a random selection of numbers. To elaborate, a set of random numbers are generated within the range of Eqn 2.2, and the function is evaluated for these numbers. Then the values obtained for the function are compared with each other and the largest of them is chosen as the maximum. The question may then arise as how can one be sure that the chosen result is actually the maximum.

The approach may be employed in two ways:

1. choosing a very large number of random values for variable x in its range, and evaluating the function for all of them to find the best solution for maximum, or
2. using a multi-stage approach, in which at first some random numbers within the range are generated and the best of them is found. Then a new set of random numbers is generated. The best solution of this set is compared with the best of the previous one, and the larger of them is saved. The approach continues in a number of iterations. The best solution obtained after a number of iterations is accepted as the maximum.

The first of the above suggestions may be acceptable as a method for simple problems. However for complicated cases and those that involve many variables, this method may prove to be inefficient. For the cases that the cost for function evaluation is high, this is not a suitable approach either. As far as the second method is concerned, a point that should be noted is that in each stage the set of randomly chosen values for x are independent of those that were chosen in the previous stage. This means that the results obtained in one stage are not used for guiding the process of choosing the points in the next stage. That is, no 'evolution' is involved in this method. Hence, many iterations may need to be carried out without any guarantee to get close to the maximum. One could consider many other variations of the above approaches, some of which may be suitable in particular cases. However, a much more suitable approach to the problem is that of the 'genetic algorithm'.

Genetic algorithm is a robust and efficient numerical search method that can deal with many optimisation problems. This algorithm works through an evolutionary strategy and this makes the method different from the approaches discussed before. The idea of the genetic algorithm is introduced in terms of an example.

2.2 ILLUSTRATIVE EXAMPLE

Consider the function

$$y = 2x(\sin x)(\sin 4x)$$

2.3

with the independent variable x being in the range

$$43 \leq x \leq 49$$

2.4

Here, y is the dependent variable and x is the independent variable, in radian. The coordinates of the global maximum point of the function are:

$$x = 48.3272512 \quad \text{and} \quad y = 89.7427884$$

The global maximum point is indicated in Fig 2.1. To show how the maximum for the function of Eqn 2.3 can be found by the genetic algorithm, the procedure is described in the sequel in a step-by-step manner.

Fig 2.1

2.3 INITIATION

In the context of the genetic algorithm, each value of x within the range is called an individual. Genetic algorithm starts with the choice of some individuals. Each value of x is generated using a random number generator (see Appendix A). The set of the chosen values of x is called a ‘population’ and each randomly generated value for x is called a ‘member’ of this population. The size of the population is the number of the members that constitute the population. For the case under consideration, an initial population with ten members is generated. The randomly generated values, that is, the members of the initial population are shown in the second column of Table 2.1. The values chosen for x are within the range given by Eqn 2.4.

Table 2.1 Initial population and corresponding fitness values

Member number	Randomly generated value of x	Fitness value (Value of y)
1	46.00185	80.81937
2	47.55866	-39.49779
3	43.21543	4.44075
4	48.24687	84.87343
5	44.94981	-49.28445
6	44.71675	12.12936
7	44.97852	-56.39631
8	43.79992	10.58896
9	45.22075	-83.01325
10	47.67090	-40.43994

2.4 PAIRING

The function introduced by Eqn 2.3 is known as the ‘fitness function’. This function is evaluated for the ten different values of the independent variable x , as given in Table 2.1. These values of y are referred to as the ‘fitness values’. The fitness values for the members of the initial population are given in the third column of Table 2.1.

The fitness value corresponding to each member of the population is a measure of the suitability of that member as a solution for the problem. The large differences between the

fitness values given in Table 2.1 indicate major differences between the members of the population in providing a solution for the problem. Since the search here is for finding the maximum of y , the members having larger fitness values are more suitable. That is, a member with the greatest value of y is closest to the required maximum value. For the initial population in this example the fourth member has the largest fitness value, as shown in Table 2.1. This value corresponds to point C as indicated in Fig 2.1.

At this point, the members of the population are chosen to act as parents to produce children. Different methods have been developed for selecting the parents. In the approach followed in the present work, the parents are chosen using the so called process of ‘tournament pairing’. In this process, each parent is selected through a competition between two randomly chosen members. To this end, two random integer numbers i and j between one and N_p (size of the population) are generated. Then the fitness values of the i^{th} and j^{th} members are compared. The fitter member is selected to be one of the parents. The other parent is chosen in a similar way. In this context member with the greater fitness value will be chosen because the objective is to find the maximum. In contrast, if the minimum is of interest, the member with smaller value is considered to be the fitter one and will be chosen as a parent.

For example, consider the case in which the randomly generated numbers i and j are 1 and 5. Therefore, the 1st and 5th members of the population are chosen to compete with each other. Referring to column 3 of Table 2.1, it is observed that the fitness values for members 1 and 5 are

$$y_1 = 80.81937 \quad \text{and} \quad y_5 = -49.28445,$$

respectively. This implies that member 1 should be chosen as the first parent. If the other two randomly chosen numbers are 2 and 4, then comparing the fitness values of the corresponding members leads to the choice of member 4 as the second parent. Thus, the chosen pair to act as parents will be members 1 and 4.

2.5 MATING

The population of members evolves through implementing the mating process. Mating takes place between the two parents selected by the tournament pairing for producing two children. These children are usually different from the parents, and will become the new members of the population. The mating is carried out in four stages.

2.5.1 Encoding

Each parent has its own characteristics, and it is expected that some of these characteristics are transferred to the children. To indicate the characteristics of the parents more clearly, they are encoded. The encoded result for a parent is referred to as a 'chromosome'. This means that like natural genetics each parent is represented by its corresponding chromosome (s). Different methods may be used for encoding. In this work a binary alphabet is used. Thus, a string of binary numbers represents each of the two parents. Each of the binary digits, which are '0' or '1', is called a 'gene' and corresponds to a gene in the natural genetics. As an example consider a 16 bit binary chromosome given as

1010101110001011

This chromosome consists of nine '1' digits and seven '0' digits each of which called a gene. The 'length' of the binary chromosome is equal to the number of the genes. For the chromosome given above, the length is equal to 16. The equivalent integer decimal value for this chromosome is calculated as follows:

$$e = 1 \times 2^{15} + 0 \times 2^{14} + 1 \times 2^{13} + 0 \times 2^{12} + 1 \times 2^{11} + 0 \times 2^{10} + 1 \times 2^9 + 1 \times 2^8 + 1 \times 2^7 + 0 \times 2^6 + 0 \times 2^5 + 0 \times 2^4 + 1 \times 2^3 + 0 \times 2^2 + 1 \times 2^1 + 1 \times 2^0 = 43915$$

Thus, the above binary chromosome represents the value of 43915. In other words, the above binary chromosome is the encoded form of the number 43915

Different lengths may be considered for a binary chromosome. In this work, a length equal to the numbers of the bits in a 'word' of computer is considered for the binary strings, typically 32. With the length of the chromosomes taken as 32, then 2^{32} different binary strings are available. The equivalent integer decimal values for these strings lie in the range of 0 to $2^{32}-1$.

Returning to the case under consideration related to Eqn 2.3 and Fig 2.1, the lower and upper limits of the variable x of Eqn 2.3 are mapped into 0 and $2^{32}-1$, respectively. Intermediate values of x are mapped into a value like e , which is calculated using the following equation

$$e = \text{Round} \left(\frac{(x - x_1) \times (e_2 - e_1)}{x_2 - x_1} + e_1 \right) \quad 2.5$$

Where, e is the equivalent integer decimal value for a binary string that will represent a parent with the floatal value of x . The minimum and maximum of the equivalent integer decimal

values for the binary strings are shown by $e1$ and $e2$, respectively. For a 32 bit binary string, $e1$ and $e2$ are equal to 0 and $2^{32}-1$, respectively. The terms $x1$ and $x2$ are the lower and upper limits of the variable x . In Eqn 2.5 ‘Round’ denotes the function that rounds a number to an integer value. The encoding process is illustrated in Fig 2.2. As indicated in this figure, the lower and upper limits of the independent variable x , that is, $x1$ and $x2$ are mapped into $e1$ and $e2$ and an intermediate value like x is mapped into e .

Fig 2.2 Encoding

For example, the two chosen parents by the pairing process (members 1 and 4) with their values as given in Table 2.1, that is,

$$x_{m1} = 46.00185 \quad \text{and} \quad x_{m4} = 48.24687,$$

will be mapped into

$$e_{m1} = 2148805376 \quad \text{and} \quad e_{m4} = 3755854592,$$

respectively. Where the subscripts m1 and m4 imply member 1 and member 4. The values of e_{m1} and e_{m4} are the equivalent integer decimal values for the two binary strings of length 32 bits, corresponding to the 1st and 4th members. These binary strings that are considered as the parent chromosomes representing the two selected members of the population are as follows:

Parent chromosome (1)	10000000000101000010101100000000
Parent chromosome (2)	11011111110111011100101100000000

2.5.2 Crossover

The most important operator of the genetic algorithm is the ‘crossover’ [12]. Crossover operates on two chromosomes that are produced in the preceding stage and swaps some of

their genes. This interchange of the genes, leads to the creation of two new chromosomes. These chromosomes represent two new individuals, like the children produced through mating between parents in nature. When crossover takes place, the two new chromosomes will consist of parts of the chromosomes of the parents, as the children inherit some of each of the parent's genetic material.

Crossover may be carried out in different ways. The popular method of crossover, namely 'point crossover' is described here. In this method, two chromosomes are taken and cut at a randomly chosen 'site'. That is, each chromosome is divided into two segments. At this stage, right-hand side segments of the chromosomes are swapped. To elaborate further, consider the two binary strings that are the chromosomes of members 1 and 4 of the population, produced in the encoding stage. A 'crossover site' k is selected randomly, between 1 and the string length minus 1, that is, between 1 and 31. Suppose that k is found as 5, so the segments of the two strings containing the genes in positions 6 to 32 are swapped. The resulting chromosomes represent two children. The process is shown in Fig 2.3. As shown in this figure, the exchanged genes of the child chromosomes are shown in bold. Since the crossover operates in a probabilistic manner then the gene exchanging between the parents may lead to producing children that have better performance, that is, represent members that are closer to the optimum.

Fig 2.3 Point crossover

2.5.3 Mutation

Crossover leads to the creation of two children that contain only the genes that were in the parents. Since the population size is limited then despite the operation of the crossover, it is possible that the genes corresponding to the ideal solution do not appear in any of the children. From another point of view, the genetic algorithm is an iterative search technique.

This means that the processes of pairing and mating occur iteratively. Gradually, the similarity of the members of the population grow, that is, the process converges to a particular solution, which may not be the global optimum. As an example, for the function whose curve is given in Fig 2.1 it may converge to point B, which is a local maximum.

‘Mutation’ is a genetic operator which is implemented to prevent the problem mentioned above. This operator occasionally changes the produced children by exchanging some of their genes. Mutation preserves the diversity of the population by introducing new members and also prevents the premature convergence. Mutation occurs probabilistically according to a chosen rate. If the mutation rate per number of the handled genes is μ , it implies that the probability for the mutation of a gene is μ . That is, if the total number of the handled genes is n and if n is large, then approximately $n\mu$ genes will be mutated. For instance, a typical value of 0.005 for μ implies that the number of the mutated genes for every 1000 genes handled is around 5. In relation to the example under consideration, in which, a child chromosome contains 32 genes, the procedure for mutation is carried out as follows.

For each gene of a child chromosome produced by crossover a random number between 0 and 1 is generated. If this random number is less than μ , then the corresponding gene is mutated. That is, the value of the gene is changed (a 1 is changed into 0 and a 0 is changed into 1).

Applying this process to the example under consideration, in one occasion for the second child the randomly generated number corresponding to the gene lying at the 13th position from the right was less than the mutation rate. The mutated gene is shown below in bold.

Child chromosome (2) 11011000000101000011101100000000

2.5.4 Decoding

The two new chromosomes that are produced through crossover and mutation represent two children. Each of these chromosomes corresponds to a value for the independent variable x . However, chromosomes are in a binary form. The corresponding decimal values are found through the decoding process, using the equation

$$x = \frac{(e - e1) \times (x2 - x1)}{e2 - e1} + x1 \quad 2.6$$

Where, x is the decimal value corresponding to a child and e is the equivalent integer decimal value of the chromosome representing that child. The minimum and maximum of the equivalent integer decimal values for the binary strings are $e1$ and $e2$, respectively. The terms $x1$ and $x2$ are the upper and lower limits of variable x . The decoding process is illustrated in Fig 2.4

Fig 2.4 Decoding

The two child chromosomes obtained in the previous stages are shown again below.

Child chromosome (1)	10000111110111011100101100000000
Child chromosome (2)	11011000000101000011101100000000

The equivalent integer decimal values for these binary chromosomes are

$$e_{c1} = 2279459584 \quad \text{and} \quad e_{c2} = 3625204480$$

where, the subscripts $c1$ and $c2$ imply child 1 and child 2. Using Eqn 2.6, the values for the children that are represented by the two new chromosomes are calculated as:

$$x_{c1} = \frac{(2279459584 - 0) \times (49 - 43)}{(2^{32} - 1) - 0} + 43$$

or

$$x_{c1} = 46.18437$$

and x_{c2} is calculated in a similar way as

$$x_{c2} = 48.06435$$

2.6 REPLACEMENT

The two children created through the mating process, explained in Section 2.5, are placed in the population as new members. To this end, two current members of the population are replaced by the new ones. The members chosen for replacement are the two least fit members of the population.

In the case of the example under consideration, the 7th and 9th members of the initial population have the least fitness values. These members together with the corresponding fitness values are shown in bold in Table 2.2. Then, these two members are eliminated from the population and are replaced by the new children. The population after replacement is given in Table 2.3.

Table 2.2 Initial population and two least fit members

Member number	Population members (Value of x)	Fitness value (Value of y)
1	46.00185	80.81937
2	47.55866	-39.49779
3	43.21543	4.44075
4	48.24687	84.87343
5	44.94981	-49.28445
6	44.71675	12.12936
7	44.97852	-56.39631
8	43.79992	10.58896
9	45.22075	-83.01325
10	47.67090	-40.43994

Consequently, by the replacement process two new members enter the population and two members die out. Referring to Table 2.3 it is observed that in this occasion, the fitness values of the new members are greater than the fitness values of the selected members for replacement. That is, the new members are fitter than the members that have been replaced. However, it should be noted that the new children may be less fit than the worst members of the population. But, even in such a case, the replacement is carried out as usual and the new children replace the two least fit members. This strategy is prudent because the new children may contain some ‘good genes’ that may improve the performance of the genetic algorithm.

As another adopted strategy, the fittest member of the population is preserved and is not replaced with new children. However, the fittest member may be updated and altered by a new member with greater fitness value that may enter the population.

Table 2.3 Population after Replacement

Member number	Value of x	Fitness value (Value of y)
1	46.00185	80.81937
2	47.55866	-39.49779
3	43.21543	4.44075
4	48.24687	84.87343
5	44.94981	-49.28445
6	44.71675	12.12936
7	48.064354	45.13744
8	43.79992	10.58896
9	46.18437	43.11304
10	47.67090	-40.43994

2.7 TERMINATION

The steps explained in Sections 2.4 to 2.6 are carried out in an iterative manner. Each iteration is referred to as an ‘evolution cycle’ and consists of the processes of ‘pairing’, ‘mating’ and ‘replacement’ as shown in Fig 2.5.

In each cycle, two children are produced and these replace two members of the population. When the number of the produced children is equal to the size of the population (N_p), then one ‘generation’ is considered to have been completed.

Fig 2.5 Evolution Cycle

Table 2.4 lists the members of the population and the corresponding fitness values, for the current example relating to the function of Eqn 2.3, after one generation is completed, that is, after the evolution cycle has been repeated for 5 times. Referring to Table 2.1, it is seen that in the initial population, the randomly generated members are scattered between the lower and upper limits of the independent variable x (43 to 49). Also, the corresponding fitness values vary in a wide range (-83.01325 to 84.87343). However, as may be seen from Table 2.4, after one generation the members of the population are congregated around some points. To investigate these points, the curve of Figure 2.1 is shown again in Fig 2.6. From Table 2.4 it may be seen that six members with values of x around 43.5 are close to point D of the curve of Fig 2.6, which is a local maximum. Also, two members with values of x around 46 are close to point B, which is another local maximum. Finally, two members of the population with values around 48 are close to point A, which is the global maximum. Comparing with the members of the initial population in Table 2.1, after one generation some of the members have become closer to the maximum points. After 8 generations the value of $y = 87.03790$ is obtained for the fittest member. After 20 generations all ten members of the population congregate around 48.32725 with fitness value equal to 89.74279. From the above description, it can be seen that as the genetic process proceeds, the fitness value of the fittest member of the population increases gradually and the best one becomes close to point A, that is, the global maximum.

The history of the variations of the fitness values of the best members of the generations for two runs the genetic process are shown in Fig 2.7. The curve specified as attempt 1, indicates the history of the variations for the case whose details were explained above. As shown in Fig 2.7, since the genetic process operates in a stochastic manner, the history of the variations for the two attempts are not identical. It may also be seen from this figure that for some successive generations (in particular, generations 6 to 11 of the second attempt) no improvement is achieved, but by continuing the process the solution is improved.

In general, the exact position of the maximum point is unknown, then the process should be terminated if no improvement is achieved during a number of successive generations. That is, if the difference between the best fitness values is small enough, it may be concluded that no improvement of the fitness values is expected anymore. In this case, the current best member of the population is taken as an 'acceptable solution'. For instance, as shown in Fig 2.7, in attempt 1, after 30 generations the curve representing the variations of the best fitness value

assumes a long flat slope. In the present work, the following equation is used as the convergence criterion for the termination of the process.

$$abs\left(\frac{b_i - b_{i-1}}{b_i}\right) \leq \varepsilon \tag{2.7}$$

Where,

- b_i and b_{i-1} are, respectively, the fitness values of the best members of the populations in the i^{th} and $(i-1)^{th}$ generations,
- ε is a small value, called the ‘convergence limit’ with a typical value of 1 E-6 and
- abs denotes the absolute value function.

Here, a question may arise, namely, could the process be terminated if the convergence criterion of Eqn 2.7 is satisfied for any two successive generations? This question is discussed below.

Table 2.4 Population after one generation

Member number	Value of x	Fitness value (Value of y)
1	43.56726	34.99488
2	43.56711	35.00437
3	43.56724	34.99562
4	45.96156	84.19287
5	48.248125	85.02154
6	45.96156	84.19289
7	43.56502	35.140875
8	43.56726	34.99487
9	48.40350	85.19215
10	43.54110	36.48863

Referring to Fig 2.7, it is seen that in attempt 2 the fitness values of the best members of generations 6 to 11 are almost the same. For more clarity, this part of the curve is magnified in Fig 2.7. Also, the best fitness value for generation 6 to 12 are given in Table 2.5. It is seen from the results given in Table 2.5 that the best fitness values of generations 6 to 9 are the same and also these values for generations 10 and 11 are identical. The convergence test of Eqn 2.7 is satisfied for each of the two successive generations in generations 6 to 11.

Fig 2.6

However, as it is seen from Table 2.5, in generation 12 the fitness value of the best member of the population is increased to 88.97125. That is, a considerable improvement is achieved for the best member of the population by continuing the genetic process. This means that only one time satisfaction of the convergence test should not be considered as enough to terminate the process.

Table2.5 Best fitness values

Generation number	Best fitness value
6	87.41229
7	87.41229
8	87.41229
9	87.41229
10	87.41232
11	87.41232
12	88.97125

In the present work, if Eqn 2.7 is satisfied for a number of successive convergence tests, say 20, then the process is terminated. The required number of the successive satisfactions of the convergence test is referred to as the ‘confirmation count’. Thus, the convergence test is

carried out after each generation. If it is satisfied consecutively as many times the confirmation count, the genetic process is terminated and the best fitness value of the last generation is taken as the solution. Assuming the value of 20 for the confirmation count, in attempt 1 of Fig 2.7, after 57 generations the algorithm converged to

$x=48.327253$ $y=89.74279$

In attempt 2 the process converged after 65 generations to

$x=48.32410$ $y=89.74013$

as shown in Fig 2.7.

Fig 2.7 History of fitness value for the best member

The maximum number of generations is another criterion that is checked for the termination. Thus, if Eqn 2.7 is not yet satisfied after a specified ‘maximum number of generations’, then the process is terminated. For example, if the maximum number of generations is specified as 500, the optimisation process is terminated after 500 generations even if the convergence the criterion is not satisfied. In this case, the best fitness value of the generation 500 is accepted as solution.

2.8 FURTHER DISCUSSION OF THE GENETIC OPERATORS

2.8.1 Significance of Mutation

Returning to the history of variations for attempt 1, for generations 8 to 10, all the members of the population have the value of x equal to 48.26764 with fitness value of 87.03790. The chromosome representing all of these members is

11100000110000001011000000000000

In this case, since all the members have the same chromosome then the operation of the pairing and crossover produce children that are identical to their parents. In this occasion in generation 11 a mutation changed the 25th bit from the right-hand side of a chromosome that had been selected for mating. That is, this gene was changed from 0 to 1. This child chromosome is given below, where the mutated gene is shown in bold.

11100001110000001011000000000000

This chromosome represents a new member with value of x equal to 48.29108 with the fitness value of 88.73727. This demonstrates that when the genetic process comes to a halt, mutation may save it from stagnation by introducing new members through changing some of the genes.

2.8.2 Two-Point Crossover

As described in section 2.5.2, in operating the point crossover, two parent binary chromosomes are cut at one randomly chosen site and each of them is divided into two segments. Then, the genes of the segments of the parent chromosomes on the right-hand side of the chosen site are exchanged. Another possible method of crossover is a 'two-point crossover', where each parent chromosome is cut at two randomly chosen sites. To illustrate this, consider the two selected parent chromosomes given in Fig 2.8. Suppose that the two randomly chosen sites are at positions 5 and 23, as shown in the figure. This divides the chromosome into three segments. Then the segments between the two sites are swapped. The chromosomes representing the children are shown in the Fig 2.8. The exchanged genes are shown in bold.

In general, a 'multi-point crossover' may be carried out where, a specified number of sites, say k , are selected randomly. Thus, each parent chromosome is divide into $k+1$ sites. Then, every other segment is swapped.

Fig 2.8 Two point Crossover

2.8.3 Uniform Crossover

The ‘uniform crossover’ is another type of crossover in which some of the genes of the parent chromosomes are selected randomly and are exchanged. To this end, in the case of 32 bit binary chromosomes, first a 32 bit string, called the ‘mask’ is generated randomly. Then, the genes of the parent chromosome whose corresponding digits in the mask are ‘0’ are exchanged. As an illustrative example consider the parent chromosomes and the randomly generated mask given in Fig 2.9. The resulting child chromosomes are also shown in this figure. The exchanged genes are shown in bold.

Parent chromosome (1)	10000000100101000010101100111100
Mask	00100000001000000001011010110110
Parent chromosome (2)	11011101110111111100101101000000
Child chromosome (1)	11011101110111111100101101110100
Child chromosome (2)	10000000100101000010101100001000

Fig 2.9 Uniform Crossover

2.9 EFFECTS OF THE GENETIC OPERATORS

Suppose that the genetic process is repeated for a number of times. Since, the genetic algorithm is a stochastic process, then the obtained solutions are not expected to be exactly the same. However, it is reassuring if the obtained results are close to each other and are congregated around the global optimum. On the other hand, it is possible that the genetic process has a premature convergence to a local optimum that may be far away from the

correct solution. In this relation, the effects of some of the genetic parameters such as the ‘mutation rate’ and the ‘population size’ on the performance of the genetic algorithm are investigated.

Let the genetic process be repeated for 500 times to find the maximum of the function of Eqn 2.3, whose related curve is given in Fig 2.6. In this case, the point crossover is employed and the following parameters are used:

mutation rate $\mu = 0.001$ and population size $N_p = 10$

On one occasion, the number of the times that the solution converged to a local maximum was equal to 275. That is, for 275 times the genetic process was terminated with a premature convergence. These solutions converged to points around the local maximums B, C and D of the curve shown in Fig 2.6. In this case, 211 solutions converged to points around B and 27 of the solutions converged to points around C. The number of the solutions converging to points around D was equal to 37. The genetic process was executed again for 500 times but with a value of 0.005 for the mutation rate. Consequently, the number of the solutions with premature convergence was reduced to 251. It is seen that by increasing the mutation rate the probability of the convergence to a local maximum is decreased. Although even for a mutation rate equal to 0.05, around 189 of the solutions converged to a point around the local optimum. This means that only increasing the mutation rate is not sufficient to prevent the algorithm to be trapped into a local maximum.

Now, the investigation is continued by increasing the size of the population and running the genetic process with the same values of the mutation rate. With the population size of 50 and the mutation rate of 0.001 the number of the solutions that converged to points around a local maximum was 96. Increasing the mutation rate to 0.05 lead to 70 solutions with premature convergence. With values of 100 and 0.05 for N_p and μ , respectively, in 5 cases premature convergence occurred for the example under consideration. Table 2.6 lists the results for different values of the mutation rate and the population size. In this table LO stands for the number of the solutions that converged to points around a local maximum.

The same procedure was carried out with the two-point and uniform crossover. The results are given in Tables 2.7 and 2.8. In relation to premature convergence, the results in Tables 2.6 to 2.8, indicate that the performance of the genetic algorithm with two-point crossover, in this

case, is better than point crossover and uniform crossover. For instance, with the values of 50 and 0.005 for N_p and μ , respectively, no premature convergence for the example under consideration was observed for the two-point crossover.

Table 2.6 Results for point crossover

	$\mu=0.001$				$\mu=0.005$				$\mu=0.05$			
N_p	10	20	50	100	10	20	50	100	10	20	50	100
LO	275	201	96	22	251	182	70	11	189	163	38	5

The investigation carried out in relation to the effects of the genetic operators may give rise to the following conclusions

- Increasing the mutation rate or the population size decreases the probability of premature convergence to a local optimum.
- Two-point crossover has a better performance than the other two variations used

Table 2.7 Results for two point crossover

	$\mu=0.001$				$\mu=0.005$				$\mu=0.05$			
N_p	10	20	50	100	10	20	50	100	10	20	50	100
LO	81	26	0	0	65	20	0	0	15	0	0	0

However, it should be noted that the values for the mutation rate and the population size are problem dependent. That is, for a particular problem, the genetic algorithm should be tuned by choosing appropriate values for these parameters. Another point to be noted is that by choosing a high rate for the mutation, the algorithm deteriorates into a random search and it moves away from being an evolutionary technique.

Table2.8 Results for uniform crossover

	$\mu=0.001$				$\mu=0.005$				$\mu=0.05$			
N_p	10	20	50	100	10	20	50	100	10	20	50	100
LO	273	193	65	9	266	188	34	7	209	154	24	1

2.10 GENETIC ALGORITHM AND CONSTRAINED PROBLEMS

As indicated in the previous sections, to find the maximum of the function given in Eqn 2.3, a member of a population in the process of the genetic algorithm could take any value within the range for the independent variable x without any restriction. In this case, the problem is said to be an unconstrained optimisation problem. However, in some problems the optimum should be found such that some constraints are satisfied. The general form of a constrained optimisation problem may be given as follows:

$$\begin{aligned}
 &\text{Minimise (Maximise)} && f(X) \\
 &\text{Subject to} && h_i(X) = 0 && i = 1, 2, \dots, n_e \\
 &&& g_j(X) \leq 0 && j = 1, 2, \dots, n_g
 \end{aligned}
 \tag{Eqn 2.8}$$

where,

- $X = [x_1 \ x_2 \ \dots \ x_n]^T$ is the vector of the design variables,
- $h_i(X)$ is the i^{th} equality constraint and
- $g_j(X)$ denotes the j^{th} inequality constraint.

In Eqn 2.8 n_e and n_g represent, respectively, the number of the equality and inequality constraints. The constraints divide the search space into two domains, the feasible domain where the constraints are satisfied and the infeasible domain where one or more of the constraints are violated.

As an illustrative example, let the fitness function and the constraint be given as follows:

$$\begin{aligned}
 f(x) &= 0.5x \\
 g(x) &= 4 - x
 \end{aligned}$$

In this case, there is no equality constraints and the objective is to minimise $f(X)$. Then, this constrained minimisation problem can be expressed as follows:

$$\begin{aligned}
 &\text{Minimise} && f(x) = 0.5x \\
 &\text{Subject to} && 4 - x \leq 0
 \end{aligned}$$

The functions $f(x)$ and $g(x)$ are represented by two straight lines as shown in Fig 2.10. The true minimum satisfying the constraint is found for x equal to 4 as shown in the figure.

Fig 2.10

In the process of the genetic algorithm, one approach in finding the best feasible solution is to check each member of the population for constraint violations. If constraints are not violated then the corresponding member is considered as a feasible solution. Continuing with this approach, the feasible solutions are compared and the best of them is chosen as the optimum solution. In this approach, no account is taken of the extent of the violation of the constraints by the members of the population. The main problem with this approach is that it is usually very time consuming.

Another approach is to find an initial population of feasible solutions and continue to generate new feasible members from this population. This approach suffers from the drawbacks of the previous approach. In addition, there is no guarantee that the individuals produced through the mating remain feasible.

However, there are some approaches in which the members of the population that violate the constraints are not rejected. The reason is that the genes of these violating members may be useful in improving the search. One approach, which is commonly used, transforms the

constrained problem into an unconstrained one. Thereafter, the unconstrained problem is optimised such that the solution is the same as for the constrained problem.

In this work, for converting the constrained problem into an unconstrained one, a method called ‘penalty function’ is employed. In this method, rather than trying to solve the constrained problem, a ‘penalty term’ representing the severity of the violation of the constraints is added to the original fitness function $f(X)$. Using the penalty function method, the general form of the unconstrained problem becomes

$$F(X) = f(X) + P(X) \quad 2.9$$

where,

- $P(X)$ is the ‘penalty term’ which is zero for a feasible solution and
- $F(X)$ is the fitness function for the unconstrained problem and is called ‘pseudo-fitness’ function.

If $F(X)$ is minimised and $P(X)$ is zero, it can be concluded that the minimum of $f(X)$ is found. Generally, two categories of penalty function formulations may be considered as follows:

1. ‘Interior penalty function methods’ in which the search for finding the optimum solution starts from a point in the feasible region. In this case, the algorithm converges to the optimum solution from the interior side of the acceptable domain.
2. ‘Exterior penalty function methods’ where, all intermediate solutions lie in the infeasible region and the algorithm converges to the solution from the outside.

In the case of an interior penalty function method the advantage is that one may stop the search and end up with a feasible solution. One drawback for such a method is that the algorithm should start with a feasible solution. For an exterior penalty function method the advantage is that the solution may be started from an infeasible point. A major shortcoming is that the search cannot be stopped with a feasible solution before the optimum is reached.

Here, the exterior penalty function that may be easily used by the genetic algorithm is explained in more detail. A number of penalty functions have been developed by various

researchers. In this work, a ‘quadratic penalty function’ is employed that imposes a penalty which is proportional to the square of the violation. Thus, the constrained optimisation of Eqn 2.8 is replaced by:

$$\begin{aligned} \text{Minimise} \quad & F(X, r) = f(X) + r \sum_{i=1}^{n_t} h_i^2(X) + r \sum_{j=1}^{n_c} \left[(g_j(X))^+ \right]^2 \\ & r = r_1, r_2, \dots, \quad r \rightarrow \infty \end{aligned} \quad \text{Eqn 2.10}$$

where, $g_j(X)^+$ means

$$g_j(X)^+ = \begin{cases} g_j(X) & \text{if } g_j(X) > 0 \\ 0 & \text{if } g_j(X) \leq 0 \end{cases} \quad \text{Eqn 2.11}$$

The positive multiplier ‘r’ performs the weighting between the objective function value and the penalty term and it is often called ‘penalty parameter’ or ‘response factor’. The reason that the constraint violation is squared is that this provides a slope of zero for the penalty at the constraint boundary, thereby ensuring a continuous slope of the pseudo-fitness function, $F(X, r)$.

Minimisation of $F(X, r)$, as an unconstrained fitness function is performed for a sequence of values of r such that the solution is forced to that of the constrained problem. In practice, an initial value for r is chosen and the minimum of F is found. The solution might be any point, not necessarily a feasible one. If the obtained solution is in the feasible domain the result is the optimum, otherwise r is increased and $F(X, r)$ is minimised again. The steps of increasing the values of r and minimising the function of $F(X, r)$ are repeated until the optimum point is in the feasible domain.

Returning to the example under consideration, the fitness function that should be minimised by the genetic algorithm will become.

$$F(X, r) = 0.5x + r \left[(4 - x)^+ \right]^2$$

Now, the genetic process is performed as usual to find the minimum of F . Suppose that the initial value of r is taken to be 0.2. Then, a value equal to 1.6875 is found for the minimum of F with a value of 2.7501 for x . This point lies in the infeasible region. By increasing r to 1 the

minimum is found at $x=3.752$ with the value of 1.9375 for F . If r is chosen to be 100, then the value of 3.9975 is obtained for x . At this point the constraint violation is equal to

$$4-3.9975=0.0025$$

Fig 2.11 shows the graphs of F for different values of r . The minimum points obtained for the pseudo-fitness functions associated with the values of 0.2 and 1 for r are shown in this figure. It can be seen from this figure that by increasing the value of r the minimum of F moves closer to the constraint boundary. It seems that to avoid an excessive number of minimisations of F , a large initial r is desirable. However, it would be better that a small initial value is considered for r and it is increased moderately. This is based on the following discussion.

Fig 2.11 Graphs for pseudo-fitness function

It is seen from Fig 2.11, that as r is increased, the curvature of F also increases. High values of curvature often lead to numerical difficulties for finding the minimum. That is, an ill-conditioning is associated with a large curvature. For instance, as shown in Fig2.11, the curve representing F associated with $r = 100$, has a large curvature at the neighbourhood of the

constraint boundary and finding the minimum in this case is more difficult than for a smooth curve. So, it is reasonable that the algorithm starts with a small value for r and if the obtained minimum point is not in the feasible region, then the value of r is increased and the optimisation process is carried out again. A flow chart for the process of the constrained optimisation by the genetic algorithm is given in Fig 2.12.

2.11 GENETIC ALGORITHM IN STRUCTURAL OPTIMISATION

The optimal design of structural systems can be classified as sizing optimal design, shape optimal design and topology optimal design. The nature of the design variable determines the type of the optimal design problem. In each type of optimal design, the objective function may be the weight or a structural response such as the frequency.

2.11.1 Sizing Optimal Design

In sizing optimal design problems, the independent variables are sizing parameters such as the cross-sectional areas or the moment of inertia of the elements. These variables may be assumed to be available as either continuous or discrete values.

2.11.2 Shape Optimal Design

In shape optimal design problems, the shape or the geometry of the structure is allowed to vary through nodal coordinates which may be taken as independent variables of the problem.

2.11.3 Topology Optimal Design

For discrete structures such as trusses topology relates to how many nodes are placed in the structure and how the nodes are connected to each other. In general, for topology optimal design, the number of the nodes and also the number of the elements connecting the nodes may vary.

In some cases, a combination of different types of optimal design may be carried out. That is, the size, shape and topology may vary during the optimisation process.

2.11.4 Illustrative Example

Consider a four bar truss, as shown in Figure 2.13, which is subjected to two vertical loads as shown. The objective is to minimise the weight of the structure by varying the cross-sectional areas of the elements as well as the coordinates of joint 1. That is, the sizing and shape

Fig 2.12 Flow chart for constrained optimisation

optimisation is carried out simultaneously. Here, the fittest structure will be the one with the least weight.

The coordinates of joint 1 are

$$x = 3.00 + \Delta x \quad y = 0.000 + \Delta y$$

where, Δx and Δy are assumed to vary within the range

$$-1.500m \leq \Delta x \leq +1.500m \quad \text{and} \quad -1.500m \leq \Delta y \leq +1.500m$$

The range is shown by dotted lines in Fig 2.13

Fig 2.13 A four bar truss

The cross-sectional areas, so called 'size variables', are discrete values and are chosen from a list of twelve possible values, as given in Table 2.9. Here, the optimisation process involves six variables. Four of these variables correspond to the values of the cross-sections of the elements of the truss (size variables) and two variables correspond to the coordinates of joint 1 (coordinate variables) which are continuous variables.

Using the process described in Sections 2.3 to 2.6, at the beginning, an initial population of members is generated randomly. Each member of the population consists of six variables. In contrast with the case explained in Sections 2.3 to 2.6, here the genetic process deals with a multivariable optimisation problem.

Table 2.9 Possible values

Item number	Cross-sec. (mm ²)	Radius of Gyration (mm)
1	182	6.5
2	254	11.0
3	325	14.1
4	453	16.0
5	707	20.0
6	906	25.5
7	1250	38.7
8	1720	39.2
9	3310	46.6
10	4970	56.1
11	5770	65.0
12	6570	74.0

Table 2.10 gives the randomly generated population with ten members. The values for the first four variables in the table relate to the identification numbers of the cross-sectional areas as given in the first column of Table 2.9, (rather than the actual values of the cross-sectional areas). For example, if the randomly chosen integer for a size variable is 4, then a value of 453 mm² is considered for the cross-sectional area of the corresponding element. Also, the radius of gyration for this element is taken to be 16.0 mm. The coordinate variables given in Table 2.10, are the values corresponding to the variations of the coordinates of node 1 in x and y directions, that is, Δx and Δy . Thus to obtain the coordinates of node 1, these variations are added to the initial values given in Fig 2.13 for the coordinates of node 1. Thus, the coordinates of node 1 will be

$$x = 3.00 + \Delta x \qquad \text{and} \qquad y = 0.0 + \Delta y$$

The fitness values for each member of the population, that is, the weight of the truss corresponding to the set of values for the variables, are given in the last column of Table 2.10. The density of 7850kg/m³ has been used for calculating the weights.

2.11.5 Genetic Algorithm and Constrained Structural Optimisation

Referring to Table 2.10, the truss representing the 7th member of the population having the least weight is chosen for more investigation. This investigation is carried out in relation to the behaviour of the truss under consideration while it is subjected to the external loads. Allowable stresses for the elements and also allowable joint displacements will be considered as follows:

Table2.10 The Initial Population

Member number	Size variables				Coord. variables		Fitness value (N)
	First var.	Second var.	Third var.	Fourth var.	Fifth var.	Sixth var.	
1	3	12	11	10	0.951	1.266	5776.1
2	4	2	8	7	0.409	0.616	1246.1
3	3	10	6	8	1.329	-1.196	3529.7
4	4	8	2	2	-1.391	-0.828	844.4
5	11	1	7	6	1.131	-0.215	2688.0
6	10	11	12	9	0.818	-0.309	7245.6
7	1	5	2	5	0.472	0.935	660.9
8	8	1	12	2	0.635	1.254	2170.4
9	6	2	11	11	1.411	1.320	4107.2
10	3	11	11	12	-0.796	1.352	6162.1

Axial stress for the elements are assumed to be limited to

$$\sigma_{\max} = 140N/mm^2$$

Allowable buckling stress, σ_b , for an element in compression is calculated using the formulation given by AISC code [32], as follows.

Firstly, coefficient C_c is obtained using the equation

$$C_c = \pi \left(\frac{2E}{F_y} \right)^{\frac{1}{2}}$$

where, E and F_y are the modulus of elasticity and the yield stress of the material, respectively. Then L_c is calculated as

$$L_c = \frac{\lambda}{C_c}$$

where, λ is the slenderness of the element.

If $\lambda \leq C_c$ then,

$$\sigma_b = \frac{F_y (1 - 0.5L_c^2)}{5/3 + (3/8)L_c - (1/8)L_c^3}$$

and otherwise,

$$\sigma_b = \frac{12\pi^2 E}{23\lambda^2}$$

Also, the maximum allowable vertical displacement of the joints is assumed to be

$$d_{\max} = \pm 25\text{mm}$$

The truss under consideration is analysed to find the stresses and joint displacements. The resulting stresses in the truss elements are given in Table 2.11. The vertical displacements of joints 1 and 2 are

$$d1 = 38\text{mm} \text{ and } d2 = 76\text{mm}$$

Table 2.11 Stresses in the elements of the truss representing the 7th member of the initial population

Element number	Length (m)	Cross-sec. area(mm ²)	Radius of gyration(mm)	Allowable stress(N/mm ²)	Axial stress (N/mm ²)
1	3.60	182.0	6.5	-3.37	-1437.3
2	4.04	707.0	20.0	140.00	+254.6
3	3.26	254.0	11.0	-11.70	-497.8
4	6.00	707.0	20.0	140.00	+138.5

Referring to Table 2.11, it is seen that the stresses in the elements 1 to 3 exceed the allowable values. In particular, the stress in element 1 is more than four hundred times greater than the allowable value. Also, if the displacement of joint 2 is compared with the allowable value, it is seen that it is more than 3 times larger. So, this truss, (member 7 of the initial population of Table 2.10), despite having the least weight, is not an acceptable design.

Now, consider the sixth member of the initial population given in Table 2.10 and the truss representing this member, as shown in Fig 2.14. The element stresses in this truss are given in Table 2.12. From this table, it can be seen that stresses of the elements are within the allowable ranges. Also, the maximum node displacement that is the deflection of joint 1, is 4.84 mm which is less than 25 mm. This truss is therefore a ‘feasible solution’ in which the

constraints are satisfied. Although, its weight is bigger than the trusses representing the other members of the population.

Fig 2.14 Truss representing the sixth member of the population

In the example under consideration, up to now the genetic algorithm has been allowed to take any value for the design variables, providing the values are within the given ranges. This approach as shown in the above example, may lead to the solutions that are not feasible. However, structural optimisation process usually deals with constrained problems. So, the genetic algorithm should involve some constraints such as limitations on stresses and displacements to ensure that the best solution is an acceptable design, that is, it is a feasible solution.

Table 2.12 Stresses in the elements of the truss representing the 6th member of the initial population

Element number	Length (m)	Cross-sec. area(mm ²)	Radius of gyration(mm)	Allowable stress(N/mm ²)	Axial stress (N/mm ²)
1	3.83	4970.0	56.1	-111.50	-52.85
2	5.05	5770.0	65.0	140.00	+47.94
3	3.96	6570.0	74.0	-120.75	-14.59
4	6.00	3310.0	46.0	140.00	+15.94

2.11.5.1 Handling of the constraints

To show how the constraints can be taken into account, the optimisation problem is formulated as follows:

Minimise the weight of the structure

$$W = \sum_{i=1}^n \rho L_i A_i \quad 2.12$$

subject to

$$\sigma_i^l \leq \sigma_i \leq \sigma_i^u \quad i = 1 \text{ to } n \quad 2.13$$

$$\sigma_i \leq \sigma_{bi} \quad 2.14$$

$$d_j^l \leq d_j \leq d_j^u \quad j = 1 \text{ to } \text{ndof} \quad 2.15$$

$$A_i^l \leq A_i \leq A_i^u \quad 2.16$$

$$x_p^l \leq x_p \leq x_p^u \quad 2.17$$

Where,

- W is the total weight of the truss and n is the total number of elements,
- ndof is the total number of degrees of freedom,
- A_i and L_i are the cross-sectional area and the length of the i^{th} element, respectively,
- ρ is the density of the material,
- σ_i is the axial stress in element i , and σ_i^l and σ_i^u are the lower and upper limits of the allowable axial stresses in element i , respectively,
- σ_{bi} is the buckling stress limit of element i ,
- d_j is the displacement at the j^{th} degree of freedom, and d_j^l and d_j^u are the lower and upper limits of displacement at the j^{th} degree of freedom, respectively,
- A_i^l and A_i^u are the lower and upper limits of the cross-sectional area of the i^{th} element, respectively, and
- x_p is the p^{th} coordinate variable, and x_p^l and x_p^u are the lower and upper limits of the p^{th} coordinate, respectively.

Eqns 2.13 to 2.17 are the set of the constraints. These constraints should not be violated in the structure that will be chosen as the optimum design. The last two constraints, expressed by Eqns 2.16 and 2.17, are satisfied automatically, because cross-sectional areas and coordinates are design variables of the problem and are chosen from the specified ranges. These design

variables should be chosen such that the constraints expressed by Eqns 2.13 to 2.15 are not violated. The set of the values for the design variables that give rise to the solutions satisfying the constraints form a 'feasible' region in the search space. A solution is called feasible if its corresponding variable values belong to the feasible region.

General ideas regarding the handling of the constraints have been already discussed in section 2.10 . As described in that section, to use the genetic algorithm as an optimisation tool, the constrained problem is converted to an unconstrained problem through adding a penalty term to the objective function. The procedure explained in Section 2.10 involved the constraints given as explicit functions of the design variables. In contrast, in the case of structural optimisation, the constraints given in Eqns 2.13 to 2.15 are implicit functions of the design variables. In this case, to find the constraint violations, the structure should be analysed for each set of the design variables. Then, the values of the stresses and displacements are calculated and compared with the allowable values.

To take the constraints into account, the 'quadratic penalty function' explained in Section 2.10 is employed. To this end, at first, Eqns 2.13 to 2.15 are rewritten as follows:

$$|\sigma_i| - |\sigma_i^a| \leq 0 \quad 2.18$$

$$|\sigma_i| - |\sigma_{bi}| \leq 0 \quad 2.19$$

$$|d_j| - |d_j^a| \leq 0 \quad 2.20$$

where,

- $\sigma_i^a = \sigma_i^u$ when $\sigma_i \geq 0$,
- $\sigma_i^a = \sigma_i^l$ when $\sigma_i < 0$,
- $d_j^a = d_j^u$ when $d_j \geq 0$ and
- $d_j^a = d_j^l$ when $d_j < 0$.

Because of the large differences between the values of stresses and displacements, to eliminate undesirable numerical difficulties the normalised form of the constraints are used.

Eqns 2.18 to 2.20 are normalised as follows:

$$\left| \frac{\sigma_i}{\sigma_i^a} \right| - 1 \leq 0 \quad 2.21$$

$$\left| \frac{\sigma_i}{\sigma_{bi}} \right| - 1 \leq 0 \quad 2.22$$

$$\left| \frac{d_j}{d_j^a} \right| - 1 \leq 0 \quad 2.23$$

The general formulation for converting a constrained problem to an unconstrained one, using the penalty function method, has been already given as Eqn 2.10. Using this equation, the unconstrained form of the structural optimisation is formulated as explained below.

The constraints in the present text are three groups of inequality constraints, as given by Eqns 2.21 to 2.23. The value of the penalty associated with each of these groups of the constraints may be calculated using the quadratic penalty function given as the last part of Eqn 2.10. As an example, for the group of the constraints represented by Eqn 2.21, the penalty value for the stresses in a typical element is calculated as

$$P_{1i} = r_1 \left[\left(\left| \frac{\sigma_i}{\sigma_i^a} \right| - 1 \right)^+ \right]^2$$

where,

$$\left(\left| \frac{\sigma_i}{\sigma_i^a} \right| - 1 \right)^+ = 0 \text{ if } \left| \frac{\sigma_i}{\sigma_i^a} \right| - 1 \leq 0, \text{ otherwise}$$

$$\left(\left| \frac{\sigma_i}{\sigma_i^a} \right| - 1 \right)^+ = \left| \frac{\sigma_i}{\sigma_i^a} \right| - 1 \text{ and}$$

r_1 is the penalty parameter for this group of the constraints. By extending the summation of P_{1i} over all elements of the structure the penalty term associated with the groups of the constraints given by Eqn 2.21 becomes

$$P_{1i} = r_1 \sum_{i=1}^n \left[\left(\left| \frac{\sigma_i}{\sigma_i^a} \right| - 1 \right)^+ \right]^2$$

The values of the penalties associated with the other groups of the constraints, given by Eqns 2.22 and 2.23 are calculated in a similar way. So, the formulation for the unconstrained form of the structural optimisation is as follows:

Minimise

$$F = \frac{W}{N_f} + r_1 \sum_{i=1}^n \left[\left(\frac{|\sigma_i|}{|\sigma_i^a|} - 1 \right)^+ \right]^2 + r_2 \sum_{i=1}^n \left[\left(\frac{|\sigma_i|}{|\sigma_{bi}|} - 1 \right)^+ \right]^2 + r_3 \sum_{j=1}^{ndof} \left[\left(\frac{|d_j|}{|d_j^a|} - 1 \right)^+ \right]^2 \quad 2.24$$

where,

- F is called a ‘pseudo-fitness function’,
- W is the weight of the structure,
- N_f is a normalisation factor and
- r_1 , r_2 and r_3 are penalty parameters.

The penalty parameters are obtained by trial and error. These parameters may have different values for various constraints. For the example under consideration, that is, the optimisation of the truss of Fig 2.13, a single parameter, namely r is used for all constraints. If r is too small, then members violating the constraints may be selected as parents too often. If r is too large then, the members violating the constraints may be completely ignored for choice as parents. However, the unfeasible solutions may have good genes that could have produced good children if they were selected. Then, the choice of an appropriate value for r is an important issue. For the example under consideration, the initial value of r is assumed to be 100.

To show how the penalty terms are calculated for the example under consideration, consider Table 2.13 that gives the results obtained for the members of the initial population. In this table the values of P_1 , P_2 and P_3 are the penalties imposed for different constraint violations and P is the total penalty for the constraint violations. Tables 2.14 and 2.15 give the details for calculating the values given in Table 2.13. For example, the values for P_1 and P_2 corresponding to the 8th member of the population are calculated using the values given in the third and last columns of Table 2.14. These values are obtained as follows:

$$P_1 = 0.129^2 + 5.47^2 + 2.047^2 = 34.127$$

and

$P_2 = 0.787^2 = 0.619$

Table 2.13 Penalties and fitness values for the members of the initial population

Member number	$W(N)$	P_1	P_2	P_3	P	F
1	5776.1	0.0	5051.6	0.3	5051.9	505247.8
2	1246.1	21.4	606.4	0.6	628.4	62852.5
3	3529.7	0.0	7335.6	1.0	7336.6	733695.3
4	844.4	2.5	16806.4	1.1	16810.1	1681084.4
5	2688.0	102.5	0.0	8.1	110.6	11086.9
6	7245.6	0.0	0.0	0.0	0.0	72.5
7	660.9	0.7	183283.0	4.4	183288.1	18328876.0
8	2170.4	34.1	0.6	0.3	35.0	3520.7
9	4107.2	25.8	83.3	0.8	109.9	11031.1
10	6162.1	0.0	614.0	0.0	614.0	61461.6

The values for buckling stress limits σ_{bi} , given in Table 2.14, are calculated as explained in Section 2.11.5

Table 2.14 Details for calculating the constraint violations

Element number	$\sigma_i(N/mm^2)$	$\frac{ \sigma_i }{ \sigma_i^a } - 1$	$\sigma_{bi}(N/mm^2)$	$\frac{ \sigma_i }{ \sigma_{bi} } - 1$
1	-158.02	+0.129	88.45	+0.787
2	+905.73	+5.470	-----	-----
3	-20.50	-0.854	128.43	-0.840
4	+426.57	+2.047	-----	-----

Table 2.15 contains the joint displacements. Using this table the value of P_3 is calculated as:

$P_3 = 0.138^2 + 0.494^2 = 0.262$

Therefore,

$P = P_1 + P_2 + P_3$

$P = 34.127+0.619+0.262 = 35.008$

Assuming the value of 100 for both r and N_f , the value of F is obtained as:

$$F = \frac{2170.4}{100} + 100 \times 35.008 = 3520.7$$

Table 2.15 Constraint violations

Degree of Freedom j	$d_j(mm)$	$\frac{ d_j }{ d_j^a } - 1$
1	+6.60 ($\Delta x1$)	-0.736
2	-28.45 ($\Delta y1$)	+0.138
3	+12.80 ($\Delta x2$)	-0.488
4	-37.35 ($\Delta y2$)	+0.494

2.11.6 Pairing

Using the tournament selection for the pairing, two members of the population are selected randomly and the one that has the smaller fitness value is chosen to be a parent. The second parent is selected in a similar way. Suppose that the 6th and 8th members of the initial population of Table 2.10 are chosen as parents. The variables corresponding to these selected members are shown in Table 2.16.

Table 2.16 Selected members by pairing

Parent Number	Size variables				Coord variables		Fitness value
	Element	Element	Element	Element	Δx	Δy	
	1	2	3	4			
1	10	11	12	9	0.818	-0.309	72.5
2	8	1	12	2	0.635	1.254	3520.7

2.11.7 Mating

The two selected parents are mated to produce two children. As described in Section 2.5, the mating process consists of four stages namely, ‘encoding’, ‘crossover’, ‘mutation’ and ‘decoding’.

2.11.7.1 Encoding and Decoding

In the present context, the first and fourth stages of the mating process, that is, 'encoding' and 'decoding' are slightly different from what has been described in Sections 2.5.1 and 2.5.4. This is because the size variables have integer values and this requires a different way of handling. To explain this, suppose that the numbers 1 and 12 are the lower and upper limits of the integer values of a variable. These are represented by i_1 and i_2 , respectively. For simplicity, suppose that an eight bit binary string is used for encoding and the integers are encoded using Eqn 2.5. Then, the lower and upper limits are mapped into 0 and 255, respectively. The other integers are mapped into the values between 0 and 255.

Using Eqn 2.6 for decoding, the binary strings whose integer decimal values are within the range 0 to 255 are used to find the corresponding integer values. For example, if the equivalent decimal value for a binary string is 93, then the corresponding value for the integer that is represented by this binary string is

$$x = \frac{93-0}{255-0} \times (12-1) + 1$$

or

$$x = 5.01$$

Then, by truncation of x the value of 5 is obtained. As another example, consider the equivalent decimal value to be equal to 115, then

$$x = 5.96$$

Therefore, again the value of 5 is obtained for x when it is truncated. That is, all the binary strings whose equivalent integer decimal values lie between 93 and 115 represent the value of 5.

A problem arises for the upper limit of the integer values, because an integer may have the value of 12 only when the equivalent integer decimal value of the binary string is equal to 255. This means that all of the integers, except the upper limit are appropriately represented, as shown in Fig 2.15. To prevent the problem, the upper limit of the integers is extended by one unit. That is, the upper limit becomes i_2+1 , where, i_2 is the upper limit of the variable. Then, an integer like i is encoded using the following equation.

Fig 2.15

$$e = Round\left(\frac{(i - i1) \times (e2 - e1)}{i2 + 1 - i1} + e1\right) \quad 2.25$$

Where, e is the equivalent integer decimal value for the binary string representing integer i . Also, $e1$ and $e2$ are the minimum and maximum of the equivalent integer decimal value of the binary strings. Fig 2.16 illustrates the encoding process. Extending the range, that is, the use of $i2+1$ as the upper limit, makes all the integers being appropriately represented by the binary strings, as shown in Fig 2.17.

Fig 2.16 Encoding

To decode an integer variable, the decimal value of the binary string representing that variable is used to find its corresponding integer value. For this purpose, the following equation is used.

$$i = trunc\left[\frac{e - e1}{e2 - e1}(i2 + 1 - i1) + i1\right] \quad 2.26$$

where, '*trunc*' indicates that the value in the brackets is truncated.

Fig 2.17

A problem may arise for decoding because of the approximate nature of the floatal values. This may happen with Eqn 2.26 when the equation gives a value less than $i1$. For example, if the value for a binary string is 0.0 then, using Eqn 2.26 the corresponding integer will be found as follows:

$$i = trunc[\frac{0.0 - 0.0}{255.0 - 0.0} \times (i2 + 1 - i1) + i1]$$

It is possible that the first term

$$\frac{0.0 - 0.0}{255.0 - 0.0}$$

is not exactly equal to 0, and it may be a rather small negative value. Then, the value which is truncated is less than $i1$, and an integer less than $i1$ will be obtained after truncation. This value which is out of the range is not acceptable. A similar situation may occur for the upper limit of the integers. That is, a value greater than $i2$ may be obtained. For instance, the value of 255 for e , may give rise to a value of 13 for i , which is out of the specified range.

To ensure that the value of the integers do not extend beyond the range, two conditions are imposed as follows:

$$i = i1 \quad \text{if} \quad i < i1$$

and

$$i = i2 \quad \text{if} \quad i > i2$$

Returning to the example under consideration, in relation to the optimisation of the truss of Fig 2.13, assuming a 32 bits ‘word’ for the computer, Eqn 2.25 is used for encoding the selected members given in Table 2.16. The results obtained for the equivalent integer decimal values are given in Table 2.17. For instance, the encoded value for the first variable of parent one is calculated as follows:

$$e = Round\left(\frac{(10-1)\times(2^{32}-1-0)}{12+1-1}+0\right)$$

or

$$e = 3221225471.$$

The fifth variable of parent one, which is a continuous variable is encoded as follows:

$$e = Round\left(\frac{(0.818-(-1.5))\times(2^{32}-1-0)}{1.5-(-1.5)}+0\right)$$

or

$$e = 3318115118.$$

Table 2.17 Equivalent integer decimal values for selected parents

Parent number	Size variables				Coord variables	
	First var.	Second var.	Third var.	Fourth var.	Fifth var.	Sixth var.
1	3221225471	3579139412	3937053354	2863311530	3318115118	1705207617
2	2505397589	0	3937053354	357913941	3057079899	3942839572

2.11.7.2 Crossover

In the example under consideration, a parent chromosome consists of six parts, each of which corresponds to a variable. In this case, the genetic algorithm deals with a multi-variable problem. This is in contrast with the case explained in Section 2.2 which was a single variable problem. The encoded values for two parents are given in Table 2.17 . Each of the values given in this table are related to a 32 bit binary string. That is, each parent chromosome consists of six binary strings, as shown in Fig 2.18. In this figure, only some of the genes of each chromosome are shown.

Fig 2.18 Binary strings for parent chromosomes

For each variable its corresponding binary strings in two parent chromosomes are taken to perform crossover. Let a point crossover be carried out for the example under consideration,

which is a six-variable problem. To this end, six random sites are chosen for the six pairs of binary strings. Then, using the procedure described in Section 2.5.2, some of the binary digits are exchanged between the binary strings. To explain more clearly, the first and fifth pairs of binary strings are chosen to show the crossover procedure. These parts of the parent chromosomes together with the corresponding parts of the resulting children are shown in Fig 2.19.

Fig 2.19 Point crossover for multivariable problem

2.11.7.3 Mutation

Mutation is implemented in the same way as described in Section 2.5.3. Each bit of the binary strings of the child chromosomes is examined for mutation. To this end, for every digit a random number between 0 and 1 is generated. If this random number is less than the mutation rate, then its corresponding gene is mutated. That is, it is converted from ‘0’ to ‘1’ and vice versa. For the case under consideration, a value of 0.005 has been assumed for the mutation rate. In one occasion, for this value of mutation rate, the binary string representing the fifth variable of the second child was mutated. That is, the seventh digit from the right-hand side was converted from 0 to 1. The mutated binary string of the second child is shown below with the bolded mutated gene.

10110110001101100110101101101110

2.11.7.4 Decoding

The coordinate variables of the problem under consideration are continuous variables. Then, the decoding process in relation to these variables is carried out using Eqn 2.6. For the size

variables, the procedure described in Section 2.11.7.1 is employed. The decoded form of the two children produced by crossover and mutation will be as shown in Table 2.18. For instance, the decoded value for the first variable of child one is obtained as follows:

$$i = trunc \left[\frac{3221214549 - 0}{(2^{32} - 1) - 0} \times (12 - 1) + 1 \right]$$
$$i = trunc[9.25] = 9$$

In the above equation, the corresponding equivalent integer decimal value for the variable under consideration is equal to 3221214549.

Table 2.18 Decoded values for children

Child number	Size variables				Coord variables	
	First var.	Second var.	Third var.	Fourth var.	Fifth var.	Sixth var.
1	9	10	12	9	0.818	-0.684
2	8	1	12	1	0.635	1.254

The decoded value for the fifth variable of child one, which is a continuous variable with an equivalent integer decimal value of 3318109787, is calculated below:

$$x = \frac{3318109787 - 0}{(2^{32} - 1) - 0} \times (1.5 - (-1.5)) + (-1.5)$$
$$x = 0.81767$$

2.11.8 Replacement

The two children produced through the mating process, shown in Table 2.18, are placed in the population as new members. To this end, two least fit members of the current population are replaced by the children. Since minimising is of interest, then two worst members of the current population are those with greatest values of fitness. Referring to Table 2.13, it is seen that the 4th and 7th members have the largest fitness values. Then, they are replaced by the two new children. It should be noted that the replacement is carried out even if the worst chromosomes are fitter than the new children, as explained in Section 2.6. The population after replacement is given in Table 2.19. In this table, the new members are shown in bold.

2.11.9 Evolution cycle

As described in Section 2.7, the ‘evolution cycle’ consists of the processes of ‘pairing’, ‘mating’ and ‘replacement’. The evolution cycle continues until the number of the produced child chromosomes is the same as the number of the chromosomes in the population.

Table 2.19 Population and new members

Member number	Size variables				Coord variables		Fitness value
	First var.	Second var.	Third var.	Fourth var.	Fifth var.	Sixth var.	
1	3	12	11	10	0.951	1.266	505247.8
2	4	2	8	7	0.409	0.616	62852.5
3	3	10	6	8	1.329	-1.196	733695.3
4	8	1	12	1	0.635	1.254	4193.5
5	11	1	7	6	1.131	-0.215	11086.9
6	10	11	12	9	0.818	-0.309	72.5
7	9	10	12	9	0.818	-0.684	67.2
8	8	1	12	2	0.635	0.125	3520.7
9	6	2	11	11	1.411	1.320	11031.1
10	3	11	11	12	-0.796	1.352	61461.6

2.11.10 Termination

In the case of the constrained optimisation which is described in this work, the optimisation process is checked for termination in two separate phases as explained below.

2.11.10.1 Termination in phase one

After a generation is completed, the best member of the population is identified. This member is represented by a truss that has the least pseudo-fitness value in comparison with the other members of the population. Suppose that the pseudo-fitness value of the truss representing the best solution of the i^{th} generation is equal to F_i . Then, using Eqn 2.7 the convergence criteria may be given as follows:

$$abs\left(\frac{F_i - F_{i-1}}{F_i}\right) \leq \varepsilon$$

2.27

where, F_i and F_{i-1} are the pseudo-fitness values of the trusses representing the best solutions of the current and the previous generations, respectively. If Eqn 2.27 is satisfied for a number of successive convergence tests, say 20, then the process is terminated in phase one. This required number of successive tests is called the ‘confirmation limit’, as described in Section 2.7. On the other hand, if Eqn 2.27 is not satisfied for the specified maximum number of generations, then the process is terminated. Fig 2.20 shows the history of the convergence in one occasion. Also, the truss representing the best solution in phase 1 is given in Fig 2.21. The values corresponding to the variables for the best solution are given in Table 2.20. The stresses in the elements of the truss representing the best solution are given in Table 2.21.

Table 2.20 Best solution

Size variables				Coord variables		Fitness value
First var.	Second var.	Third var.	Fourth var.	Fifth var.	Sixth var.	
9	7	8	5	0.644	1.255	21.693

Fig 2.20 History of convergence in phase 1

2.11.10.2 Termination in phase two

As shown in Table 2.21, the axial stress in element 4 of the truss representing the best solution in phase one exceeds the allowable stress. That is, the optimum obtained is not feasible. Then, the process is repeated with a new value for the penalty parameter. At this stage, the genetic process starts with the population produced after the algorithm converged to an unfeasible

solution in phase one. That is, the search to find the optimum starts from a point that may be close to the optimum.

Table 2.21 Stresses in the elements of the best solution in phase one

Element number	1	2	3	4
Axial stress	-82.17	132.31	-78.17	152.76

Continuing the procedure, it may converge to an optimum solution which is feasible. On one occasion this feasible solution was found while the penalty parameter took the value of 10000. In this case, the penalty parameter, that is r , was increased incrementally by 100.

Fig 2.21 Truss representing the solution in phase 1

As indicated in this example, the feasible solution was obtained after a considerable number of trials. However, if the initial value of the penalty parameter is chosen properly, the number of trials will be decreased. The truss representing the feasible optimum solution is shown in Fig 2.22. Also, the element stresses as well as variables (size and coordinate) for this truss are given in Tables 2.22 and 2.23, respectively.

Table 2.22 Stresses for feasible optimum solution

Element number	Cross-sectional area (mm ²)	Axial stress (N/ mm ²)	Allowable stress (N/ mm ²)
1	3310	-82.93	-101.66
2	1250	115.51	140.00
3	1720	-85.36	-106.90
4	906	135.88	140.00

The weight of this truss is equal to 2157 N. Vertical displacements for joints 1 and 2 are 4.96 mm and 13.10 mm, respectively, which are less than the allowable value.

Table 2.23 Feasible optimum solution

Size variables				Coord variables		Fitness value
First var.	Second var.	Third var.	Fourth var.	Fifth var.	Sixth var.	
9	7	8	6	0.565	1.417	21.57

Fig 2.22 Truss representing the feasible optimum solution

2.12 A CHECK FOR THE ACCURACY OF THE DEVELOPED TECHNIQUE

In the previous sections the procedure developed was employed for optimising the truss of Fig 2.13 while the coordinates of node 1 and also the cross-sectional areas of the elements were considered as independent variables. To indicate the accuracy of the algorithm, the technique developed in this chapter is used for optimising the weight of the truss shown in Fig 2.23. This truss is a special case which is derived from the truss of Fig 2.13. As shown in Fig 23, the coordinates of node 1 are

$X = 3.00\text{ m} \quad Y = 1.50\text{ m}$

This truss which is subjected to vertical loads at nodes 1 and 2, is a statically determinate structure and the element forces may be calculated independent of the amount of the cross-sectional areas of the elements. The internal forces of the truss are given in Table 2.24. This truss is designed for carrying these internal forces. To this end, the assumptions described in

section 2.11.5 are used for allowable axial stresses and also allowable buckling stresses. In this case, no constraint is imposed on the node displacements. The cross-sectional areas and the radius of gyrations for the elements of the designed truss are also given in Table 2.24.

Table 2.24 Stresses in designed truss

Element number	Element axial force (kN)	Cross-sectional area (mm ²)	Radius of gyration (mm)	Stress (N/mm ²)
1	-268.33	2717	39.0	-98.76
2	+89.44	639	-----	139.97
3	-178.89	2030	33.7	-88.12
4	+160.00	1143	-----	139.97

Now, the genetic algorithm is used for minimising the weight of the truss of Fig 2.23 while only the cross-sectional areas of the elements are considered as independent variables of the problem. The set of the twelve possible values listed in Table 2.9 are modified as listed in Table 2.25.

Table 2.25 Possible values

Item number	Cross-sec. (mm ²)	Radius of Gyration (mm)
1	182	6.5
2	254	11.0
3	325	14.1
4	453	16.0
5	639	17.0
6	707	20.0
7	906	25.5
8	1143	29.0
9	1250	38.7
10	1720	39.2
11	2030	33.7
12	2717	39.0

As it is seen, this table embodies the cross-sectional areas and the radius of gyrations obtained by designing of the truss of Fig 2.23. With this set of possible values the genetic process is carried out for minimising the weight of the truss. The result obtained as the best solution by genetic algorithm is the same as for the designed structure. That is the resulting values for the section properties are the same as the values given in Table 2.24 which are the exact values

obtained by designing. This indicates that the genetic algorithm has searched the whole domain of the possible values and has explored the global optimum.

Fig 2.23

CHAPTER 3

A Genetic Approach for Topological Optimisation of Double Layer Grids

3.1 INTRODUCTION

In this chapter, at first the genetic algorithm developed in chapter 2 is employed to establish a method for determination of the degrees of importance of the elements of a double layer grid. To this end, a double layer grid with square on square pattern is considered as the base grid. Then, the procedure for obtaining the degree of importance (portancy) of an element of the base grid is explained in detail. Also, in this chapter, the portancy values obtained for the elements of the base grid are used for comparing the reduced grids. That is, a method is proposed, by which different topologies relating to a particular base grid may be compared with each other.

3.2 ESTABLISHING THE MAIN CONCEPTS

One of the main objectives of this study is to investigate the possibility of assigning a degree of 'importance' to each element of the base grid. It is desirable that the importance of each element be expressible quantitatively, such that two different elements of the base grid may be compared in terms of their corresponding 'importance'. A question may arise at this point, namely, what could be the 'sense' of importance for an element of the grid in the present context?

In general, the configuration of a double layer grid is chosen based on architectural requirements and is designed for transferring the loads to the supports through its elements. The importance of an element may then be regarded as the degree of its contribution in carrying the load. That is, the elements that carry more forces may be regarded as more important.

However, carrying the load should be associated with a reasonable behaviour for the structure. That is, the stresses and displacements should not exceed the allowable values. To have a grid with a desirable behaviour, the grid is designed and the cross-sectional areas are allocated to the elements of the grid. The cross-sectional areas may be allocated through an optimisation process. In this sense, an element with greater cross-sectional area may be regarded as a more important element.

It is seen that assigning a degree of importance to an element of the base grid may be carried out from different viewpoints. In this chapter a procedure is developed to determine the degree of importance for the elements of the base grid and then the results are discussed and compared with each other. In the present context the term ‘portancy’ is used to indicate the degree of ‘importance’ of an element.

Here, the attention is focussed on the investigation of the importance of the elements of the base grid in carrying the loads. Consider the double layer grid whose plan and side views are shown in Fig 3.1. This grid, which is referred to as a base grid is supported at eight bottom layer nodes indicated by little circles as shown. The support indicated by S1 is constrained in X, Y and Z directions and support S2 is constrained in Y and Z directions. The other supports are constrained in the Z direction only. The top and bottom layer elements of the grid are all of the same length L and the depth of the grid, namely d , is given by

$$d = \frac{\sqrt{2}}{2} L \quad 3.1$$

This choice of the depth for the grid will make the web elements of the same length as that of the top and bottom elements.

The grid is subjected to equal vertical concentrated loads of magnitude P at all the top layer nodes. The modulus of elasticity of the material of which the grid is made is E and the cross-sectional areas of all the elements are equal to A . The grid is assumed to behave linearly.

Fig 3.1

A procedure will be established later for finding the portancies of the elements of the base grid of Fig 3.1. This procedure relies on the analytical results for a number of reduced grids. It is desirable to obtain these analytical results in terms of the parameters P , E , A and L . To show how the result of the analysis can be expressed in terms of P , E , A and L , consider a typical element of the grid. Suppose that this element makes the angles α , β and γ with the coordinate axes as shown in Fig 3.2. Assuming pin-connection for the grid, the stiffness matrix of this element in the global coordinate system may be given as:

$$Km = \begin{bmatrix} \frac{EA}{L}T & -\frac{EA}{L}T \\ -\frac{EA}{L}T & \frac{EA}{L}T \end{bmatrix}$$

or

$$Km = \frac{EA}{L} \begin{bmatrix} T & -T \\ -T & T \end{bmatrix}$$

Here, T is the matrix for transformation from the local coordinate system to the global coordinate system. The transformation matrix T may be given as:

$$T = \begin{bmatrix} \cos^2 \alpha & \cos \alpha \cos \beta & \cos \alpha \cos \gamma \\ \cos \alpha \cos \beta & \cos^2 \beta & \cos \beta \cos \gamma \\ \cos \alpha \cos \gamma & \cos \beta \cos \gamma & \cos^2 \gamma \end{bmatrix}$$

The element stiffness matrix Km may then be written in the form:

$$Km = \frac{EA}{L} \bar{K}m \tag{3.2}$$

Where,

$$\bar{K}m = \begin{bmatrix} T & -T \\ -T & T \end{bmatrix} \tag{3.3}$$

The elements of matrix $\bar{K}m$ are only dependent on the angles α , β and γ . Therefore, the overall stiffness matrix of the grid, which is built by assembling the stiffness matrices of the elements, may be given as:

$$K = \frac{EA}{L} \bar{K} \tag{3.4}$$

Fig 3.2 Angles of a typical element with the coordinate axes

In Eqn 3.4, the term EA/L may be factored out because this term is the same for all the elements of the grid. The matrix $\bar{K}$ will then be independent of E , A and L . In the stiffness method, the relation between the node displacements and the external forces may be given as:

$$KD = W \quad 3.5$$

Where,

- K is the overall stiffness matrix of the structure,
- D is the nodal displacement vector and
- W is the external load vector.

Substituting Eqn 3.4 into Eqn 3.5,

$$\frac{EA}{L} \bar{K} D = W$$

or

$$\frac{EA}{L} \bar{K} D = P \bar{W} \quad 3.6$$

Where, $\bar{W}$ is the external load vector with the nodal external load P factored out. From Eqn 3.6, the nodal displacement vector may be obtained as

$$D = \frac{PL}{EA} \bar{K}^{-1} \bar{W}$$

or

$$D = \frac{PL}{EA} \bar{D}$$

where,

$$\bar{D} = \bar{K}^{-1} \bar{W}$$

$\bar{D}$ is the displacement vector of the structure with the term PL/EA factored out. Therefore, it is seen that the nodal displacements are proportional to the factor PL/EA .

The force-displacement equation for an element of the grid may be given as:

$$Fm = Km Dm \quad 3.7$$

where,

- Fm is the force vector of the element,
- Km is the stiffness matrix of the element and
- Dm is the nodal displacement vector of the element.

The vector Dm , which is a sub-vector of vector D , is proportional to PL/EA and is

$$Dm = \frac{PL}{EA} \bar{Dm} \quad 3.8$$

where,

$\bar{Dm}$ is the nodal displacement vector of the element with the term PL/EA factored out.

Substituting Eqns 3.2 and 3.8 into Eqn 3.7,

$$Fm = \frac{EA}{L} \bar{Km} \times \frac{PL}{EA} \bar{Dm}$$

or

$$Fm = P \bar{Km} \bar{Dm}$$

Thus, the element force vector Fm is proportional to P .

In practice, for analysing a grid by the computer, the values of the parameters P , E , A and L may be taken to be equal to 1. After the analysis, the resulting values for the internal forces based on this analysis are multiplied by P . Also, the nodal displacements may be found by multiplying the values from the analysis by PL/EA .

Also, for a case in which the values of L and A are not the same for the elements of the grid, the internal forces and the nodal displacements may still be given in terms of P , E , A and L . However, in this case, A and L are the cross-sectional area and the length of a particular element of the grid respectively, and the cross-sectional areas and the length of the other elements are given as proportions of A and L , respectively.

Incidentally, in this work a graphical convention is used for the presentation of the internal forces in the elements of the grid. This convention is illustrated in Fig 3.3. This figure shows the internal forces in the base grid of Fig 3.1 under an external loading consisting of equal downward concentrated loads applied at all the top layer nodes of the grid. In Fig 3.3 each element is drawn with a thickness proportional to the absolute value of its internal force. Thus, a tensile force and a compressive force of the same magnitude are indicated by lines of the same thickness. Note that the grid is analysed as a pin-jointed system and therefore there are only axial forces in the elements. The element(s) with the maximum internal force (tension or compression) in Fig 3.3 is shown with lines of around 1.2 mm thick and any other element is shown by a line whose thickness indicates the internal force in proportion to the thickness of the element(s) with the maximum internal force. Of course, a graphical representation like the one shown in Fig 3.3 is not suitable for accurate determination of the values of the internal forces but it provides a convenient way of obtaining a general appreciation of the pattern of the internal force distribution in the grid.

Returning to the discussion regarding the importance of the elements, as may be seen from Fig 3.3, some of the elements carry small internal forces while others are under higher internal forces. To improve the efficiency of the structure, one may consider removal of some of the elements that carry small forces since this is bound to reduce the weight of the structure. However, the removal of some of the elements will change the force distribution.

Actually, the base grid of Fig 3.1 has a rather dense configuration. In practice, the tendency is to use grids that are obtained by removing a number of elements from the base grid. This is prompted by the desire to have a grid with a 'lighter looking' configuration. This would also help in allowing the natural light through when translucent cladding is used. For example, the base grid of Fig 3.1 may be reduced as shown in Figs 3.4 to 3.7. Each of these configurations is created by removing 32 elements from the base grid. The removed elements are indicated by dashed lines. A question may arise at this point, namely, which one of the reduced grids of

Figs 3.4 to 3.7 is the best engineering choice, assuming that as regarded as the architectural requirements the grids of Figs 3.4 to 3.7 are equally acceptable

Fig 3.3 Force distribution for the base grid

At a first look, using engineering judgment and referring to the force distribution of the base grid, given in Fig 3.3, it may be concluded that the reduced grid of Fig 3.7 is less suitable in comparison with the other reduced grids, given in Figs 3.4 to 3.6. The reason is that some of the bottom elements are removed from the middle region in the grid of Fig 3.7, since these removed elements may be found to have an important role in carrying the loads.

In order to find the best reduced grid, one may carry out an optimisation process to find the optimum weights of the reduced grids. Then, the grid associated with the least weight could be considered as the best one. This is an approach that may be carried out using the optimisation methods available in the literature. However, in this study the goal is to develop a procedure in which different topologies derived from the base grid may be compared with each other in a simple manner and without the complete analysis and optimisation of the grids. This procedure involves the use of 'genetic algorithm' to find a criterion by which a designer may decide on the best topology.

Fig 3.4 A reduced grid

Fig 3.5 Another reduced grid

Fig 3.6 Another reduced grid

Fig 3.7 Another reduced grid

3.3 APPLICATION OF GENETIC ALGORITHM

The main concepts of the genetic algorithm have already been described in chapter 2. As indicated in that chapter, the genetic algorithm starts by creating an initial population of members which are generated randomly. This population evolves using the ‘pairing’, ‘crossover’ and ‘mutation’ operations. The procedure for implementing the genetic algorithm in relation to the evaluation of reduced grids is explained step by step through an example in the sequel.

Consider the double layer grid with a square on square pattern given in Fig 3.8. In this figure, the top layer elements are indicated by thick lines while the bottom and the web elements are shown by thin lines. This grid which is considered as a base grid, is supported at four bottom layer nodes indicated by little circles as shown. In Fig 3.8, support S1 is constrained in X, Y and Z directions and support S2 is constrained in Y and Z directions. The other supports are constrained in the Z direction only.

Fig 3.8 A base grid

The grid of Fig 3.8 consists of 72 elements all of which are of the same length L . For all the members of the grid being of the same length, the depth of the base grid should be equal to $L/\sqrt{2}$. The elements of the grid are numbered as shown in Fig 3.8. The base grid of Fig 3.8 is a statically indeterminate structure with 4 degrees of indeterminacy. The grid is subjected to equal downward concentrated loads of magnitude of P applied at all the top layer nodes.

3.3.1 Initiation

The genetic process starts with an initial population of members each of which is a chromosome. A chromosome represents a reduced grid which is derived from the base grid of Fig 3.8. In the reduced grid the support arrangements and the load conditions are the same as for the base grid. Fig 3.9 indicates a reduced grid that has been generated randomly. As shown in this figure, the reduced grid has four missing elements that are shown by dotted lines. Each chromosome consists of a number of '1' and '0' digits. The number of these digits is equal to the number of the elements of the base grid. For the case under consideration, the number of the digits is equal to 72. A digit 1 in a chromosome indicates the presence of an element of the base grid in the reduced grid and a digit 0 indicates the absence of an element of the base grid in the reduced grid. The digits 1 and 0 are the genes of the chromosome. The chromosome representing the reduced grid of Fig 3.9 is shown in Fig 3.10.

Fig 3.9 An example of a reduced grid

stable grids. Although, the mutation may change some of the genes, but as discussed in chapter 2, the mutation rate is rather small and the probability for mutation to be of help is too low.

For the case of the base grid of Fig 3.8, on one occasion it was found that a suitable value for the element presence factor C was 0.92. In this occasion, nine members of the initial population of one hundred members were the chromosomes which represented stable grids.

3.3.2 Fitness Function

As discussed in chapter 2, the genetic process proceeds by selecting members of the initial population for mating. However, before the mating process is performed, the members of the population are 'evaluated'. The evaluation of members is carried out based on the 'fitness values'. The fitness value assigned to a member is used to measure how 'good' that member is in a particular context. For the problem under consideration, a fitness function is defined as explained below.

Consider two different reduced grids that are obtained by random selection from the base grid of Fig 3.8. Suppose that these grids are statically stable, and let the grids be subjected to linear analysis with support conditions and loads the same as the base grid. These two reduced grids are compared in terms of their internal forces. The grid with smaller summation of absolute values of internal forces is chosen as the 'better' grid. The reason for this will be explained later. The fitness function is given as

$$\text{Fitness} = \frac{s}{S} \quad 3.9$$

Where, s and S denote the summations of the absolute values of the internal forces of the reduced grid and that of the base grid, respectively. In this context, the phrase 'summation of absolute values of internal forces' is abbreviated to 'summation of internal forces'. Table 3.1 lists the fitness values of some of the members of the initial population generated in one occasion during the running of the genetic process. These fitness values are related to the members representing stable reduced grids. The fitness value for a member representing an unstable grid will be discussed later. As shown in Table 3.1, the fitness values for the members of the initial population of the example under consideration are within the range of 1.00-5.08.

Table 3.1 Fitness values of some members of the initial population

Member Number	Number of elements of reduced grid	Fitness value
21	71	1.00
36	68	2.83
43	68	2.33
48	70	1.67
53	68	1.00
58	70	1.00
91	70	1.00
94	68	5.08
98	69	1.00

The summation of the internal forces is chosen as a quantity that is used for comparing the reduced grids. This choice is based on the following argument. Suppose that all the elements of a double layer grid are of the same length. A simple way of designing a grid will be to analyse the structure once, assuming the same cross-sectional areas for all elements of the grid. Then, the cross-sectional areas can be allocated to the elements based on the results of the analysis. These allocated cross-sectional areas will be proportional to the internal forces of the elements. The weight of the structure is then given by the following equation.

$$\text{Weight} = \sum \gamma L A \quad 3.10$$

Where, γ is the specific weight of the material used, L is the length of an element, A is the cross-sectional area of the element and the summation extends over all the elements of the grid. Since γ and L are the same for all the elements, then the above equation becomes

$$\text{Weight} = \gamma L \sum A \quad 3.11$$

Assuming the same allowable stresses for tension and compression, namely, σ , the relation between the internal force F and the cross-sectional area A of an element will be

$$F = \sigma A \quad 3.12$$

or

$$A = F / \sigma \quad 3.13$$

Substituting Eqn 3.13 in Eqn 3.11,

$$\text{Weight} = \frac{\gamma L}{\sigma} \sum F \quad 3.14$$

Thus, it may be concluded that the summation of the internal forces in the elements is proportional to the weight of the grid. This means that the weight of the grid is increased if the summation of the internal forces are increased and vice versa. Since, having a lighter structure is usually desirable, then smaller summation of internal forces may be considered as a measure of suitability of the grid.

One of the assumptions in obtaining Eqn 3.14 was that all the elements of the grid have the same length. This is quite common in double layer grids, where, the elements are of the same length. However, it is believed that even if the elements are not of the same length, Eqn 3.14 is approximately true. The second assumption was that one can produce a simple design for a double layer grid based on a single linear analysis of the grid with all the elements having the same cross-sectional areas. Actually, this is a process that was widely used by the designers of double layer grids before the days of computer. That is, using the internal forces obtained from a single analysis, the elements of the grid were designed. However, by experience and engineering judgment some modifications may have been carried out in relation to the element cross-sectional areas. That is, for a particular element with internal force more than the average of the internal forces, the allocated cross-sectional area may have been increased and the cross-sectional area may have been decreased for an element with a small force.

After the grid is designed based on the procedure outlined above, the allocated cross-sectional areas for the elements of the grid may be different. However, if the double layer grid is analysed again considering the allocated cross-sectional areas, it will be found that although the internal forces may be different from those obtained assuming equal cross-sectional areas, but the principal pattern of the force distribution will not be changed greatly.

Here, it should be emphasised that the explanation given above, in relation to assumption of uniform length and cross-sectional areas, does not imply that the procedure is proposed for actual design purposes. Also, it is not proposed that Eqn 3.14 may be used for weight optimisation. At this point, the aim is to show that the fitness function of Eqn 3.9 is chosen on the basis of a reasonable argument and it can be regarded as a reliable criterion for comparing the reduced grids.

Returning to the discussion concerning the procedure of the genetic algorithm, the fitness values for the members of the initial population may be calculated using Eqn 3.9. As indicated

in chapter 2, the genetic process works based on the selection of the members of the population for mating. This selection is based on the fitness values of the members. Considering Eqn 3.9 as the fitness function, a member with a smaller fitness value, will have more chance of being selected.

Here, it should be noted that Eqn 3.9 cannot be used for calculating the fitness of a member of the population whose corresponding grid is not statically stable. A member that represents a statically unstable grid may be dealt with in different ways. Normally one may discard such a member and only accept the members representing statically stable grids. However, the policy adopted in this work is that a member of the population that represents a statistically unstable grid is given a low probability of selection for mating, rather than being discarded. To elaborate, a suitably large fitness value is given to such a member so that it has a small chance of being selected for mating. This fitness value is larger than the fitness values of all members representing statistically stable grids.

A question may arise at this point, namely, what significance may be imagined for a member representing an unstable grid and why it is not discarded? Also, one may wonder why such a member is given a chance to be in the population? The answer is that, sometimes the genetic process is stagnated with the progress coming to a halt. That is, the genetic operators, namely crossover and mutation, are not able to make progress in the evolution of the solution with the available genes in the chromosomes. In such occasions, some new genes are needed to enter the population. A member of population representing an unstable grid may have some good genes that may be useful to improve the performance of the genetic algorithm. Indeed, the role of such a member is similar to mutation which may be helpful to relieve the genetic algorithm from stagnation.

As discussed above, having members representing unstable grids in the population with a small chance of being selected may be useful. If such members are given a high chance of being selected for mating, it is possible that they dominate the stable members and most of the members of the population may become those representing unstable grids. In this case, the procedure cannot approach the desired solution. For the example under consideration, the fitness value assigned to the members representing unstable grids is taken as 3 times that of the fitness value of the base grid.

3.3.3 Pairing

Here, the tournament pairing discussed in chapter 2 is employed. That is, two chromosomes are randomly chosen from the population and they are compared in terms of their fitness values. The chromosome with the smaller fitness value will be chosen as a parent chromosome. Then, the same procedure is repeated to choose the other parent chromosome.

3.3.4 Mating

Mating process is performed with two parent chromosomes selected by tournament pairing. The mating process consists of two steps, namely 'crossover' and 'mutation'.

3.3.4.1 Crossover

The two selected parent chromosomes (selected through the tournament pairing) are operated upon with and some of their genes being exchanged by subjecting them to the process of crossover. Here, a type of crossover, called, 'uniform crossover' is used. To perform the uniform crossover, a string of 1 and 0 digits, called a 'mask', is generated randomly. The number of the digits of this string is equal to the number of the digits of a chromosome in the population. For generation of each digit of the mask a random number between 0 and 1 is generated. If this random number is greater than 0.5, the corresponding digit of the mask will be equal to 1, otherwise, it will be equal to 0.

For the example under consideration, the mask consists of 72 digits. To perform the crossover, those genes of the parents whose corresponding digits in the mask are 0, are exchanged and those that correspond to a digit 1 in the mask are left alone. An example of two parent chromosomes together with a mask is shown in Fig 3.11. Also shown in this figure, are the resulting two child chromosomes. The exchanged genes in the example of Fig 3.11 are shown in bold. Each of the child chromosomes represents a new reduced grid. The reduced grids represented by the two parent chromosomes are given in Figs 3.12 and 3.13. Also, the reduced grids represented by two children are shown in Figs 3.14 and 3.15.

3.3.4.2 Mutation

Mutation takes place occasionally and changes some of the genes of the child chromosomes randomly. The frequency of the mutation is specified by the 'mutation rate'. For instance, if the mutation rate is 0.02, then, two genes in every 100 genes handled are expected to be mutated. Each gene of the child chromosomes may be subjected to the mutation.

Fig 3.12 Reduced grid represented by parent 1

Fig 3.13 Reduced grid represented by parent 2

Fig 3.14 Reduced grid represented by child 1

Fig 3.15 Reduced grid represented by child 2

Fig 3.16 The grid represented by a mutated chromosome

The process of pairing, mating and replacement are repeated until the number of the generated child chromosomes is equal to the number of the members of the initial population. That is, the cycle is continued until one generation is completed. For instance, in the current example, the cycle will be repeated 50 times to generate 100 new members of the population.

3.3.6 Termination

When one generation is completed, the best solution of that generation, that is, the chromosome with the least value of fitness is found. Experience shows that normally the fitness value of the best solution becomes smaller gradually. Here, a criterion is needed to terminate the process. In this work, the following equation is used as the convergence criterion.

$$\frac{b_{i-1} - b_i}{b_i} \leq \varepsilon \quad 3.15$$

In the above equation, b_{i-1} and b_i are the fitness values for the best members of the previous and the current generations, respectively, and ε is a small value, typically, 0.001. If this equation is true for a number of successive generations, typically, 30, then the process is terminated. However, in some cases, the genetic algorithm does not converge and it should be terminated with another criterion. The maximum number of generations is chosen as this

criterion which is used for termination. Then, if Eqn 3.15 is not satisfied after the maximum number of generations, the process is terminated.

3.4 PORTANCY MAP

Actually, one of the goals of the procedure developed here is to establish a method by which the importance of an element of a double layer grid may be expressed numerically. This method is explained in the sequel.

Suppose that the genetic process is carried out once. The result is a reduced grid with the least value of the summation of the internal forces. For instance, Fig 3.17 shows a reduced grid that has been obtained for an application of the genetic process in which the grid of Fig 3.1 has been considered as the base grid. In this reduced grid the eliminated elements are indicated by dashed lines. The force distribution corresponding to this reduced grid is shown in Fig 3.18. Now, let the genetic process be carried out again. A possible resulting reduced grid and its corresponding force distribution are shown in Figs 3.19 and 3.20. Comparing these figures with those obtained for the first running of the genetic process, it is seen that they are not quite similar. The reason for the difference is that the genetic algorithm works in a stochastic manner. Therefore, by executing the process using different initial seed numbers the results are probabilistically different and the analytical results are bound to be different.

Suppose that the genetic process is executed several times, say 'r'. Then, there are r reduced grids each of which is an optimum solution obtained by the genetic technique. Now, for each element of the base grid, the absolute values of the internal forces of that element in these r reduced grids are added together. For the cases in which this particular element is absent from a reduced grid, the value of zero is considered for its internal force. As an example, suppose that the genetic process is repeated ten times for the base grid of Fig 3.1. Table 3.2 lists the summations of the internal forces for a selected set of the elements of the base grid. These selected elements are indicated by double lines in Fig 3.21. Then, the value corresponding to each element of the base grid is divided by the maximum of the values for all the elements of the base grid. In the example considered the overall maximum value corresponds to element D, shown in bold in Table 3.2. The result of the division will be a number between 0 and 1 for each element as shown in Table 3.2. Each of these values is referred to as the 'portancy' of an element.

Fig 3.17 Optimum reduced grid

Maximum force = 10.68 P

Fig 3.18 Force distribution in the optimum reduced grid

Fig 3.19 Another optimum reduced grid

Maximum force = 11.21 P

Fig 3.20 Force distribution in another optimum reduced grid

To obtain a general appreciation of the portancy values of the elements of the base grid, the results are shown graphically. That is, each element of the base grid is drawn in proportion to its portancy. The result is called a ‘portancy map’. Fig 3.22 shows a portancy map based on a ten times repeat of the genetic process.

Table 3.2 Results for ten times repetition

Element	Summation of internal forces	Portancy
A	7.05	0.08
B	35.87	0.40
C	49.42	0.55
D	89.28	1.00
E	13.93	0.16
F	70.26	0.79
G	2.33	0.03
H	72.08	0.81
I	1.42	0.02
J	29.95	0.34
K	14.14	0.16

The portancy map indicates the degree of importance of each element of the base grid. In this context two aspects of importance are considered for an element. One aspect is the role of an element in the statically stability. Another aspect is the contribution of the element in carrying the loads, while the fitness function is minimised. A portancy map which is produced based on several optimised grids indicates the relative importance of the elements from view points of both of the above considerations.

A portancy map may be imagined as a map representing an average of the results obtained by repeating the optimisation process. A question may arise at this point, namely, how many times the process should be repeated in order to give rise to a reliable portancy map. In this relation, one may carry out a statistical investigation. To elaborate, the force distribution corresponding to each resulting reduced grid may be considered as a sample that has been obtained in a stochastic procedure. Then, the required number for repeating the process may be found based on a statistical analysis such that a ‘good’ average is obtained for these samples. However, in this work a simple procedure is proposed for this purpose and this will be explained in detail in the sequel. This simple procedure is based on the following discussion.

Fig 3.21 Base grid and selected elements

Fig 3.22 Portancy map for ten repetitions

Returning to Figs 3.18 and 3.20, the force distributions given in these figures are obtained assuming the number of the genes of each chromosome in the population is equal to the number of the elements of the base grid. While the genetic process proceeds, each gene of a chromosome may experience changes independent from the other genes of that chromosome. Therefore, although the base grid under consideration is a grid with at least two axes of symmetry, as shown in Fig 3.23, the genes representing the elements in the symmetrical positions are not necessarily the same. For instance, suppose that the gene corresponding to element E1 in Fig 3.23 is 1. The genes corresponding to elements E2 to E4 may be 0 or 1. Then a resulting reduced grid such as the one given in Fig 3.17 is not normally symmetrical. As a result, the force distributions corresponding to these reduced grids are not symmetrical, as shown in Figs 3.18 and 3.20.

Fig 3.23 Base grid and symmetry axes

Now, consider the portancy map shown in Fig 3.22 which is produced by ten repetitions of the genetic process. By comparing Figs 3.18 and 3.20 with the portancy map of Fig 3.22, it may be seen that whereas the results in Figs 3.18 and 3.20 have a 'poor' symmetry, the portancy map of Fig 3.22 has a 'better' symmetry. Now, let the portancy map of Fig 3.22 be

compared with the portancy map of Fig 3.24 which is based on twenty repetitions of the genetic process. As it is seen from these figures, the portancy map shows a better symmetry for the 20 times repeat. Experience shows that the symmetry is improved while the number of the repetitions of the process is increased although, a complete symmetry, may not be achieved.

In this work, the anticipated symmetry for the portancy values of the elements is used as a criterion to find the number of the times that the genetic process should be repeated. To elaborate, each resulting reduced grid which is the best solution given by the genetic algorithm, is obtained in a random manner. The symmetry of the portancy map is an assurance that the genetic algorithm has explored all the domain of the search space randomly and it has no bias to some particular parts of the search space. Then, the symmetry may be considered as a suitable criterion for the determination of the number of the times necessary for repeating the genetic process. Since the complete symmetry cannot be achieved, then the symmetry is checked for the elements with more contribution in carrying the loads. That is, the number of the repetitions of the genetic process is controlled such that the symmetry is satisfied for the elements with the highest portancies.

Here, the procedure for checking the symmetry is explained in relation to the base grid of Fig 3.1. This grid has four axes of symmetry two of which are shown in Fig 3.23. Consider elements E1, E2, E3, and E4 of this grid that are in the symmetrical positions. The portancies of these elements are expected to be almost the same. Suppose that at one occasion the genetic process is carried out once, and the resulting portancy values for the elements under consideration are as follows:

<u>Element</u>	<u>Portancy</u>
E1	0.8315
E2	0.8480
E3	0.8078
E4	1.0000

The average for these portancies is equal to 0.8718 and the absolute values of differences between the portancies of these four elements and the average are as follows:

Fig 3.24 Portancy map for twenty repetitions

<u>Element</u>	<u>Portancy difference with average</u>
E1	0.0403
E2	0.0238
E3	0.0640
E4	0.1282

The obtained values are divided by the average. The results which are the proportional differences are shown below:

<u>Element</u>	<u>Proportional difference</u>
E1	0.0462
E2	0.0273
E3	0.0734
E4	0.1470

Now, suppose that the genetic process is repeated ten times. The portancy values for these elements on that occasion are as follows:

<u>Element</u>	<u>Portancy</u>
E1	0.9266
E2	0.9492
E3	0.9747
E4	0.9115

The average of these portancies is equal to 0.9405 and the portancy differences with their average are as follows:

<u>Element</u>	<u>Portancy difference with average</u>
E1	0.0139
E2	0.0087
E3	0.0342
E4	0.0290

The proportional differences are as below

<u>Element</u>	<u>Proportional difference</u>
E1	0.0148
E2	0.0093
E3	0.0364
E4	0.0308

The maximum value of the proportional differences for the one time repetition case given before is equal to 0.1470. The value of this maximum for the ten times repetition case is equal to 0.0364. It is seen that the value of this maximum is decreased substantially with the increase of the repetitions.

Decreasing the proportional differences for the elements in the symmetrical positions may help to define a criterion for controlling the number of the repetitions of the genetic process. Based on this criterion the process is repeated until the maximum value of the proportional differences for the elements in the symmetrical positions become less than a small value, namely, η . A typical value for η may be chosen to be 0.001. Thus, after each time completing the genetic process, the proportional differences for the elements in the

symmetrical positions are calculated. If these values are smaller than η , then the program is terminated.

Returning to the base grid of Fig 3.1 with 648 elements, there are 171 groups of elements each of which contains a number of elements that are in symmetrical positions. For instance, the four elements E1 to E4 indicated in Fig 3.24 correspond to one group, while another group contains only two elements E5 and E6. One could have required that the proportional differences for all the groups of the elements of the base grid are less than η . However, it is sufficient for the checking to be carried out for a couple of the groups of the elements that have the highest portancy values. For the example under consideration, two groups of the symmetrical elements with the highest portancies are checked. Fig 3.25 shows a portancy map for the base grid of Fig 3.1. This portancy map is obtained based on 339 times repetitions of the genetic process. In this example a value of 0.001 has been considered for η . A flow chart of the process for obtaining the portancy map is given in Fig 3.26. The stages of the process are carried out through a number of computer programs written by the author. A description of these programs is given in Appendix B.

Fig 3.25 Portancy map

Fig 3.26 Flow chart of the process for obtaining the portancy map

Now, let the portancy map shown in Fig 3.25 be investigated in more detail. As explained before, the portancy map is used for graphically illustrating the degrees of importance of the elements of the base grid. The numerical value of the portancies expressing the importance of an element is between 0 and 1. For example, elements E1 to E4 of the base grid which are indicated in Fig 3.24 have the portancies 0.9545, 0.9549, 0.9552 and 0.9556, respectively. These portancies correspond to four elements of the double layer grid which are in symmetrical positions. The average of the portancies of these elements is equal to 0.9551 and the corresponding proportional differences for elements E1 to E4 are 0.0006, 0.0002, 0.0002 and 0.0005, respectively. It is seen that the maximum of these values is less than η which is assumed to be 0.001. That is, the criterion considered for symmetry is satisfied. Here, it should be noted that for drawing the portancy map, the portancy values have been classified in 9 groups. Each group contains the portancy values corresponding to a specified range. The ranges for this classification that have been used in this work are listed in Table 3.3.

The portancy map provides an overall view of the element portancies. So, it cannot be used to find the accurate portancy of a particular element. However, the accurate values of the portancies of the elements of the base grid are saved in a file and may be used when the accurate values are of interest.

Referring to the portancy map of Fig 3.25, the elements with high portancies are the elements that are expected to have large internal forces. For example, the web elements near the supports and the top and bottom layer elements in the middle region of the grid are usually the elements with large internal forces. These elements are seen to be represented by thick lines in the portancy map of Fig 3.25. On the other hand, the portancy map is based upon a number of reduced grids each of which is the result of an optimisation process. In the optimisation process two aspects have been considered for obtaining the optimum solution. One aspect is the statically stability and the other aspect is the magnitude of the internal force associated with each element. It may then be concluded that an element of high portancy has appeared in the majority of the reduced grids and it has carried large loads. An element may have a high portancy because it has an

Table 3.3 Portancy groups

Group	Rang of portancy values
1	0.0-0.2
2	0.2-0.3
3	0.3-0.4
4	0.4-0.5
5	0.5-0.6
6	0.6-0.7
7	0.7-0.8
8	0.8-0.9
9	0.9-1.0

important role in the static stability of the grid and carries large internal forces. Therefore, one of the main benefits of the portancy map is that a designer may obtain an overall view of the contribution of the elements in carrying the loads. This overall view is useful in designing an efficient grid. For a particular support conditions and loading arrangement, the portancy of an element of the base grid is a specification that describes how important that element is at its position in the grid. However, the portancy of a particular element may vary when the support conditions and the external loads are changed.

3.5 SOME INVESTIGATIONS IN RELATION TO THE PORTANCY MAP

3.5.1 Statistical Investigations

To find the portancy map of Fig 3.25, it was assumed that all the elements of the grid have the same cross-sectional area. Also, it was assumed that the plan of the grid is square, and therefore, all the top and bottom layer elements are of the same length. Furthermore, the depth of the grid was chosen such that the web elements have the same length as the top and bottom layer elements. The effects of these assumptions on the portancy map are investigated as follows. For this investigation two different cases are considered. First, suppose that the cross-sectional areas are not the same. As an example, three different values are considered for the cross-sectional areas. Namely, all the web elements are assumed to have a cross-sectional areas equal to A . For the elements of the bottom and top layers the cross-sectional areas are considered to be $2A$ and $3A$, respectively. Fig 3.27 shows the portancy map obtained for this case. In another case, besides the stated variations of the cross-sectional areas of the elements, different lengths are considered for the elements of the base grid. Here, the elements of the bottom and top layers have the lengths equal to L unit length. For the web elements the length of $0.7L$ unit length is considered. The portancy map obtained for this case is shown in Fig 3.28. It can be seen from Figs 3.27 and 3.28 that these portancy maps are very similar to the portancy map of Fig 3.25.

Here, a statistical investigation is carried out to see what may be regarded as similarity in terms of statistical parameters. To this end, the portancy values corresponding to the portancy maps of Figs 3.25, 3.27 and 3.28 are used as statistical data. This is justifiable because the portancy values are produced through a stochastic process and are therefore randomly obtained values. To elaborate, considering the procedure used for obtaining the portancy values, it starts by generating random values and involves genetic operators such as selection, crossover and mutation which all work using random numbers. Consequently, the values are obtained through a random process and may be used as statistical data.

Fig 3.27 Portancy map for different cross-sectional areas

Fig 3.28 Portancy map for different lengths

To find out how similar are two sets of data, first the ‘mean’ (average) of each set of data is calculated. It is also important to know how the data is spread about its mean. ‘Variance’ is a measure that indicates how far away data are from the mean. For the case under consideration, statistical investigation is carried out as follows:

1. The mean of the portancies are calculated for all groups of the elements in the symmetrical positions. For the base grid under consideration (Fig 3.1), there are 171 such groups of elements. For instance, one of these groups contains elements E1 to E4 indicated in Fig 3.23. Then, there are 171 mean values that are considered as statistical data and will be sorted in descending order.
2. Then the mean and variance are calculated for different subsets of data. To elaborate, for the first ten values of the sorted data the values of mean and variance are calculated. The mean and standard deviation are also calculated for the first 20, 50, 100 and 150 as well as all the 171 values.

The standard deviation for each of these groups of data is calculated using the equation

$$\sigma^2 = \frac{\sum (x - \mu)^2}{N} \quad 3.16$$

where,

- σ^2 is the variance of the set of data,
- x is an item of the data,
- N is the number of the items in the data and
- μ is the mean for the set of data and is equal to

$$\mu = \frac{\sum x}{N}$$

The results obtained for three different cases, whose corresponding portancy maps are shown in Figs 3.25, 3.27 and 3.28, are listed in Table 3.4. From this table, it is seen that for each group of data the results are close to each other. For instance, for the group of data corresponding to 20 items, the mean has a value about 0.7 for different cases and also the values of variances are about 0.02. It is therefore seen that the data obtained for three different cases show an acceptable similarity.

Table 3.4 Data and statistical parameters

Statistical parameters	Cases	The number of data in a group					
		10	20	50	100	150	171
Mean	Case 1	0.904	0.771	0.503	0.315	0.226	0.200
	Case 2	0.879	0.738	0.474	0.292	0.208	0.184
	Case 3	0.885	0.738	0.470	0.291	0.209	0.186
Variance	Case 1	0.004	0.022	0.065	0.068	0.061	0.059
	Case 2	0.006	0.024	0.064	0.065	0.058	0.055
	Case 3	0.005	0.026	0.067	0.066	0.057	0.054

Now, investigation for evaluating the sensitivity of the portancy values to the variations of the cross-sectional areas and the element lengths is carried out in another way. To this end, first it is assumed that all the elements of the base grid are of the same length and the cross-sectional areas are varied. In this investigation 16 sets are considered for the cross-sectional areas of the elements (CS) as listed in Table 3.5. For simplicity, the cross-sectional areas of the elements of each layer are considered to be the same. Therefore, three types of cross-sections are considered for the grid. In Table 3.5, the first set of the cross-sectional areas relating to case 1 is the same as that was used for obtaining the portancy map of Fig 3.25. The portancy values of this map are referred to as 'base data'. The other cases are compared with the base data. Here, the portancy values relating to 16 different cases are involved as 16 set of data each of which generated through a stochastic process. To find how similar is each set of data with the base data, a statistical investigation is carried out as follows.

As a criterion for similarity between groups of data, the 'error sum of squares' [33] denoted by SSE is calculated as below:

$$SSE_j = \sum_{i=1}^N (p_i - q_{ij})^2 \quad 3.17$$

where,

- SSE_j is the error sum of squares for j^{th} set of data,
- N is the number of the elements of the base grid,
- P_i is the portancy of the i^{th} element of the base grid whose portancy values are considered as base data and

- q_{ij} is the portancy value of the i^{th} element of the base grid with j^{th} set of the cross-sectional areas.

SSE_j for the data corresponding to case one is zero. The larger SSE_j , the less similarity between the portancy values of the base grid with the cross-sectional areas of case j and the portancy values of the map of Fig 3.25.

Table 3.5 Cross-sectional areas for different cases

Case	C.S for the top layer elements	CS for the bottom layer elements	CS for the web elements
1	A	A	A
2	2A	A	A
3	3A	A	A
4	4A	A	A
5	0.8A	A	A
6	0.5A	A	A
7	A	2A	A
8	A	3A	A
9	A	4A	A
10	A	0.8A	A
11	A	0.5A	A
12	A	A	2A
13	A	A	3A
14	A	A	4A
15	A	A	0.8A
16	A	A	0.5A

In Table 3.6, are listed the raw and also normalised values of SSE_j . The normalised values, namely e_j , are calculated as follows:

$$e_j = \frac{SSE_j}{\sum p_i} \quad 3.18$$

The graph indicating the variations of e_j is shown in Fig 3.29. As it is seen from this figure and also from Table 3.6, in most cases the value of e_j is around zero. Except for cases 13 and 14 in which, the differences are noticeable. As it may be seen from Table 3.5, for the cases 13 and 14 the cross-sectional areas of the web elements have been considered respectively, to be

3 and 4 times of the top and bottom layer elements. This is not a usual choice for practical designs, and therefore, the results related to these two cases can be ignored.

Table 3.6 Errors for different cases

Case	SSE	e
1	0.000	0.000
2	0.586	0.005
3	0.803	0.007
4	0.891	0.007
5	0.306	0.003
6	0.897	0.007
7	0.308	0.003
8	0.631	0.005
9	1.000	0.008
10	0.0706	0.001
11	0.725	0.006
12	1.271	0.010
13	3.766	0.031
14	4.571	0.038
15	0.164	0.001
16	0.583	0.005

To investigate the effects of the variations of lengths of the elements on the similarity of portancy maps, the depth of the grid is changed. Due to the changes in the depth, the lengths of the web elements will differ from the top and bottom elements. Thereafter, the statistical investigation is carried out in the same manner explained for the case in which the cross-sectional areas were considered being changed. Here, five cases are considered and the error sum of squares is calculated for each case. The results are listed in Table 3.7. In this table, the results related to the portancy map of Fig 3.25 are also included (Case 3). As it is seen from this table, the normalised values of errors are rather small. This implies that there is an acceptable similarity between the set of portancy values of the elements of the base grid for different lengths that may be considered for the elements of the base grid.

Eventually, it may be concluded from statistical investigations that the portancy may be considered as a concept independent of the dimensions of the elements of the base grid. That is, the portancy maps are almost the same even when the lengths or the cross-sectional areas

of the elements are changed. However, as will be shown later, the portancy map is highly dependent on the support conditions.

Fig 3.29 Variations of errors

3.5.2 Sensitivity of Portancy Map to Parameters Used by Genetic Approach

The portancy map of Fig 3.25 was obtained based on the following assumptions:

- The size of the initial population was 100,
- the mutation rate was taken as 0.005 and
- the penalty value considered for statically unstable structures was 3 times the fitness value of the base grid.

Table 3.7 Errors for different cases

Case	Depth of the grid	<i>SSE</i>	<i>e</i>
1	$0.3\sqrt{2}L$	0.470	0.004
2	$0.4\sqrt{2}L$	0.163	0.001
3	$0.5\sqrt{2}L$	0.000	0.000
4	$0.6\sqrt{2}L$	0.215	0.002
5	$0.8\sqrt{2}L$	1.194	0.010
6	$\sqrt{2}L$	2.654	0.022

Now, each of these parameters is varied and the effects of the changes are investigated through a statistical study. First, the size of the population is decreased to 50 and the portancy values are obtained. Here, the other parameters are the same as used for the case of the portancy map of Fig 3.25. In another case, the mutation rate is changed to 0.01 and the other parameters remain constant. With this assumption for the mutation rate, the portancy values of the elements of the base grid of Fig 3.1 are found. In relation to the penalty considered for statically unstable structures, two different assumptions are considered. As the first

assumption, the penalty is taken 10 times of the fitness value of the base grid, that is, the value of 10 is assumed for the penalty. As the second assumption, after each generation the penalty for statically unstable structures is taken as two times the fitness values of the worst member of the previous generation. This study shows that the portancy maps obtained based on the above assumptions are similar. This similarity is investigated through a statistical study. To this end, the mean and variance are calculated for different groups of data. The numerical results are listed in Table 3.8.

In Table 3.8, the statistical values in case 1 correspond to the portancy values obtained for the portancy map of Fig 3.25. The statistical values obtained for the population size of 50 are listed as case 2. Also, statistical values for case 3 relates to the mutation rate of 0.01. The values listed as case 4 and case 5 correspond to the two different assumptions considered for the penalty values assigned to the statically unstable structures.

As it is seen from Table 3.8, for each group of data considered for different cases the results are close to each other. For instance, for the group of data corresponding to 20 items, the mean has a value about 0.77 for different cases and also the variance has a value about 0.02. So, it may be concluded that the data obtained for five different cases show an acceptable similarity.

Table 3.8 Data and statistical parameters

Statistical parameters	Cases	The number of data in a group					
		10	20	50	100	150	171
Mean	Case 1	0.904	0.771	0.503	0.315	0.226	0.200
	Case 2	0.901	0.776	0.509	0.320	0.231	0.205
	Case 3	0.894	0.778	0.510	0.327	0.239	0.214
	Case 4	0.900	0.768	0.499	0.311	0.223	0.198
	Case 5	0.900	0.765	0.498	0.312	0.223	0.198
Variance	Case 1	0.004	0.022	0.065	0.068	0.061	0.059
	Case 2	0.005	0.020	0.064	0.068	0.062	0.059
	Case 3	0.005	0.018	0.062	0.066	0.060	0.057
	Case 4	0.004	0.022	0.064	0.068	0.061	0.058
	Case 5	0.004	0.022	0.064	0.068	0.061	0.058

3.6 EFFECTS OF THE SUPPORT ARRANGEMENTS ON THE PORTANCY MAP

To investigate the effects of different support arrangements on the element portancies, some commonly used types of support conditions are considered for the case of the double layer grid of Fig 3.1. These support conditions are as follows:

- Supports at four top layer nodes
- Supports at all nodes around the bottom layer
- Supports at eight top layer nodes

Consider the support arrangement shown in Fig 3.30 where the grid is supported at four top layer nodes. In this figure, support S1 is constrained in directions X, Y and Z. Support S2 is constrained in directions Y and Z and the other support are constrained in the Z direction only.

Fig 3.30 Base grid

The grid is subjected to equal concentrated loads at all the top layer nodes, in the negative Z direction. The portancy map associated with the base grid of Fig 3.30 is shown in Fig 3.31. Comparing Figs 3.25 and 3.31, it is seen that some of the elements that have large portancies in the case of Fig 3.25 have small portancies in Fig 3.31. For instance, the elements in the middle regions of the top and bottom layers have small portancies as shown in Fig 3.31. However, some of the elements of the base grid of Fig 3.30 have greater portancies in comparison with the elements of the base grid of Fig 3.1 which are at the same positions. For example, the top and bottom layer elements lying in the side regions of the base grid of Fig 3.30 have greater portancies as shown in Fig 3.31.

Fig 3.31 Portancy map

Now, consider the support arrangements shown in Fig 3.32, where the grid is supported at all nodes on the edges of the bottom layer. As indicated in this figure, support S1 is constrained in X, Y and Z directions. Also, support S2 is constrained in directions Y and Z and the other supports are constrained in the Z direction only. The grid is subjected to equal downward concentrated loads applied at all the top layer nodes. The procedure described before for obtaining the portancy map of Fig 3.25 is carried out for the base grid of Fig 3.32. The portancy map associated with this base grid is shown in Fig 3.33. This portancy map has been obtained based on 475 repetitions of the genetic process.

Fig 3.32 Base grid

Comparing the portancy maps of Figs 3.25 and 3.33, some similarities may be seen between these figures, in particular, for the top and bottom elements in the middle regions of the double layer grids. This is reasonable, because of the similarity between two cases. That is, they have the same configurations and loads with somewhat similar support conditions. In both base grids of Figs 3.1 and 3.32 the supports are arranged at the nodes on the edges of the bottom layer. Although, a fewer number of supports are considered for the base grid of Fig 3.1.

The procedure developed in Section 3.4 is carried out to find the portancy map for the double layer grid of Fig 3.34 with the support arrangement shown in the figure. Here, the base grid is supported at eight top layer nodes near the centre of the grid. With this type of support arrangement the grid acts as a cantilever roof. In this example, support S1 is constrained in X, Y and Z directions, support S2 is constrained in Y and Z directions and the other supports are

constrained in the Z direction only. The loading arrangement is the same as for the previous case.

Fig 3.33 Portancy Map

The portancy map obtained for the base grid of Fig 3.34 is shown in Fig 3.35. This portancy map is based on the result of 242 repetitions of the genetic process. That is, after 242 times running, the criterion for the symmetry has been satisfied. In this case, a value of 0.001 is assumed for η as the symmetry criterion. As may be seen from Fig 3.35, the top and bottom layer elements lying in the middle part of the grid, in the region of the supports, have the greatest portancies. Also, it is seen that the more distant an element is from the middle part the smaller is its portancy.

3.7 COMPARING REDUCED GRIDS USING THE PORTANCY MAP

The portancy values of the elements of the base grid may be used for comparing the reduced grids to find the most suitable one. Referring to Figs 3.4 to 3.7, it is seen that the patterns of element removal are different for the reduced grids, although the number of the removed elements is the same for all of them (namely, 32 elements). For instance, in the reduced grid of Fig 3.5 the elements have been removed from the regions near the supports, while in the reduced grid of Fig 3.7 the removed elements belong to the middle region of the grid.

Fig 3.34 Base grid

Also, in the reduced grids of Figs 3.4 and 3.6 the elements have been removed from the places between the supports and the middle regions of the grids. For comparing the reduced grids of Figs 3.4 to 3.7, the portancy values of the removed elements of each reduced grid are added together. Here, the portancy values of the elements of the base grid of Fig 3.1 are used. The results are listed in Table 3.9.

Table 3.9 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.4	1.5
Grid of Fig 3.5	6.5
Grid of Fig 3.6	8.2
Grid of Fig 3.7	13.3

As it is seen from Table 3.9, the summations of the portancy values of the removed elements vary in a wide range between 1.5 and 13.3. Comparing these values with each other, it may be concluded that for a grid that its corresponding value of summation of portancies is greater, the removed elements have higher portancies, and therefore, more important elements have been eliminated from the base grid for generating that reduced grid. For instance, comparing the values corresponding to the reduced grids of Figs 3.4 and 3.7, the base grid has lost more important elements for producing the reduced grid of Fig 3.7. So, it may be concluded that if both of these reduced grids are acceptable from the viewpoint of architecture, the reduced grid of Fig 3.4 may be chosen as the more suitable one. Here, it should be noted that this comparison is valid only if the support conditions of the reduced grids are the same as the support condition of the base grid of Fig 3.1

Fig 3.35 Portancy map

To find the portancy map of Fig 3.25, the absolute values of the internal forces of the optimum reduced grids are added to each other. In this case, no difference is considered for the elements which are in tension and those elements of the base grid which are in compression. To investigate the influence of this assumption on the results, the portancy maps are obtained with the internal forces of the compressive elements are multiplied by a factor, namely, β . That is, the internal forces of these elements are modified. Since it is not known

that the internal forces of the compressive elements should be increased or decreased, then for the factor of β four different values equal to 0.50, 0.75, 1.25 and 1.5 are considered. That is, for two cases the internal forces of the compressive elements are decreased by multiplying them by $\beta < 1$ and for the other two cases, the internal forces of these elements are increased by multiplying them by the factor $\beta > 1$. The portancy maps associated with different values of β are shown in Figs 3.36 to 3.39. Now, the reduced grids of Figs 3.4 to 3.7 are evaluated in terms of the portancies of their corresponding elements, using the portancy maps given in Figs 3.36 to 3.39. The results are listed in Table 3.10

As it is seen from Table 3.10, although the values of the summations of the portancy values of the removed elements are changed, but the rankings of these values for different values of β have not changed and are the same as the rankings given in Table 3.9. The rankings given in Table 3.9 are in fact for the case that β has been considered to be 1. For a better comparison, the results for this case have been repeated in Table 3.10.

Table 3.10 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements				
	$\beta=0.50$	$\beta=0.75$	$\beta=1.00$	$\beta=1.25$	$\beta=1.50$
Grid of Fig 3.4	1.4	1.4	1.5	1.1	0.9
Grid of Fig 3.5	6.1	6.6	6.5	5.8	4.9
Grid of Fig 3.6	8.4	8.7	8.2	6.8	5.8
Grid of Fig 3.7	14.2	14.4	13.3	10.6	8.5

3.7.1 Weight Optimisation of Reduced Grids

To investigate the reliability of the portancy map as a tool for comparing the reduced grids, a weight optimisation process is carried out. That is, the minimum weight of each of the reduced grids of Figs 3.4 to 3.7 are obtained with the support arrangements and load conditions remaining constant for all of the reduced grids. In this optimisation process, since each grid has four symmetry axes, (as shown in Fig 3.40), then the cross-sectional areas of the elements of 1/8th of the double layer grid may be considered as the independent variables of the optimisation problem.

Fig 3.36 Portancy map for $\beta = 0.5$

Fig 3.37 Portancy map for $\beta = 0.75$

Fig 3.38 Portancy map for $\beta = 1.25$ Fig 3.39 Portancy map for $\beta = 1.50$

Fig 3.40 Reduced grid and its symmtery axes

Suppose that the reduced grid of Fig 3.4 has dimensions 36 m in X and Y directions as shown in Fig 3.40. The depth of the double layer grid, that is, the vertical distance between the centres of the top and bottom layer elements is taken as 2.8 m. With this value of depth, the web elements of the grid are of the same lengths as the top and bottom layer elements. The grid is subjected to equal downward concentrated loads of magnitude 32 kN at all the top layer nodes. Modulus of elasticity is considered to be 200 kN/mm² and the yield stress is assumed to be equal to 240 N/mm². The density of the material is considered to be 7850 kg/m³. The allowable axial stresses of the elements are assumed to be limited to 140 N/mm². The allowable buckling stresses for the compressive elements are calculated using the procedure explained in Section 2.11.5. The allowable vertical displacements of the joints are assumed to be limited to 1/400th of the length of a side of the top layer.

The elements of the structure are steel tubes. Both the outside and inside diameters of the tubes may vary during the optimisation process. To reduce the number of the variables of the problem, the thickness of each tube is taken to be equal to 1/15th of its outside diameter. Then the inside diameter is equal to:

$$d_{in} = d_{out} - \frac{2}{15} \times d_{out} = \frac{13}{15} \times d_{out}$$

where, d_{in} and d_{out} are the inside and outside diameters of a tube, respectively.

The cross sectional area of an element is calculated as follows

$$A = \frac{\pi}{4} \times (d_{out}^2 - d_{in}^2) = 0.196 \times d_{out}^2$$

where, A is the cross-sectional area.

Thus, the outside diameters of the elements are considered as the independent variables of the optimisation problem. The number of the independent variables is equal to the number of the elements in 1/8th of the double layer grid. For the case of the reduced grid of Fig 3.4 this number is equal to 85. A range is specified such that all independent variables, that is, the outside diameters of the tubes remain within that range. For the example of Fig 3.40, this range is assumed to be 60-150 mm.

The genetic approach developed in Chapter 2 is employed for minimising the weight of each of the reduced grids of Figs 3.4 to 3.7. The minimum weights obtained on one occasion for

the grids together with their corresponding summations of the portancies of the removed elements are listed in Table 3.11

Table 3.11 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 3.4	229.6	1.5
Grid of Fig 3.5	232.4	6.5
Grid of Fig 3.6	237.4	8.2
Grid of Fig 3.7	270.2	13.3

As it is seen from Table 3.11, for the cases of Figs 3.4 to 3.7, the results obtained from the weight optimisation are consistent with the results obtained by comparing the summation of the portancy values. To elaborate, comparing the grids of Figs 3.4 to 3.7, using the summations of the portancies leads to the choice of the grid of Fig 3.4 as the more suitable reduced grid. On the other hand, from Table 3.11, it is seen that the grid of Fig 3.4 is lighter than the grids of Figs 3.5 to 3.7. That is, choosing the grid of Fig 3.4 is associated with less weight and thus this grid is preferred to the other grids, provided that all of these grids are acceptable from the other viewpoints.

Referring to Table 3.11 again, for obtaining the minimum weights of the grids of Figs 3.4 to 3.7, the depth of the grid is assumed to be 2.8 m. For this value of depth, all the elements of the grid have the same length. To investigate the sensitivity of the results to this assumption, the depth of the grid is taken as 1.8 m. That is, the depth of the grid is assumed to be 1/20th of the length of a side of the top layer. With this value for depth, the elements of the web of the grid are not of the same length as the top and bottom layer elements. In this case, the results obtained for the minimum weights together with the summation of the portancies of the removed elements of the reduced grids are listed in Table 3.12.

As may be seen from Table 3.12, the ranks of the minimum weights obtained for the reduced grids of Figs 3.4 to 3.7 are again consistent with the ranks obtained based on the summations of the portancies of the removed elements. Here, it should be noted that comparing the reduced grids according to their corresponding minimum weights is carried out to show that

the concept of portancy is based on strong logic. That is, by comparing the grids from the viewpoint of the minimum weights associated with the grids, the results confirm the reliability of the portancy values in a satisfactory manner.

Table 3.12 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 3.4	248.0	1.5
Grid of Fig 3.5	259.8	6.5
Grid of Fig 3.6	266.8	8.2
Grid of Fig 3.7	362.7	13.3

3.7.2 Comparing the Reduced Grids with Other Support Arrangements

Continuing the discussion concerning the comparison of the reduced grids in terms of the summations of the portancies of the removed elements, the grids of Figs 3.4 to 3.7 with support arrangements as the base grid of Fig 3.30 are compared with each other. This comparison is carried out based on the portancy values used for the portancy map of Fig 3.31. The results are listed in Table 3.13.

Table 3.13 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.4	5.5
Grid of Fig 3.5	5.4
Grid of Fig 3.6	4.1
Grid of Fig 3.7	3.2

Comparing the rankings associated with the summations of the portancies of the removed elements listed in Tables 3.11 and 3.13, it is seen that the reduced grid of Fig 3.7 which has the lowest rank in Table 3.11 is of the highest rank in Table 3.13. This is reasonable because of the manner in which the double layer grid is supported at four near-corner nodes. Thus, the elements in the middle part of the grid have less contribution in carrying the loads, and therefore, the base grid loses less important elements if the removed elements belong to this

part of the grid. Another point relating to the values listed in Table 3.13 is that the summations of the portancies of the removed elements are almost close to each other for all the reduced grids of Figs 3.4 to 3.7. For example, these values are 5.5 and 5.4 for the grids of Figs 3.4 and 3.5, respectively. This means that these two reduced grids are almost of the same degree of suitability.

The weight optimisation procedure is carried out for the reduced grids of Figs 3.4 to 3.7 with the support arrangements indicated in Fig 3.30. Considering the length of 36 m for the grid dimensions in X and Y directions and the depth of 2.8 m, the results obtained for minimum weights of the reduced grids are listed in Table 3.14, together with the summations of the portancies of the removed elements. In this case the outside diameters of the tubes are in the rang 100-250 mm. As it is seen from Table 3.14, the optimum weights of the reduced grids are not too different and are spread in the range of 584.1 to 588.7 kN. The ranks of the weights are almost consistent with the ranks of the portancies, except for the grids of Figs 3.4 and 3.5.

Table 3.14 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 3.4	587.5	5.5
Grid of Fig 3.5	588.7	5.4
Grid of Fig 3.6	586.5	4.1
Grid of Fig 3.7	584.1	3.2

Here, it should be emphasised that the weight is not the only feature of a structure that may be used as a criterion for comparing the suitability of the structures. For example, suppose that the cost minimisation of a space structure is of interest. In this case, the cost of the joints used for connecting the elements of the structure constitutes a major part of the expenses. However, the joint costs are not incorporated in the weight optimisation process and, therefore, it does not follow that the lighter structure is necessarily of lower cost. So, in this context, the optimum weights obtained for the reduced grids are involved as benchmarks for evaluating the reliability of the approach developed in this work. However, this approach leads to the creation of the portancy map, which contains valuable information in relation to

the positions of the elements that have more contribution in carrying the loads. That is, in the portancy map the principal force paths are identified. So, The comparison of two reduced grids derived from a base grid with the same numbers of removed elements, leads to the choice of the reduced grid that has lost less number of its elements that have more contribution in carrying the loads. This choice by itself is of considerable importance and, therefore, the proposed approach may be used as a powerful tool for comparing the reduced grids.

With the support conditions indicated in Fig 3.32, the reduced grids of Figs 3.4 to 3.7 are compared with each other with respect to the summations of the portancies of their corresponding removed elements. The portancy values used for the portancy map of Fig 3.33 are used for this comparison. The results are listed in Table 3.15.

Table 3.15 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.4	10.2
Grid of Fig 3.5	8.0
Grid of Fig 3.6	13.3
Grid of Fig 3.7	15.8

Comparing the results listed in Tables 3.9 and 3.15, it is seen that the reduced grid of Fig 3.4 which has the rank one in Table 3.9 is of rank two in Table 3.15. Also, for the reduced grid of Fig 3.5 its rank has been changed from two in Table 3.9 to one in Table 3.15. This is reasonable, because for the case of the reduced grid of Fig 3.5 with support conditions as the base grid of Fig 3.1, the elements have been removed from regions near the supports that have great portancy values. That is, the summations of the portancy values of the removed elements of the reduced grid of Fig 3.5 will be greater than that of the reduced grid of Fig 3.4. However, for the support conditions of Fig 3.32, the loads have been transmitted to more supports and thus the elements near the supports have less portancy values. Therefore, the summations of the portancy values of the removed elements of the reduced grid of Fig 3.5 will be smaller than those of the reduced grid of Fig 3.4.

Now, let the weight optimisation be carried out for the reduced grids of Figs 3.4 to 3.7 with the support conditions similar to that of the base grid of Fig 3.32. Assuming the length of 36 metre for the grid dimensions in X and Y directions and considering the depth of 2.8 m for the reduced grids, the genetic process is carried out and the minimum weights of the reduced grids are obtained. For this case, the outside diameters of the tubes are in the range 60-150 millimetres. The results are listed in Table 3.16. Also, in this table the summations of the portancies of the removed elements of the reduced grids are listed again. As it may be seen from Table 3.16, the rank of the minimum weight obtained for each reduced grid is consistent with the rank of its corresponding summation of the portancies of the removed elements.

Continuing the investigation of the effects of the support conditions, as the next example the reduced grids of Figs 3.4 to 3.7 are supported at eight top layer nodes as shown for the base grid of Fig 3.34. In this case, the portancy values obtained for the portancy map of Fig 3.35 are used for comparing the reduced grids of Figs 3.4 to 3.7. The results are listed in Table 3.17.

Table 3.16 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 3.4	214.4	10.2
Grid of Fig 3.5	212.2	8.0
Grid of Fig 3.6	217.7	13.3
Grid of Fig 3.7	229.5	15.8

As it may be seen from Table 3.17, the summations of the portancies of the removed elements of the reduced grids of Figs 3.4 and 3.5 are smaller than those of the grids of Figs 3.6 and 3.7. This is reasonable because the base grid of Fig 3.34 operates as a cantilever plate when it is subjected to vertical loads. In this case, the elements in the middle region of the grid and also those near the supports have more contributions in carrying the loads. Hence, the reduced grids of Figs 3.6 and 3.7 which are obtained by removing equal numbers of elements from these critical regions of the base grid are less suitable in comparison with the reduced grids of Figs 3.4 and 3.5.

Table 3.17 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.4	9.0
Grid of Fig 3.5	8.9
Grid of Fig 3.6	17.5
Grid of Fig 3.7	16.0

The weight optimisation procedure is carried out for the reduced grids of Figs 3.4 to 3.7 with the support arrangements indicated in Fig 3.34. Considering the length of 36 m for the grid dimensions in X and Y directions and the depth of 2.8 m, the results obtained for the minimum weights of the reduced grids are listed in Table 3.18, together with the summations of the portancies of the removed elements. For this case, the outside diameters of the tubes are in the range 80-250 mm. As it is seen from Table 3.18, the optimum weights of the reduced grids of Figs 3.4 and 3.5 are close to each other. And, the optimum weights obtained for the reduced grids of Figs 3.6 and 3.7 are not too different and the ranks of the minimum weights are almost consistent with the ranks of the portancies of the removed elements.

Table 3.18 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 3.4	421.4	9.0
Grid of Fig 3.5	421.6	8.9
Grid of Fig 3.6	436.9	17.5
Grid of Fig 3.7	433.5	16.0

3.8 EFFECTS OF THE LOADING ARRANGEMENT ON THE PORTANCY MAP

In the preceding discussion the portancy maps were obtained for different support conditions, but for one type of loading arrangement. In those cases, the base grids were subjected to equal concentrated loads at all the top layer nodes. Now, let the base grid of Fig 3.1 be subjected to another loading arrangement. To this end, half of the top layer nodes are under the effect of equal concentrated loads of magnitude P in the negative Z direction. These top layer nodes are

located on one side of the horizontal axis of symmetry. This axis of symmetry is shown in Fig 3.23. The portancy map obtained for this case is shown in Fig 3.41.

As may be seen from this figure, half of the double layer grid that has been subjected to the loads involves more elements of high portancy. Now, the portancy values obtained for the construction of the portancy map of Fig 3.41 are used for comparing the reduced grids of Figs 3.4 to 3.7. The results are listed in Table 3.19. Comparing the ranks of the reduced grids listed in this table with those listed in Table 3.11, it is seen that the ranks of the reduced grids for two load conditions are similar.

Table 3.19 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.4	3.1
Grid of Fig 3.5	5.5
Grid of Fig 3.6	7.0
Grid of Fig 3.7	10.9

As another load condition, four central top layer nodes of the base grid of Fig 3.1 are subjected to equal concentrated loads of magnitude P in the negative Z direction. The portancy map associated with this loading arrangement is shown in Fig 3.42. As it may be seen from this figure, the elements of the middle regions of the top and bottom layers have the largest portancy values in comparison with the other elements of the base grid.

The portancy map of Fig 3.42 is used for comparing the reduced grids of Figs 3.4 to 3.7. The results are listed in Table 3.20. Comparing the results obtained for this case with those listed in Table 3.19, it is seen again that the ranks of the reduced grids are similar to the previous cases.

Table 3.20 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.4	1.6
Grid of Fig 3.5	4.9
Grid of Fig 3.6	6.7
Grid of Fig 3.7	16.0

Fig 3.41 Portancy map

Fig 3.42 Portancy map

Here, another investigation is carried out in relation to the effects of the variations of the support conditions and loading arrangements. To this end, the previous loading arrangements used for obtaining the portancy maps of Figs 3.41 and 3.42 are applied on the base grid of Fig 3.1 with the support conditions similar to Figs 3.30 and 3.32. Fig 3.43 shows the portancy map obtained by subjecting half of the top layer nodes of the base grid to equal vertical loads. Also shown in Fig 3.44 is the portancy map obtained by applying four concentrated vertical loads at the four central top layer nodes. As indicated in these figures, the support conditions are the same as that of Fig 3.32. With these two loading arrangements and with the support conditions similar to the base grid of Fig 3.30, the resulting portancy maps are shown in Figs 3.45 and 3.46.

The portancy maps of Figs 3.43 to 3.46 are used for comparing a number of reduced grids. Here, in addition to the reduced grids of Figs 3.4 to 3.7, the reduced grids of Figs 3.47 and 3.48 are also used for this comparison. The summations of the portancies of the removed elements for different cases are listed in Table 3.21. In this table, as it is seen from the leftmost column, the reduced grids are classified into two groups. This grouping is based on the patterns of the holes in the grids.

Table 3.21 Results for different loading arrangements and support conditions

Grid		Support conditions 1			Support conditions 2			Support conditions 3		
		Loading arrangement			Loading arrangement			Loading arrangement		
		(a)	(b)	(c)	(a)	(b)	(c)	(a)	(b)	(c)
Group 1	Grid of Fig 3.4	1.5	3.1	1.6	10.2	6.0	4.9	5.5	3.0	8.6
	Grid of Fig 3.47	11.9	9.4	15.3	15.3	12.0	14.8	4.8	2.2	15.0
	Grid of Fig 3.48	3.0	2.8	0.4	1.4	1.0	0.2	11.2	6.0	6.0
Group 2	Grid of Fig 3.5	6.5	5.4	4.9	8.0	5.6	4.4	5.4	3.3	6.9
	Grid of Fig 3.6	8.2	6.9	6.7	13.3	9.8	7.7	4.1	2.7	10.2
	Grid of Fig 3.7	13.3	10.9	16.0	15.8	13.5	16.8	3.2	2.0	17.5

Fig 3.43 Portancy map

Fig 3.44 Portancy map

Fig 3.45 Portancy map

Fig 3.46 Portancy map

Fig 3.47 A reduced grid

Fig 3.48 A reduced grid

The support conditions 1 in Table 3.21 is used for the case of the supports indicated in Fig 3.1. The support conditions 2 and 3 are used for the cases of the supports shown in Figs 3.32 and 3.30, respectively. Also, loading arrangement (a) refers to the loading used for obtaining the portancy map of Fig 3.25 and the loading arrangements (b) and (c) refer to the loadings applied for obtaining the portancy maps of Figs 3.41 and 3.42, respectively.

As it is seen from Table 3.21, for the support conditions 2, the ranks of all of the reduced grids for different loading arrangements are similar. That is, for this support arrangement, the results obtained by using the portancy maps for different loading conditions are the same. Also, from this table it may be seen that for the support arrangement of case one, the ranks obtained for all the reduced grids listed in the table are consistent for the loading arrangements (b) and (c). For the loading arrangement (a) the ranks of the reduced grids within each group are consistent. Also, by comparing all the reduced grids under this loading arrangement, it is seen that the ranks of the reduced grids are almost consistent. However, for the support conditions of case 3, with the loading arrangements (a) and (b), the ranks of the reduced grids within each group are consistent. The investigation carried out indicates that as the number of the supports is decreased the degree of the consistency of the ranks of the reduced grids is decreased when different types of loading are applied. Considering the whole set of results in Table 3.21, one may conclude that, in general, for every support arrangement, the ranks of different reduced grids under different loading conditions are more or less the same.

3.9 PORTANCY MAP FOR DENSER DOUBLE LAYER GRIDS

So far, the developed algorithm has been used in relation to the base grids with patterns of square on square. As shown in Figs 3.1, 3.30 and 3.32 as well as 3.34, each side of the top layers of the base grids consist of nine chords of length L . Now, let each side of the top layer of the base grid consist of 11 chords of length L . That is, the investigation is carried out in relation to a larger double layer grid. This double layer grid is shown in Fig 3.49. Figs 3.50 to 3.54 indicate five reduced grids each of which is derived from the base grid of Fig 3.49 by removing 32 elements. Another group of reduced grids is the grids shown in Figs 3.55 and 3.56. Each of these reduced grids are created by eliminating 40 elements from the base grid of Fig 3.49. Also, the grids of Figs 3.57 to 3.59 are considered as another group of reduced grids derived from the base grid of Fig 3.49 by removing 72 elements.

Fig 3.49 Base grid

The base grid of Fig 3.49 is supported at eight bottom layer nodes as indicated in the figure. Here, support S1 is constrained in X , Y and Z directions and support S2 is constrained in Y and Z directions. The other supports are constrained in the Z direction only. The base grid is subjected to equal downward concentrated loads of magnitude P applied at all the top layer nodes. The procedure explained in Section 3.4 is employed to build the corresponding portancy map. This portancy map is shown in Fig 3.60. The map has been obtained by 244 repetitions of the genetic process. Comparing the portancy maps of Figs 3.25 and 3.60, it is seen that the general pattern of the portancy distributions for the two cases are similar. That is,

Fig 3.50 A reduced grid

Fig 3.51 Another reduced grid

Fig 3.52 Another reduced grid

Fig 3.53 Another reduced grid

Fig 3.54 Another reduced grid

Fig 3.55 Another reduced grid

Fig 3.56 Another reduced grid

Fig 3.57 Another reduced grid

Fig 3.58 Another reduced grid

Fig 3.59 Another reduced grid

again the elements in the middle regions of the top and bottom layers as well as the elements near the supports have the greatest portancy values. In other words, the principal force paths for both cases are similar.

Fig 3.60 Portancy Map

Now, the portancy values of the map of Fig 3.60 are used for comparing the reduced grids of Figs 3.50 to 3.59. These reduced grids are assumed to be supported as the base grid of Fig 3.49. The reduced grids of Figs 3.50 to 3.59 are divided into three groups based on the differences in the numbers of the elements that have been removed in each case. For the first group, that is, the reduced grids of Figs 3.50 to 3.54, the summations of the portancies of the removed elements are listed in Table 3.22.

Table 3.22 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.50	1.4
Grid of Fig 3.51	9.6
Grid of Fig 3.52	14.2
Grid of Fig 3.53	7.5
Grid of Fig 3.54	12.2

For the second group of the reduced grids, that is, the reduced grids of Figs 3.55 and 3.56, the summations of the portancies of the removed elements are listed in Table 3.23. Also, the summations of the portancies of the elements of the reduced grids of Figs 3.57 to 3.59 are listed in Table 3.24.

Table 3.23 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.55	11.2
Grid of Fig 3.56	15.9

Tables 3.22 to 3.24 give the summations of the portancies of the removed elements for three different groups of reduced grids. In these tables, a reduced grid in a particular group can be compared only with another reduced grid of that group. Therefore, using the method described for comparing the grids, a reduced grid from the first group of reduced grids with 32 elements cannot be compared with a reduced grid from the third group with 72 removed elements.

Table 3.24 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 3.57	14.3
Grid of Fig 3.58	12.6
Grid of Fig 3.59	25.5

To find a criterion for comparing two reduced grids with different numbers of removed elements, the average of the portancies of the removed elements for each grid is calculated. That is, the summation of the portancies is divided by the number of the removed elements of the reduced grid. Now, the average values obtained for all the reduced grids may be used for comparing the reduced grids with different numbers of removed elements. For the cases under consideration, that is, the reduced grids of Figs 3.50 to 3.59, the results are listed in Table 3.25. According to the average values listed in Table 3.25, two reduced grids may be compared with each other and the grid with a lower average value is considered as the more suitable one. For instance, the average for the reduced grid of Fig 3.52 with 32 removed elements is 0.44, while this value is 0.18 for the reduced grid of Fig 3.58 with 72 removed elements. Therefore, the reduced grid of Fig 3.58 is considered as more suitable. Now, let the weight optimisation process be carried out to find the minimum weights for these two reduced grids.

On one occasion, the minimum weights of 739.1 kN and 680.3 kN were found for the reduced grids of Figs 3.52 and 3.58, respectively. This result verifies the conclusion obtained by comparing the reduced grids with respect to the average portancies of the removed elements. Consequently, it may be concluded that the proposed method may be used for comparing any pair of reduced grids derived from a base grid.

Table 3.25 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements	Average of portancies of removed elements	Number of removed elements	Rank
Grid of Fig 3.50	1.4	0.04	32	1
Grid of Fig 3.51	9.6	0.30	32	6
Grid of Fig 3.52	14.2	0.44	32	10
Grid of Fig 3.53	7.5	0.23	32	4
Grid of Fig 3.54	12.2	0.38	32	8
Grid of Fig 3.55	11.2	0.28	40	5
Grid of Fig 3.56	15.9	0.39	40	9
Grid of Fig 3.57	14.3	0.20	72	3
Grid of Fig 3.58	12.6	0.18	72	2
Grid of Fig 3.59	25.5	0.35	72	7

3.9.1 Denser Double Layer Grids with Other Support Conditions

Now, let the base grid of Fig 3.49 be supported at all the edge nodes of the bottom layer as shown in Fig 3.61. The portancy map associated with this support arrangement is shown in Fig 3.62. This map has been obtained by 207 repetitions of the genetic process as explained in Section 3.4. At support S1, in Fig 3.61, the degrees of freedom in X, Y and Z directions are restrained. For support S2, the degrees of freedom in the Y and Z directions are restrained. Other supports are constrained in the Z direction only. The base grid is subjected to equal downward loads of magnitude P applied at all the top layer nodes.

Comparing the maps of Figs 3.33 and 3.62, it is seen that these two portancy maps have similar characteristics, although, the portancy map of Fig 3.62 corresponds to a denser base grid. Now, using the portancy values of the map of Fig 3.62, the reduced grids of Figs 3.50 to 3.59 are compared with each other with respect to the summations of the portancies of the

removed elements. For all these reduced grids the support conditions are considered to be the same as shown in Fig 3.61. The results are listed in Table 3.26.

Fig 3.61 Base grid

In Table 3.26, the summations of the portancies of the removed elements for the reduced grids are listed together with the averages of the portancies. Also given in this table are the ranks of the reduced grids according to the corresponding averages. As it is seen from this table, the most suitable reduced grid, that is, the grid of Fig 3.50 belongs to the first group of reduced grids with 32 removed elements. Also, the worst reduced grid, that is, the grid of Fig 3.52 is within this group. Comparing the reduced grids of Figs 3.52 and 3.57 with 32 and 72 removed

elements, respectively, it shows that the reduced grid of Fig 3.57 with the average of 0.16 is more suitable. This comparison is confirmed by the result of the weight optimisation, where, in one occasion the minimum weights obtained for the reduced grids of Figs 3.52 and 3.58 were 503.9 kN and 475.8 kN, respectively.

Fig 3.62 Portancy Map

Continuing the investigation in relation to the effects of the support arrangements on the portancy map, the base grid of Fig 3.49 is considered to be supported at four top layer nodes, as shown in Fig 3.63. The resulting portancy map is shown in Fig 3.64. This map is obtained based on 201 times running the genetic process. That is, after 201 repetitions the anticipated symmetry has been obtained for the portancy map.

Comparing the portancy maps of Figs 3.31 and 3.64, it is seen that the principal force paths are similar for the two base grids, although the base grid used for the portancy map of Fig 3.64 is denser than that used for the map of Fig 3.31. Now, let the reduced grids of Figs 3.50 to 3.59 be compared based on the portancy values of the map of Fig 3.64. For all these reduced grids, the support arrangements are considered to be the same as shown in Fig 3.63. The results are listed in Table 3.27.

Table 3.26 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements	Average of portancies of removed elements	Number of removed elements	Rank
Grid of Fig 3.50	3.0	0.09	32	1
Grid of Fig 3.51	12.7	0.40	32	6
Grid of Fig 3.52	15.6	0.49	32	10
Grid of Fig 3.53	8.8	0.28	32	4
Grid of Fig 3.54	14.6	0.46	32	8
Grid of Fig 3.55	12.8	0.32	40	5
Grid of Fig 3.56	18.7	0.47	40	9
Grid of Fig 3.57	11.2	0.16	72	2
Grid of Fig 3.58	15.8	0.22	72	3
Grid of Fig 3.59	31.4	0.44	72	7

As it is seen from Table 3.27, the reduced grid of Fig 3.57 has the lowest rank, whereas this reduced grid with the support arrangement of Fig 3.62 had the second best rank. This is understandable, because in this grid most of the removed elements belong to the side regions of the top and bottom layers of the grid. Also, a number of the removed elements in this grid are in areas near the supports.

Table 3.27 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements	Average of portancies of removed elements	Number of removed elements	Rank
Grid of Fig 3.50	5.0	0.160	32	9
Grid of Fig 3.51	4.5	0.141	32	7
Grid of Fig 3.52	3.4	0.106	32	2
Grid of Fig 3.53	4.6	0.144	32	8
Grid of Fig 3.54	3.6	0.113	32	3
Grid of Fig 3.55	5.2	0.130	40	5
Grid of Fig 3.56	4.2	0.105	40	1
Grid of Fig 3.57	15.8	0.219	72	10
Grid of Fig 3.58	10.1	0.140	72	6
Grid of Fig 3.59	8.7	0.121	72	4

Fig 3.63 Base grid

As it may be seen from the portancy map of Fig 3.64, all these regions contain elements with high portancies. Also, it is seen from Table 3.27, that the reduced grid of Fig 3.56 has the rank 1 (the highest rank). In this reduced grid, the removed elements are in the middle regions of the grid, which contain the elements with low portancies. Now, let the weight optimisation process be carried out to find the minimum weights for the reduced grids of Fig 3.56 and 3.57, that is, the grids with the highest and lowest ranks. On one occasion, the minimum weights of 735.4 kN and 789.6 kN were obtained for the reduced grids of Figs 3.56 and 3.57,

respectively. This result is consistent with that obtained based on comparing the averages of the portancy values of the removed elements.

Fig 3.64 Portancy Map

CHAPTER 4

Double Layer Grids with Other Patterns

4.1 INTRODUCTION

In this chapter, the technique developed in Chapter 3 is employed in relation to some other configurations. To this end, at first, the double layer grids with square on diagonal pattern are studied. Then, two types of double layer grids with configurations based on the triangle on triangle pattern are investigated. In this chapter the portancy maps relating the cases under consideration are obtained. Using the resulting maps, a number of reduced grids corresponding to each case are compared with each other to find the most suitable topologies.

4.2 DOUBLE LAYER GRIDS WITH SQUARE ON DIAGONAL PATTERN

Consider the double layer grid shown in Fig 4.1. This double layer grid belongs to a family of configurations which are based on the square on diagonal pattern. In this grid, the top layer has a square pattern and the bottom layer has a diagonal pattern (except, of course, for the edge elements). The top and bottom layers of the grid of Fig 4.1 are interconnected by inclined web elements. In this figure, the top layer elements are indicated by thick lines and the bottom layer, as well as the web elements, are indicated by thin lines. In the plan view of the grid shown in Fig 4.1, most of the inclined web elements are hidden by the top layer

Fig 4.1 Base grid with square on diagonal pattern

elements. To avoid this viewing problem, an 'oblique view' of the grid is shown in Fig 4.2. The view in Fig 4.2 is an isometric view with an oblique view direction such that all the elements of the grid are conveniently seen.

Fig 4.2 Oblique view

The base grid of Fig 4.1 is supported at all the edge nodes of the bottom layer. In this grid, support S1 is constrained in X, Y and Z directions. Support S2 is constrained in Y and Z directions and the other supports are constrained in the Z direction only. The grid is under the effect of a system of equal downward concentrated loads of magnitude P applied at all the top layer nodes.

The top layer elements have equal length L , and therefore, the bottom layer elements have the length $L/\sqrt{2}$. The depth of the base grid is taken as $L/\sqrt{2}$. With this choice for the depth of the grid, the web elements have the length L . The procedure described in Chapter 3 is

employed for obtaining the portancies of the elements of the base grid of Fig 4.1. The resulting map is shown in Fig 4.3. This portancy map has been obtained based on the results of 826 repetitions of the genetic process. To have a clearer view of the element portancies of different layers of the base grid, the graphical presentation of the portancy values for the top, bottom and web elements are shown separately in Figs 4.4 to 4.6, respectively. It should be noted that for drawing these maps the element thickness is taken as three times larger than those used for drawing Fig 4.3

As it may be seen from Fig 4.4, the top layer of the base grid contains a considerable number of the elements with high portancies, which are in the middle areas of this layer. On the other hand, as shown in Fig 4.6, most of the web elements are the elements with low portancy values, except for a few elements near some of the supports that have greater portancies. Also, it is noticeable that the elements of the middle region of the bottom layer are not elements with high portancies (see Fig 4.5).

Figs 4.7 to 4.9 show the oblique views of three reduced grids that are derived from the base grid of Fig 4.1. Each of these reduced grids is created by eliminating 48 elements from the base grid. In these figures, the removed elements are shown by dotted lines.

Now, let the portancy values for the grid of Fig 4.1 be used for comparing the reduced grids of Figs 4.7 to 4.9. It is assumed that these reduced grids are supported in the same way as that of the base grid of Fig 4.1. The summations of the portancies of the removed elements of the reduced grids are listed in Table 4.1. It is seen from this table that the reduced grids of Figs 4.7 and 4.9 are almost of the same degree of suitability. Drawing attention to the portancy map of the bottom layer of Fig 4.5, it turns out that for creating the reduced grid of Fig 4.8, some of the elements of the base grid that have high portancy values are removed. So, this reduced grid is less desirable, as may be seen from Table 4.1.

The optimisation process is carried out to find the minimum weights for the reduced grids of Figs 4.7 to 4.9. The length of each element of the top layer is assumed to be 4.00 m. With this assumption, the span of the grid, that is, the distance between the parallel edges of the bottom layer is 36.00 m. The depth of the grid is taken as 2.80 m. The reduced grids are loaded at all the top layer nodes with equal downward concentrated loads of 24 kN . The elements of the grids are assumed to be tube elements with outside diameters within the range 60-150 mm.

Fig 4.3 Portancy map

Fig 4.4 Portancy map of top layer

Fig 4.5 portancy map of bottom layer

Fig 4.6 Portancy map of web elements

Fig 4.7 A reduced grid

Fig 4.8 Another reduced grid

Fig 4.9 Another reduced grid

The minimum weights obtained on one occasion are listed in Table 4.2, together with the summations of the portancy values. As it is seen from this table, the ranks of the reduced grids based on the summations of the portancies are consistent with the ranks obtained based on the weight optimisation.

Table 4.1 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.7	9.3
Grid of Fig 4.8	11.8
Grid of Fig 4.9	9.2

4.2.1 Effects of the Support Conditions on the Portancy Map

In order to investigate the effects of the support conditions on the portancy map, the support arrangement shown in Fig 4.10 is considered for the base grid. As shown in this figure, the base grid is supported at four top layer corner nodes. At support S1 the degrees of freedom in

X, Y and Z directions are restrained. For support S2 the degrees of freedom in Y and Z directions are restrained. The other supports are constrained in Z direction only. The loading system consists of vertical downward loads of magnitude P applied at all the top layer nodes.

Table 4.2 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 4.7	258.6	9.3
Grid of Fig 4.8	263.0	11.8
Grid of Fig 4.9	256.6	9.2

Applying the genetic technique in relation to the base grid of Fig 4.10, gives rise to the portancy map of Fig 4.11. This map is obtained based on 1000 times running the genetic process. To have a clearer view of the element portancies, the maps related to the top, bottom and web elements are also shown separately in Figs 4.12 to 4.14, respectively. In these figures the thickness used for drawing the maps is three times larger than those used for drawing Fig 4.11. As it is seen from Fig 4.12, the side elements of the top layer are the elements with high portancy values. Also, as shown in Fig 4.13, the bottom elements within the diagonal regions have large portancies. All the web elements are the elements with low portancy values, except for some of the elements near to the supports (see Fig 4.14).

The reduced grids of Figs 4.7 to 4.9 are compared with respect to the summations of the portancies of the removed elements, using the portancy values obtained for the elements of the base grid of Fig 4.10. The results are listed in Table 4.3. Comparing the results given in Tables 4.1 and 4.3, it is seen that in both cases, (that is, for two different support arrangements) the reduced grid of Fig 4.8 has the lowest rank (worst case).

The weight optimisation is carried out to find the minimum weights of the reduced grids of Figs 4.7 to 4.9. The grid dimensions and the load magnitude in this case are the same as those for the case of Fig 4.1. In the present case, the outside diameters of the tubes are within the range 80-250 mm. The minimum weights obtained in one occasion together with the summations of the portancies of the removed elements are listed in Table 4.4. It is seen from

this table, that the results based on the weight optimisation are consistent with the results based on the summations of the portancies.

Fig 4.10

Now, consider the support conditions shown in Fig 4.15, where the supports are at some of the top layer nodes. In this figure, support S1 is constrained in X , Y and Z directions and support S2 is constrained in Y and Z directions. The other supports are constrained in the Z direction only. The grid is subjected to equal concentrated loads of magnitude P applied at all the top layer nodes in the negative Z direction.

The genetic process is carried out to find the portancy map of the base grid of Fig 4.15. The resulting map which is obtained based on 200 repetitions of the genetic process is shown in

Fig 4.11 Portancy map

Fig 4.12 Portancy map of top layer

Fig 4.13 portancy map of bottom layer

Fig 4.14 Portancy map of web elements

Fig 4.16. Also, the maps indicating the portancy distributions in different layers of the base grid are shown in Figs 4.17 to 4.19. These figures are drawn with line thickness three times larger than that in Fig 4.16. As it may be seen from these figures, the top layer elements of high portancy values are within the middle region of the top layer. In the bottom layer, the elements of high portancies are in the regions around the central area. Most of the web elements have low portancy values, except those near the supports.

Table 4.3 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.7	6.9
Grid of Fig 4.8	8.0
Grid of Fig 4.9	1.7

Now, the portancy values of the maps of Fig 4.17 to 4.19 are used for comparing the reduced grids of Figs 4.7 to 4.9. The results are listed in Table 4.5. Comparisons of the results listed in Tables 4.1, 4.3 and 4.5, show that in all cases the reduced grid of Fig 4.8 has the lowest rank.

Table 4.4 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 4.7	499.1	6.9
Grid of Fig 4.8	525.8	8.0
Grid of Fig 4.9	485.3	1.7

The genetic technique is employed to find the minimum weights of the reduced grids of Figs 4.7 to 4.9 with the support arrangement being the same as that of the base grid of Fig 4.15. The loading arrangement is the same as the previous case and the outside diameters of tabular elements are within the range 80-250 mm. The resulting minimum weights are listed in Table 4.6. Also, listed in this table are the summations of the portancy values of the removed elements. As it is seen from this table, the ranks of the reduced grids based on the minimum weights are consistent with the results obtained based on the summations of the portancy values.

Table 4.5 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.7	9.8
Grid of Fig 4.8	11.4
Grid of Fig 4.9	7.1

4.2.2 Denser Double Layer Grids with Square on Diagonal Pattern

At this point, a denser configuration with square on diagonal pattern is considered as the base grid. For this case, as shown in Fig 4.20, the top layer edges have 10 elements of length L in comparison with the base grid of Fig 4.1 whose top layer edges have 8 elements of length L . The grid is subjected to equal vertical loads of magnitude P applied at the top layer nodes in the negative Z direction. With the support arrangement indicated in Fig 4.20, the portancy map shown in Fig 4.21 is obtained. This map is based on the results of 105 times running the genetic process. To have a clearer view, the maps representing the top, bottom and web element portancies are shown separately in Figs 4.22 to 4.24, respectively. Comparing the maps of Figs 4.3 and 4.21, it is seen that the pattern of the portancy distributions are similar for two cases.

Table 4.6 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 4.7	215.4	9.8
Grid of Fig 4.8	225.2	11.4
Grid of Fig 4.9	206.2	7.1

Now, the maps of Figs 4.22 to 4.24 are used for comparing the reduced grids of Figs 4.25 to 4.30 considering the summations of the portancies of the removed elements. The results are given in Table 4.7. As it is seen from Table 4.7, the reduced grids of Figs 4.25 and 4.30 have the highest and lowest ranks, respectively. Now, let the weight optimisation process be carried out to find the minimum weights for these two reduced grids. The support conditions for these reduced grids are considered to be the same as shown in Fig 4.20 for the base grid.

Fig 4.15

Table 4.7 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.25	8.2
Grid of Fig 4.26	10.6
Grid of Fig 4.27	11.2
Grid of Fig 4.28	9.6
Grid of Fig 4.29	9.4
Grid of Fig 4.30	12.4

Fig 4.16 Portancy map

Fig 4.17 Portancy map of top layer

Fig 4.18 Portancy map of bottom layer

Fig 4.19 Portancy map of web elements

On one occasion, the minimum weights of 576.8 kN and 598.3 kN were found for the reduced grids of Figs 4.25 and 4.30, respectively. These results confirm the conclusions obtained based on the comparison of the reduced grids with respect to the summations of the portancies.

Fig 4.20 A denser base grid

Continuing the investigation in relation to the effects of the support conditions, the base grid under consideration, is assumed to be supported as shown in Fig 4.31. This base grid is subjected to equal downward concentrated loads of magnitude P applied at all the top layer nodes. The resulting portancy map, which is based on 200 repetitions the genetic process is shown in Fig 4.32. Also, the maps related to the top, bottom and web elements are shown separately in Figs 4.33 to 4.35. Comparing the map of Fig 4.32 with the portancy map of Fig 4.11 it is seen that the principal paths of the internal forces are similar, although, the portancy map of Fig 4.32 belongs to a denser base grid.

Fig 4.21 Portancy map

Fig 4.22 Portancy map of top layer

Fig 4.23 Portancy map of bottom layer

Fig 4.24 Portancy map of web elements

Fig 4.25 Another reduced grid

Fig 4.26 Another reduced grid

Fig 4.27 Another reduced grid

Fig 4.28 Another reduced grid

Fig 4.29 Another reduced grid

Fig 4.30 Another reduced grid

The portancy map of Fig 3.32 is used for comparing the reduced grids of Figs 4.25 to 4.30 with respect to the summations of the portancies of the removed elements. The results are listed in Table 4.8.

Fig 4.31

As it is seen from Table 4.8, the reduced grids of Figs 4.27 and 4.29 have the lowest and highest ranks, respectively. Here, the genetic process is carried out to find the minimum weights of these two reduced grids. In one occasion, the weights of 1432 kN and 1284 kN were obtained for the reduced grids of Figs 4.27 and 4.29, respectively. That is, the reduced grid of Fig 4.29 is a lighter structure. This conclusion verifies the results obtained based on the portancy values.

Table 4.8 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.25	6.3
Grid of Fig 4.26	6.9
Grid of Fig 4.27	9.6
Grid of Fig 4.28	3.8
Grid of Fig 4.29	2.4
Grid of Fig 4.30	4.7

Now, the support arrangement shown in Fig 4.36 is considered for the base grid. Applying equal downward vertical loads of magnitude P at all the top layer nodes, the resulting portancy map is shown in Fig 4.37. This map is obtained based on 200 repetitions of the genetic process. The maps representing the top, bottom and web element portancies are shown separately in Figs 4.38 to 4.40. Comparing the portancy maps of Figs 4.16 and 4.37, it may be concluded that the patterns of the portancy distributions in both cases are similar. The portancy values of the map of Fig 4.37 are used for comparing the reduced grids of Figs 4.25 to 4.30. The results are listed in Table 4.9

Table 4.9 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.25	7.9
Grid of Fig 4.26	11.5
Grid of Fig 4.27	12.5
Grid of Fig 4.28	7.2
Grid of Fig 4.29	8.2
Grid of Fig 4.30	12.2

As it is seen from this table, the reduced grids of Figs 4.27 and 4.28 have the lowest and highest ranks, respectively. The weight optimisation process is carried out to find the minimum weights of these two reduced grids. On one occasion the minimum weights of 516 kN and 507 kN were found for the reduced grids of Figs 4.27 and 4.28, respectively. So, the minimum weights of these two reduced grids confirm the results obtained based on the summations of the portancies.

Fig 4.32 Portancy map

Fig 4.33 Portancy map of top layer

Fig 4.34 Portancy map of bottom layer

Fig 4.35 Portancy map of web elements

Fig 4.36

Fig 4.37 Portancy map

Fig 4.38 Portancy map of top layer

Fig 4.39 Portancy map of bottom layer

Fig 4.40 Portancy map of web elements

4.3 A HEXAGONAL DOUBLE LAYER GRID WITH TRIANGLE ON TRIANGLE OFFSET PATTERN

Consider the double layer grid whose plan and side view are shown in Fig 4.41. This grid belongs to a family of double layer grids with the configuration based on the triangle on triangle offset pattern. In Fig 4.41, the top layer elements are shown by thick lines and the bottom layer elements as well as the web elements are indicated by thin lines. Both top and bottom layers have triangular patterns and are interconnected by inclined web elements. This grid with the triangle on triangle offset pattern may be used as a base grid for generation of a variety of patterns. For example, the grids of Figs 4.42 to 4.45 are reduced grids with triangle on triangle offset patterns derived from the base grid of Fig 4.41. Each reduced grid is created by eliminating a total of 72 elements from the top, bottom and web elements of the base grid.

All the elements of the top and bottom layers of the base grid of Fig 4.41 are assumed to be of length L . The depth of the grid, that is, the vertical distance between the top and bottom layers is taken as L as well. With this value of depth, the web elements have the length $1.15L$. The

base grid of Fig 4.41 is supported at 12 top layer nodes as indicated in the figure by little circles. Support S_1 is constrained in X , Y and Z directions. Support S_2 is constrained in Y and Z directions and the other supports are constrained in the Z direction only. The base grid is considered to be under equal downward concentrated loads applied at all the top layer nodes.

Now, the genetic technique is employed to find the portancy map of the base grid of Fig 4.41. Fig 4.46 shows the resulting map based on 200 repetitions of the genetic process. For a clearer view, the maps representing the portancy values of the top, bottom and web elements are also shown separately in Figs 4.47 to 4.49. As it is seen from Figs 4.47 and 4.48, the top and bottom elements in the middle parts of the grid have large portancy values. As shown in Fig 4.49, only the web elements near the supports have large portancy values and the other elements of the web have low portancies.

Using the portancy values of the elements of the base grid of Fig 4.41, the reduced grids of Figs 4.42 to 4.45 are compared with respect to the summations of the portancies of the removed elements. The results are listed in Table 4.10. As it is seen from this table, the difference between the summations of the portancies for the reduced grids of Figs 4.43 and 4.44 is rather small. This means that these two reduced grids have almost the same degree of suitability. Also, as Table 4.11 shows, the reduced grids of Figs 4.42 and 4.45 are

Fig 4.41

Fig 4.42
A reduced grid

Fig 4.43 Another
reduced grid

Fig 4.44 Another reduced grid

Fig 4.45 Another reduced grid

Fig 4.46 Portancy map

Fig 4.47 Portancy map
of top layer

Fig 4.48 Portancy map of bottom layer

Fig 4.49 Portancy map of web elements

both more suitable than the reduced grids of Figs 4.43 and 4.44. This is reasonable, because as it may be seen from maps of Figs 4.47 to 4.49, the elements removed from the base grid for creation of the reduced grids of Figs 4.43 and 4.44 have larger portancies in comparison with the elements removed for generation of the reduced grids of Figs 4.42 and 4.45.

Table 4.10 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.42	20.0
Grid of Fig 4.43	28.6
Grid of Fig 4.44	28.2
Grid of Fig 4.45	21.2

The genetic process is employed to find the minimum weights of the reduced grids of Figs 4.42 to 4.45 with support conditions of Fig 4.41. To this end, the length of each element of the top and bottom layers is taken as 4.00 m. Then, the diameter of the top layer of each grid is 56.00 m. The depth of the grids is assumed to be 2.80 m and the elements of the grids are considered to be tubes with outside diameters in the range 80-250 mm. Each reduced grid is subjected to equal downward concentrated loads of magnitude 24.0 kN applied at all the top layer nodes. The minimum weights obtained in one occasion for the reduced grids of Figs 4.42 to 4.45 are listed in Table 4.11, together with the summations of the portancies. As it is seen from this table, the ranks of the reduced grids based the minimum weights are fully consistent with the ranks obtained based on the summations of the portancies of the removed elements.

Table 4.11 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Summation of portancies of removed elements
Grid of Fig 4.42	653.1	20.0
Grid of Fig 4.43	688.0	28.6
Grid of Fig 4.44	685.4	28.2
Grid of Fig 4.45	666.4	21.2

4.3.1 Effects of the Support Conditions on the Portancy Map

To investigate the effects of the support conditions, let the base grid of Fig 4.41 be supported at six top layer nodes as shown in Fig 4.50. In this case, support S1 is constrained in X, Y and Z directions, support S2 is constrained in Y and Z directions and the other supports are constrained in the Z direction only. The base grid is under the effect of a system of equal downward concentrated loads of magnitude of P applied at all the top layer nodes.

Fig 4.50

Employing the genetic technique, the resulting portancy map is shown in Fig 4.51. This map is obtained based on 200 repetitions of the genetic process. Also, the maps representing the portancy values of the top, bottom and web elements are shown separately in Figs 4.52 to 4.54. As it may be seen from Figs 4.52 and 4.53, the top and bottom layer elements lying along the diameters are the elements with high portancy values.

Fig 4.51 Portancy map

Fig 4.52 Portancy map
of top layer

Fig 4.53 Portancy map
of bottom layer

Fig 4.54 Portancy map
of web elements

Also, it is seen from Figs 4.52 and 4.53, that the top and bottom layer elements parallel to the edges of the base grid have relatively large portancy values and some of these elements which are closer to the edge have more contribution in carrying the loads. Furthermore, the bottom layer elements in the middle part of the grid have large portancy values. On the other hand, as it is seen from Fig 4.54, all of the web elements have low portancy values, except for the elements near the supports that have large portancies.

Now, the portancy values of the elements of the base grid of Fig 4.50 are used for evaluating the reduced grids of Figs 4.43 to 4.45 with respect to the summations of the portancies of the removed elements. The results are listed in Table 4.12.

Table 4.12 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.42	16.1
Grid of Fig 4.43	20.4
Grid of Fig 4.44	18.1
Grid of Fig 4.45	15.3

Table 4.12 shows that the reduced grids of Figs 4.43 and 4.44 whose corresponding removed elements are close to the centre of the grid are less suitable. Comparing the patterns used for removing the elements of the base grid for creating these reduced grids, it is seen that these two patterns are only slightly different. To elaborate, the removed elements from the bottom and web elements of the base grid are the same. Also, 6 of 18 top layer elements which are removed from the base grid for generating the reduced grids of Figs 4.43 and 4.44 are identical. Therefore, each of these two reduced grid is created by eliminating 72 elements from the base grid, while 66 of the removed elements being identical for these two reduced grids. However, the difference between the summations of the portancies of the removed elements for these two reduced grids is noticeable. This situation provides an example of the important role that may be considered for the portancy map in reaching a suitable decision regarding the choice of reduced grids even when the reduced grids may have certain similarities. While, at the first view and by only engineering judgment it may not be possible to make a suitable decision.

Now, let the weight optimisation be carried out to find the minimum weights of the reduced grids of Figs 4.43 and 4.44 with support conditions of Fig 4.50. On one occasion, the weights of 883 kN and 874 kN were obtained for the reduced grids of Figs 4.43 and 4.44, respectively. This confirms the results obtained based on the summations of the portancy values.

As another support arrangement, let the base grid with triangle on triangle pattern be supported as shown in Fig 4.55. As shown in this figure, all the bottom layer edge nodes are considered as supports. In this figure, support S1 is constrained in X, Y and Z directions and support S2 is constrained in Y and Z directions. The other supports are constrained in the Z direction only. The base grid is subjected to equal concentrated loads of magnitude P applied at all the top layer nodes in the negative Z direction.

Fig 4.55

Using the genetic technique, the portancy map of the base grid of Fig 4.55 is obtained. The resulting map, shown in Fig 4.56, is produced based on the results of 200 repetitions of the genetic process. The maps relating to the top, bottom and web elements are shown separately in Figs 4.57 to 4.59. As it is seen from Figs 4.57 and 4.58, the elements of the middle regions of the top and bottom layers are the elements of high portancies. Also, as shown in Fig 4.59, the web elements near the supports have larger portancy values in comparison with the elements in the middle areas.

Now, using the portancy values obtained for the base grid of Fig 4.55, let the reduced grids of Figs 4.42 to 4.45 be compared with respect to the summations of the portancy values of the removed elements. The results are listed in Table 4.13. As it is seen from this table, for the reduced grids of Figs 4.42 and 4.45, the summations of the portancies are close to each other. In both of these reduced grids the removed elements belong to the side regions of the base grid. Also, the difference between the summations of the portancy values for the reduced grids of Figs 4.43 and 4.44 are rather small. These reduced grids are generated by removing a number of elements from the middle parts of the base grid, where the top and bottom layers have a large numbers of the elements with high portancies.

Table 4.13 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements
Grid of Fig 4.42	23.3
Grid of Fig 4.43	30.6
Grid of Fig 4.44	31.3
Grid of Fig 4.45	22.6

The genetic technique is employed to find the optimum weights of the reduced grids of Figs 4.44 and 4.45 with the support conditions of Fig 4.55. That is, the minimum weights of the reduced grids with the lowest and highest ranks in Table 4.13 are found. In one occasion, the weights of 685 kN and 666 kN were obtained for the reduced grids of Figs 4.44 and 4.45, respectively. So, the resulting minimum weights confirm the ranks of these two reduced grids obtained based on the summations of the portancies of the removed elements.

Fig 4.56 Portancy map

Fig 4.57 Portancy map
of top layer

Fig 4.58 Portancy map of bottom layer

Fig 4.59 Portancy map of web elements

4.4 A TRIANGULAR DOUBLE LAYER GRID WITH TRIANGLE ON TRIANGLE OFFSET PATTERN

Consider the double layer grid whose plan and side views are shown in Fig 4.60. The configuration of this grid is based on the triangle on triangle offset pattern. In Fig 4.60, the top layer elements are shown by thick lines and the bottom layer as well as the web elements are shown by thin lines. The double layer grid of Fig 4.60 has 780 elements and it may be used as a base grid for generation of a number of reduced grids. For example, consider the double layer grids shown in Figs 4.61 and 4.62. Each of these grids is derived from the base grid of Fig 4.60 by removing 36 elements. Another group of reduced grids is shown in Figs 4.63 and 4.64, where each of the reduced grids is created by eliminating 48 elements from the base grid.

The base grid of Fig 4.60 is assumed to be supported at six bottom layer nodes. As shown in Fig 4.60, the supports are indicated by little circles. In this figure, support S1 is constrained in X, Y and Z directions, support S2 is constrained in Y and Z directions and the other supports are constrained in the Z direction only. The grid is under the effect of equal downward concentrated loads of magnitude P applied at all the top layer nodes.

The genetic technique is employed for obtaining the portancy map of the base grid of Fig 4.60. The resulting map based on 200 repetitions of the genetic process is shown in Fig 4.65. For a clearer view, the maps representing the element portancies of the top, bottom and web elements are also shown separately in Figs 4.66 to 4.68, respectively.

As shown in Fig 4.66, some of the edge top layer elements as well as some of the elements in the middle part of this layer have relatively large portancy values. Also, as it is seen from Fig 4.67, the elements in the middle region of the bottom layer as well as the elements in the corner areas of this layer have low portancies. On the other hand, as Fig 4.68 shows, the web elements near the supports have large portancy values and the other elements have low portancies.

Now, the portancy values of the elements of the base grid of Fig 4.60 are used for comparing the reduced grids of Figs 4.61 to 4.64. The results are listed in Table 4.14. Since the numbers of the removed elements of the reduced grids of Figs 4.61 and 4.62 are different from those of the reduced grids of Figs 4.63 and 4.64, the averages of the portancies of the removed

Plan view

Side view

Fig 4.60

Fig 4.61
A reduced grid

Fig 4.62 Another
reduced grid

Fig 4.63 Another reduced grid

Fig 4.64 Another reduced grid

Fig 4.65
Portancy map

Fig 4.66 Portancy map
of top layer

Fig 4.67 Portancy map of bottom layer

Fig 4.68 Portancy map of web elements

elements are used for comparing the reduced grids. As it may be seen from this table, both of the reduced grids of Figs 4.63 and 4.64 are more suitable in comparison with the reduced grids of Fig 4.61 and 4.62, although, a larger number of elements are removed from the base grid of Fig 4.60 for creation of the reduced grids of Figs 4.63 and 4.64.

Table 4.14 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements	Average of portancies of removed elements	Number of removed elements
Grid of Fig 4.61	3.9	0.11	36
Grid of Fig 4.62	4.5	0.13	36
Grid of Fig 4.63	4.1	0.09	48
Grid of Fig 4.64	4.7	0.10	48

Focussing attention on the patterns used for removing the elements in producing the reduced grids of Figs 4.61 to 4.64, it is seen that the reduced grids of Figs 4.63 and 4.64, are respectively the same as the reduced grids of Figs 4.61 and 4.62 with some extra removed elements. To elaborate, the reduced grids of Figs 4.63 and 4.64 are generated by eliminating the same elements from the central parts of the reduced grids of Figs 4.61 and 4.62, respectively. On the other hand, as it is seen from Figs 4.66 to 4.68, these central elements have low portancy values. Therefore, the summations of the portancies of the removed elements for the reduced grids of Figs 4.63 and 4.64 have not been increased appreciably in comparison with the summations of the portancies of the removed elements of the reduced grids of Figs 4.61 and 4.62. So, the averages for the reduced grids of Figs 4.63 and 4.64 are less than those of the reduced grids of Figs 4.61 and 4.62. Therefore, it may be concluded that the portancy map provides the possibility of finding more suitable reduced grids with larger number of removed elements.

The weight optimisation technique is carried out to find the minimum weights of the reduced grids of Figs 4.61 to 4.64 with the support conditions of Fig 4.60. To this end, the lengths of the elements of the top and bottom layer grids are taken as 4.0 m. Also, the depth of the grid is assumed to be 2.8 m. The outside diameters of the tubular elements are within the range 80-250 mm. The reduced grids are assumed to be subjected to equal downward concentrated loads of magnitude 24 kN applied at all the top layer nodes in the Z direction. Table 4.15 shows the minimum weights obtained in one occasion, together with the averages of the

portancies of the removed elements. As it is seen from this table, the ranks of the reduced grids based on the minimum weights are consistent with the ranks based on the averages of the portancies of the removed elements.

Table 4.15 Comparing the grids using minimum weights and portancy values

Grid	Minimum weight (kN)	Average of the portancies of removed elements
Grid of Fig 4.61	967	0.11
Grid of Fig 4.62	981	0.13
Grid of Fig 4.63	946	0.09
Grid of Fig 4.64	958	0.10

4.4.1 Effects of the Support Conditions on the Portancy Map

To investigate the effects of the support conditions on the portancy map of Fig 4.65, the supports arrangement shown in Fig 4.69 is considered. As shown in this figure, the base grid is supported at all the bottom layer nodes. Support S1 is constrained in X, Y and Z directions, support S2 is constrained in Y and Z directions and the other supports are constrained in the Z direction only. The grid is under the effect of a system of equal downward concentrated loads of magnitude P applied at all the top layer nodes in the Z direction.

The genetic process is employed to find the portancy map of the base grid of Fig 4.69. The resulting map based on 200 repetitions of the genetic process is shown in Fig 4.70. Also, the maps relating to the top, bottom and web elements are shown separately in Figs 4.71 to 4.73, respectively. In these figures the scale of the line thickness used for drawing is two times larger than that used for the map of Fig 4.70. As shown in Figs 4.71 and 4.72, the elements parallel to the edges of the base grid which are between the edges and the centre of the grid have low portancies. Furthermore, the web elements near the supports in the middle part of the edges of the bottom layer have large portancy values (see Fig 4.73).

Now, let the reduced grids of Figs 4.61 to 4.64 be compared using the portancy values of the elements of the base grid of Fig 4.69. The results are listed in Table 4.16. As it is seen from this table, the reduced grid of Fig 4.61 with 36 removed elements is the most suitable grid and

Fig 4.69

the reduced grid of Figs 4.64 with 48 removed elements has the lowest rank. Also, both reduced grids of Figs 4.63 and 4.64 with 48 removed elements are less suitable than the reduced grids of Figs 4.61 and 4.62 with 36 removed elements. This is because the reduced grids of Figs 4.63 and 4.64 are generated, respectively, by eliminating 12 extra elements from the central parts of the reduced grids of Figs 4.61 and 4.62. However, the central areas contain the elements with high portancy values. So, the summations of the portancy values of the removed elements for the reduced grids of Figs 4.63 and 4.64 are increased appreciably. Therefore, the averages of the portancies for these two reduced grids are greater than those for the grids of Figs 4.61 and 4.62.

Fig 4.70
Portancy map

Fig 4.71 Portancy map
of top layer

Fig 4.72 Portancy map
of bottom layer

Fig 4.73 Portancy map
of web elements

Table 4.16

Grid	Summation of portancies of removed elements	Average of portancies of removed elements	Number of removed elements
Grid of Fig 4.61	8.0	0.22	36
Grid of Fig 4.62	9.0	0.25	36
Grid of Fig 4.63	12.5	0.26	48
Grid of Fig 4.64	13.5	0.28	48

The optimisation process is carried out to find the minimum weights of the reduced grids of Figs 4.61 and 4.64, with the support conditions of Fig 4.69. That is the minimum weights for the reduced grids of highest and lowest ranks are found. In one occasion, the minimum weights of 787 kN and 804 kN were obtained for the reduced grids of Figs 4.61 and 4.64, respectively. This confirms the results obtained based on the averages of the portancy values.

Now, consider the support arrangement shown in Fig 4.74, where the base grid is supported at six top layer nodes. In this figure, support S1 is constrained in X, Y and Z directions. Support S2 is constrained in Y and Z directions and the other supports are constrained in the Z direction only. The base grid is subjected to equal concentrated loads applied at all the top layer nodes in the negative Z direction.

Employing the genetic technique, the portancy map associated with the base grid of Fig 4.74 is obtained. The resulting map obtained by 200 repetitions of the genetic process is shown in Fig 4.75. The maps representing the portancy values of the top, bottom and web elements are also shown separately in Figs 4.76 to 4.78, respectively. It should be noted that the scale of the line thickness used for drawing Figs 4.76 to 4.78 is two times larger than that used for the portancy map of Fig 4.75. As Figs 4.78 and 4.77 show, the elements in the middle parts of the top and bottom layers have low portancies. Also, most of the web elements have low portancy values, except for the elements near the supports that have large portancy values (see Fig 4.78).

Now, let the portancy map of Fig 4.75 be used for evaluating the reduced grids of Figs 4.61 to 4.64. The results are listed in Table 4.17. This table shows that the reduced grid of Fig 4.64 is the most suitable one. This grid has been created by removing 48 elements from the central

region of the base grid, where most of the elements have low portancy values. On the other hand, the reduced grid of Fig 4.61, as Table 4.17 shows, is the worst reduced grid. This is reasonable, because this grid is generated by removing 36 elements from the regions which contain the most important top and bottom layer elements of the base grid.

Fig 4.74

Fig 4.75
Portancy map

Fig 4.76 Portancy map
of top layer

Fig 4.77 Portancy map of bottom layer

Fig 4.78 Portancy map of web elements

The weight optimisation is carried out to find the minimum weights of the reduced grids of Figs 4.61 and 4.64. In this case, the support arrangement of Fig 4.74 is considered for these two reduced grids. In one occasion, the weights of 1617 kN and 1547 kN were found for the grids of Figs 4.61 and 4.64, respectively. This confirms the results obtained based on the averages of the portancies of the removed elements.

Table 4.17 Comparing the grids using portancy values

Grid	Summation of portancies of removed elements	Average of portancies of removed elements	Number of removed elements
Grid of Fig 4.61	6.9	0.19	36
Grid of Fig 4.62	3.1	0.09	36
Grid of Fig 4.63	7.2	0.15	48
Grid of Fig 4.64	3.4	0.07	48

CHAPTER 5

Conclusions and Suggestions for Future Work

5.1 INTRODUCTION

In this chapter, first an outline of the work reported in the previous chapters as well as their conclusions are presented. Then, some guidelines for future work are given.

5.2 OUTLINE OF THE WORK AND CONCLUSIONS

In the present work, the genetic algorithm was employed to establish a new methodology for topological studies of double layer grids. In Chapter 2, the fundamental procedure of the genetic algorithm was explained. The steps for developing the methodology and applying it for studying different types of double layer grids were discussed in detail in Chapters 3 and 4. The conclusions of the work carried out in Chapters 2, 3 and 4 are described in the sequel.

Studies carried out in Chapter 2 show that the genetic algorithm is a robust technique that can deal with different optimisation problems. Some aspects of the genetic process developed in Chapter 2 may be highlighted as follows:

- Genetic algorithm involves a number of parameters each of which has an influence on the performance of the process. Studies carried out in this work show that choosing

suitable values for these parameters is of great importance for preventing the failure of the process.

- Basically, the genetic algorithm is for unconstrained problems. However, it was shown that it could also deal with constrained optimisation problems.
- The convergence behaviour of the algorithm indicates that the genetic process developed in Chapter 2 has a reasonable behaviour, not being prone to a zigzag performance.

In Chapter 3, the genetic technique was employed for establishing an approach that could be used for studying double layer grids from the topological viewpoint. In this chapter, a new concept, namely, 'portancy' was introduced. The portancy of an element of the double layer grid is used to indicate the importance of the element in carrying the loads. The densest configuration of a family of double layer grids with square on square pattern was considered as a 'base grid' and the portancies of its elements were found using the approach developed in Chapter 3.

The procedure for applying the genetic technique to find the portancy values of the elements of a base grid was explained step by step through an example in Chapter 3. Also, the concept of 'portancy map' was introduced as a graphical indication of the element portancies. Some statistical studies were carried out for the investigation of the sensitivity of the portancy map to the variations in some structural aspects such as the cross-sectional areas and the lengths of the elements of the base grid. These studies show that the variations in these aspects do not affect the portancy maps significantly.

One of the important aspects of the work carried out in this Thesis is that the optimisation is dealt with in a probabilistic manner. To elaborate, the optimisation techniques are usually implemented to find deterministic optimum solutions. However, in this work, the portancy map is created based on a number of optimum solutions each of which is obtained through a random process. It was shown that, although the portancy map is produced through a random process, it possesses a symmetrical form.

In practice, the portancy map introduced in this Thesis may be used as follows:

- The portancy map is useful for a designer to have an accurate judgment about the positions of the elements that are more important, that is, the elements that have more

contributions in carrying the loads. Using the map, a designer may easily decide about the regions from which the elements may be removed such that the loss of the loading capacity of the structure is minimised.

- The portancy values obtained for a base grid can be used for comparing the reduced grids derived from the base grid. That is, the grids with different topologies can be compared with each other for choosing the most suitable one. Applying the proposed method in relation to a number of base grids indicate the suitability of the method for this purpose. To investigate the reliability of the proposed method, an optimisation process was carried out to find the minimum weights of the reduced grids. The results obtained from the weight optimisation process are generally consistent with the results based on the portancy approach.
- Studies show that the pattern of the disposition of the openings in a reduced grid affects its degree of suitability of the grids. So, using the portancy values, a suitable pattern may be found for placing the openings such that the elements of the reduced grid contribute more effectively in carrying the loads.

In chapter 3, the effects of the support conditions on the portancy map were investigated by considering a number of commonly used support arrangements for the base grid. It was found that the portancy values of the elements of the base grid for a particular loading arrangement are highly dependent on the support conditions. This is reasonable because the behaviour of a structure varies when the support arrangement is changed. So, a reduced grid that has the most suitable configuration with a particular support conditions may be the worst one with another support arrangement.

The effects of the loading arrangement on the results were also studied in Chapter 3. In practice, a grid may experience different types of loadings during its lifetime and it is expected that the structure has an acceptable behaviour when it is subjected to various loading arrangements. Studies carried out in this Thesis show that the portancy maps of a grid obtained for different loading arrangements lead to similar results. That is, the degree of desirability of a reduced grid is not changed when the grid is subjected to various loading arrangements.

In Chapter 4, various patterns were considered for the base grid and the procedure developed in Chapter 3 was used for topological studies of these patterns. The results obtained in

Chapter 4 show that the genetic process developed in this Thesis is suitable for any kind of patterns that may be considered for the base grid.

As another significant conclusion of the work, it should be pointed out that the method developed in this Thesis may be applied independent of the actual dimensions of the elements of the base grid. Also, the method may be used with any number of elements for the base grid.

Studies carried out by the author indicate that when the approximate values of portancies are of interest, then the portancy map obtained through once analysing the base grid may be useful. To elaborate, in this case, the base grid is analysed and then, the absolute values of the element forces are divided by the maximum internal force in the base grid. The results are numerical values between zero and one that may be regarded as approximate element portancies.

5.3 SUGGESTIONS FOR FUTURE WORK

Some suggestions for the extension of the present research are as follows:

- Double layer grids with other patterns may be considered as the base grids and the resulting portancy maps may be used for obtaining the optimum topologies.
- The possibility of extending the proposed technique to other space structures may be examined. For instance, some space structures such as barrel vaults and domes may be suitable for these investigations.
- Applying the approach developed in this work to three layer grids may be considered as the subject of an investigation.
- The concept of 'portancy' proposed in this Thesis is in relation to a case where the grid is subjected to static loads. The possibility of extension of this concept to dynamic loads may be investigated.

APPENDICES

A: RANDOM NUMBERS

As described in chapter 2 to 4, the genetic algorithm relies due to its stochastic nature on random numbers. The quality of the results produced by the genetic process depends on the quality of the random numbers. A great many random numbers are required for a genetic process. It is therefore essential that they be generated as quickly and efficiently as possible.

In operating the genetic algorithm, random numbers are used which are uniformly distributed within the unit interval $[0,1]$, that is, numbers that fall within the interval $[0,1]$ with equal likelihood. In this appendix, some methods are investigated for generating such random numbers. Indeed, these numbers are not really random numbers, since they are generated in reproducible sequences by deterministic techniques. However, if the generated numbers are satisfying a variety of statistical tests for randomness, it can be assumed that these numbers are truly random. Such numbers are referred to as 'pseudo random numbers'.

A.1 DESIRABLE SPECIFICATIONS FOR A RANDOM GENERATOR

Ideally, a pseudo random number generator should possess the following desirable characters.

1. *Good statistical characteristics*

The most important desired properties are of course the statistical properties. That is, the generated sequences of pseudo random numbers are expected to exhibit the same properties as truly random numbers. The random behaviour of these generated numbers is determined by a number of different statistical tests [34].

2. *Computational efficiency.*

Since, a stochastic process such as genetic algorithm requires a huge number of random numbers, the random number generator should provide these numbers using as little computer time as possible. Moreover, the random number generator should not require extensive computer memory.

3. *Long period*

Since sequence of pseudo random numbers is generated based on deterministic formulas, then the sequence will eventually begin to repeat itself after a certain number of steps. The size of the non-repeating sequence is called 'period'. The period is desired to be as long as possible.

From a practical viewpoint, the period should be sufficiently large such that the random numbers do not repeat themselves during a single genetic process.

4. Reproducibility

Reproducibility is important for debugging and for understanding a stochastic process. Then, it may be desirable to generate the exact same sequence of random numbers for a special starting point.

A.2 RANDOM NUMBER GENERATORS

Most modern random number generators are based upon the use of ‘congruent numbers’ [34]. Suppose a positive integer given, M , which is called a ‘modulus’. The two numbers A and B are congruent modulo M , if $(A-B)$ is some integral multiple of M that is, if

$$A - B = kM$$

where, k is an integer. This relationship may be written as

$$A \equiv B \pmod{M}$$

where, the symbol ‘ $\equiv$ ’ denotes congruence.

For a given integer A , the smallest nonnegative integer R which is congruent to $A \pmod{M}$ is called a ‘residue modulo M ’. Thus,

$$R \equiv A \pmod{M} \quad 0 \leq R \leq M$$

Each value of A will have its own corresponding residue. There are however, only M distinct residues whose values range from 0 to $M-1$.

A ‘power residue’ is the smallest nonnegative integer, P_i , that is congruent to $A^i \pmod{M}$ where, A is a given integer and i is a positive integer exponent. Thus,

$$P_i \equiv A^i \pmod{M}$$

A.2.1 Power Residue Method

This method which is also called, ‘multiplicative congruential method’ is based upon the use of the ‘power residues’. This is a simple and popular method for generating the random numbers. This random number generator makes use of the following recursive congruential relationship.

$$N_i \equiv AN_{i-1} \pmod{M}$$

where, N_i and N_{i-1} are successive random integers and A is a multiplier. M and A are specified by the user. For instance, suppose that the set of values for N_0 , A and M are given as below:

$$N_0 = 3 \quad A = 7 \quad M = 20$$

The sequence of generated numbers are obtained as follows:

$$\begin{aligned} N_0 &= 3 \\ N_1 &= (3 \times 7) \bmod 20 = 1 \\ N_2 &= (1 \times 7) \bmod 20 = 7 \\ N_3 &= (7 \times 7) \bmod 20 = 9 \\ N_4 &= (9 \times 7) \bmod 20 = 3 \end{aligned}$$

As indicated in the above example, N_4 is equal to N_0 . Continuing the generation of numbers implies that N_5 is equal to N_1 and so on. It is seen that the sequence repeats itself after a certain number of steps.

In order that the generated numbers by ‘power residue method’ exhibit acceptable random behaviour, it is essential that the values for M , N_0 and A be chosen carefully. To this end, set of rules which are commonly used may be given as follows:

- The ‘modulus’, M , should be chosen as large as possible in order to maximise the period of the random number sequence.
- The multiplier, A , should be chosen such that the correlation between successive generated numbers is minimised, while at the same time obtaining the largest possible period.
- The initial value, N_0 , which is called ‘seed’, can be any positive integer whose value is less than M .

Two suggestion for A and M , presented by experts in the field, are given in Table A.1 [35].

A.2.2 Mixed Congruential Method

The mixed congruential method is based upon the use of the following congruential relationship.

$$N_i = (AN_{i-1} + B) \bmod M$$

where, N_i and N_{i-1} are successive random integer numbers and the parameters A , B and M are specified integer constants. The constant parameters should be chosen carefully such that the rules described in relation to the ‘power residue method’ are satisfied. That is, the period for the resulting random numbers is maximised and the correlation between successive generated numbers is minimised. Table A.2 indicates three suggestions presented by researchers for the constant parameters [35].

Table A.1 Proposed parameters for random generators based on power residue method

Name	A	M	Period	Reference
LGM	16807	$2^{31} - 1$	$2^{31} - 2$	Lewis, Goodman, Miller (1969)
PRB	630360016	$2^{31} - 1$	$2^{31} - 2$	Payne, Rabung, Bogyo (1969)

As seen from Table A.2, the mixed congruential method will result in sequences of random numbers whose period is equal to M . The mixed congruential method is therefore known as ‘full-period’ method.

Table A.2 Proposed parameters for random generators based on mixed congruential method

Name	A	B	M	Period	Reference
Marsg	69069	1	2^{32}	2^{32}	Marsaglia (1972)
Atari ST	3141592621	1	2^{32}	2^{32}	from the OS ROM
rand	1103515245	12345	2^{31}	2^{31}	Unix

In contrast with ‘power residue’ method, the mixed congruential method has been found by some experts to give poor results [Ref 34]. That is, the numbers sequence generated are statically less random than those produced by the power residue method. Moreover, the method is slower than the power residue method. For these reasons, the mixed congruential method is used less often than the power residue method, despite the fact that its period may be larger.

In this work, a random generator based on the ‘power residue’ method is employed whose corresponding constants A and M are given in the first row of Table A.1, that is, the random generator named ‘LGM’.

B: DESCRIPTION OF PROVIDED CODE

In Chapter 3, the stages of the procedure for obtaining the portancy map were explained in detail and the flow chart of the procedure was given in Fig 3.26. As may one see from this figure, the process starts by configuration processing of the base grid. In this work, the configuration processing involves 'formex algebra'. In fact, formex algebra is a mathematical system that provides a convenient tool for processing of configuration. The basic ideas of formex algebra were developed in the early 1970's [36] and the first textbook in this field was published in 1984 [37]. A concise description of the concepts is described in a later publication [38]. In order to apply the concepts of formex algebra for processing the configurations, a convenient medium is required. The programming language 'Formian' has been developed for formex configuration processing [38]. So, using the Formian the configuration of the base grid is generated.

As explained in Chapter 3, the main part of the procedure for obtaining the portancy map consists of the stages of the genetic process. This part of the work is carried out through a number of computer programs written by the author. The necessity of writing the computer programs is discussed as follows.

Genetic algorithm is a relatively new technique and the background of applying this technique in structural optimisation is not too long. Therefore, the available computer programs produced by the others can deal with particular problems. Also, the subject of this thesis is a new concept and the research in relation to this subject implies investigation of the effects of different parameters. So, it was necessary to write a number of computer programs meeting these requirements. On the other hand, the problem under investigation involves a huge number of structural analyses. To have a fast tool for structural analysis a subroutine routine was written by the author based on the stiffness method. An outline of some of the subroutines is given as follows.

Since random numbers are widely used in different stages of the genetic process, then a reliable random generator should be employed. To this end, a program is written based on the random generator named 'LGM' (see Appendix A). The internal time on the computer is used as initial seed number. In the subroutine provided for generation of chromosomes representing

reduced grids, the 'presence factor' for generating each gene of the chromosomes is taken as 0.95. Also, for each of the other stages of the genetic process such as pairing, crossover, mutation, replacement and terminations a subroutine has been provided.

Portancy map which is a graphical indication of the portancy values is created based on the results of the genetic process. Actually, these results are the portancy values of the elements of the base grid. For drawing the portancy map, the elements of the base grid are classified into a number of groups according to their corresponding portancy values. The ranges given in Table 3.3 are used for this purpose. Then, for each of these groups of elements a binary file (formex file) is generated. Each of these formex files is taken by the Formian for drawing the portancy map.

Here, more details are given in relation to generation of the formex files corresponding to a portancy map. As an example, in the current program TOP1 denotes the formex file relating to the elements of the top layer with portancy values between 0.0 and 0.2. As it is explained in Ref 34, a formex which is a binary file consists of a heading followed by a body. The heading of a formex contains information about the type and dimensions of the formex held by the file. The contents of the heading for the formex TOP1 are as follows.

- For the type of the formex an integer value of 2 is considered because the formex under consideration is a floatal formex.
- Grade of the formex, that is, the number of 'uniples' in a 'signet' is 3.
- Plexitude of the formex, that is, the number of the signets in a 'candle' is 2.
- Total number of the signets of the formex is two times the number of the elements in the group of elements under consideration.
- Order of formex, that is, the number of candles is equal to the number of the elements in the group under consideration.

The routine written for generating the formex file TOP1 using C programming language is given as below.

```
OUT=fopen("TOP1.fmx","wb");
```

```
sgt=2*Top1Number;//Top1Number stands for the number of elements
type =2;//formex is floatal
```



```

plx =2; //plx stands for the Plexitude of formex
grd= 3; //grd stands for the Grade of formex
ord =Top1Numbr;//ord stands for the Order of formex

fwrite(&type,sizeof(int),1,OUT);
fwrite(&grd,sizeof(int),1,OUT);
fwrite(&plx,sizeof(int),1,OUT);
fwrite(&sgt,sizeof(int),1,OUT);//sgt stands for total number of signets in formex
fwrite(&ord,sizeof(int),1,OUT);
for(i=0;i<Top1Number;++i)
{
XYZ[0]=TopCo1[i][0];
XYZ[1]=TopCo1[i][1];
XYZ[2]=TopCo1[i][2];
XYZ[3]=TopCo2[i][0];
XYZ[4]=TopCo2[i][1];
XYZ[5]=TopCo2[i][2];
fwrite(XYZ,sizeof(float),6,OUT);
}
fclose(OUT);

```

Where,

- XYZ is the array containing the uniples,
- TopCo1 is the array that consists of the coordinates of the beginning of an element and
- TopCo2 is the array containing the coordinates of the end of an element.

For drawing the portancy map of the elements whose relating formex file is TOP1 the following Formian commands are used.

```

Take TOP1;
Use lw (0.1);
Draw TOP1;

```

Thus, the portancy map of the top elements of the base grid with portancy values in the range 0.0-0.2 is drawn with the line width of 0.1 mm.

REFERENCES

-
- [1] ARORA J S, Introduction to Optimal Design, *McGraw-Hill, New York*, 1989.
- [2] RAO S S, Engineering Optimisation-Theory and Applications, *New Age International, New Dehli*, 1998.
- [3] KIRSCH U, Structural Optimisation: Fundamental and Applications, *Springer-Verlag*, 1993.
- [4] VANDERPLAATS G N, Numerical Optimisation Techniques for Engineering Design, *McGraw-Hill, New York*, 1984.
- [5] HAFTKA R T and GURDAL Z, Elements of Structural Optimisation, *Kluwer Academic Publishers*, 1992.
- [6] DARWIN C, On the Origin of Species by Means of Natural Selection or the Preservations of Favoured Races in the Struggle for Life, *London, John Murray*, 1859.
- [7] JENKINS W M, Towards Structural Optimisation via the Genetic Algorithm, *Computers and Structures*, 1991, Vol. 40, No. 5, pp. 1321-1327.
- [8] HOLLAND J H, Adaptive Plans Optimal for Payoff-Only Environments, *In Proceeding of the Second International Conference on System Sciences*, 1969, pp. 917-920.
- [9] HOLLAND J H, Adaptation in Natural and Artificial Systems, *Ann Arbor: University of Michigan Press*, 1975.
- [10] GOLDBERG D E, Computer Aided Gas Pipeline Operation Using Genetic Algorithm and Rule Learning, *PhD Dissertation, University of Michigan*, Ann Arbor, 1983.
- [11] GOLDBERG D E, Genetic Algorithms in Search, Optimisation and Machine Learning, *Addison-Wesley Publishing Company, Inc.*, 1989.
- [12] DAVIS L, Handbook of Genetic Algorithms, *Van Nostrand Reinhold*, 1991.

-
- [13] FALKENAUER E, Genetic Algorithms and Grouping Problems, *John Wiley & Sons*, 1998.
- [14] MICHALEWICZ Z, Genetic Algorithm + Data Structures = Evolution Programs, *Springer-Verlag Berlin Heidelberg*, 1992.
- [15] HAUPT R and HAUPT S E, Practical Genetic Algorithm, *John Willey and Sons*, 1997.
- [16] GOLDBERG D E and SAMTANI M. P, Engineering Optimisation via Genetic Algorithm, *Proceeding of 9th Conference on Electronic Computation, ASCE*, 1986, pp. 471-482.
- [17] RAJEEVE S and KRISHNAMOORTHY C S, Discrete Optimisation of Structures Using Genetic Algorithm, *Journal of Structural Engineering*, Vol. 118, No. 5, 1992, pp. 1233-1249.
- [18] ADELI, H and CHENG N T, Integrated Genetic Algorithm for Optimisation of Space Structures, *Journal of Aerospace Engineering*, Vol. 6 No. 4, 1993, pp. 315-329.
- [19] WU S J and CHOW P T, Steady-State Genetic Algorithms for Discrete Optimisation of Trusses, *Computers and Structures*, Vol. 56, No. 6, 1995, pp. 979-991.
- [20] WU S J and CHOW P T, Integrated Discrete and Configuration Optimisation of Trusses Using Genetic Algorithm, *Computers and Structures*, Vol. 55, No. 4, 1995, pp. 695-702.
- [21] YANG J and SOH C K, Structural Optimisation by Genetic Algorithms with Tournament Selection, *Journal of Computing in Civil Engineering*, Vol. 11, No. 3, 1997, pp. 195-200.
- [22] HAJELA P and LEE E, Genetic Algorithms in Truss Topological Optimisation, *International Journal of Solids and Structures*, Vol. 32, No. 22, 1995, pp. 3341-3357.
- [23] ROZVANI G I N, Application of the COC Algorithm in Layout Optimisation, *Proceeding of International Conference on Engineering Optimisation in design Process, Karlsruhe, Springer, Berlin*, 1990, pp. 59-70.

- [24] DORN W C, GOMORY R E and GREENBERG H J, Automatic Design of Optimal Structures, *Journal of Mechanics*, No. 3 1964, pp. 25-52.
- [25] BENDSØE M P, Optimisation of Structural Topology, Shape and Material, *Springer-Verlag, Heidelberg*, 1995.
- [26] OHSAKI M, Genetic Algorithm for Topology Optimisation of Trusses, *Computers and Structures*, Vol. 57, No. 2, 1995, pp. 219-225.
- [27] GRIERSON D E and PAK W H, Optimal Sizing, Geometrical and Topological Design Using a Genetic Algorithm, *Structural Optimisation*, No. 6, 1993, pp. 151-159.
- [28] RAJAN S D, Sizing, Shape, and Topology Design Optimisation of Trusses Using Genetic Algorithm, *Journal of Structural Engineering*, Vol. 121, No. 10, 1995, pp. 1480-1487.
- [29] RAJEEVE S and KRISHNAMOORTHY C S, Genetic Algorithm-Based Methodologies for Design Optimisation of Trusses, *Journal of Structural Engineering*, Vol. 123, No. 3, 1997, pp. 350-358.
- [30] SHESTHA S M and GHABOUSHI J, Evolution of Optimum Structural Shapes Using Genetic Algorithm, *Journal of Structural Engineering*, Vol. 124, No. 11, 1998, pp.1331-1338.
- [31] DEB K and GULATI S, Design of Truss-Structures for Minimum Weight Using Genetic Algorithms, *Finite Elements in Analysis and Design*, Elsevier, No. 37, 2001, pp. 447-465.
- [32] SALMON C G, Steel Structures, 3rd Edition, *Harper and Row Publisher, New York*, 1990.
- [33] STEPHENS L J, Beginning Statistics, *McGraw-Hill*, 1998.
- [34] GOTTFRIED B S, Elements of Stochastic Process Simulation, *Englewood Cliffs, Prentice Hall*, 1984.

- [35] REPLEY B D, Thoughts of Pseudorandom Number Generators, *Journal of Computational and Applied Mathematics*, No. 31,1990, pp.153-163.
- [36] NOOSHIN H, Algebraic Representation and Processing of Structural Configurations, *International Journal of Computers and Structures*, 1975, pp. 119-130.
- [37] NOOSHIN H, Formex Configuration Processing in Structural Engineering, *Elsevier Applied Science*, 1984.
- [38] NOOSHIN H AND DISNEY P, Formian 2, *Multi-Science Publishing Company Ltd*, 1997.

UNIVERSITY OF SURREY LIBRARY