

SOLVING 2D-STRIP PACKING PROBLEM USING GENETIC ALGORITHM

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ABSTRACT

The main focus of this thesis is to solve the 2D strip-packing problem specifically for use in the garments industries of Bangladesh. Garments industry is one of the biggest export industries of Bangladesh. One of the routine works of all garments company is to cut shape of clothes from long strip of cloth. The current technique for placing the shapes and cutting are both done manually which is not only time consuming but also minimally optimized. We realized that this process of placing shapes can be automated. However the problem itself is classified as NP-Hard problem. In this thesis we tried to solve the problem using Genetic Algorithm keeping the orientation of the shapes fixed. This requirement of keeping the orientation fixed is posed by the nature of the way clothes have to be cut out. In this research we surveyed most of the works that has been done to solve similar problems and developed our new algorithm which solves the garments industries' problem specifically. We developed software that tests our new algorithm and presents the user with graphical output of the final placement of the shapes. Our software can also take several input parameters which are either software specific or Genetic Algorithm specific.

TABLE OF CONTENTS

Chapter 1 INTRODUCTION	1
1.1 Introduction	2
1.2 Objective	2
1.3 Motivation.....	2
1.4 Problem Formulation	3
1.5 Optimality of the solution	3
1.6 Genetic Algorithm.....	3
1.7 Methodology of the thesis	4
1.8 Conclusion	5
Chapter 2 CANDIDATE APPROACHES	6
2.1 Introduction	7
2.2 Rectangular Bounding-Box Approach.....	7
2.3 Positional and Rotational Encoding of Polygon Placement Method, using GA [5]	7
2.4 NFP Method [4]	7
2.5 Gravity Center NFP [4].....	8
2.6 Conclusion	9
Chapter 3 GENETIC ALGORITHM	10
3.1 Genetic Algorithm (GA).....	11
3.2 Fitness	11
3.3 Cross-over.....	11
3.4 Mutation	12
3.5 Conclusion	13
Chapter 4 DEVELOPED ALGORITHM	14
4.1 Developed Algorithm	15
4.2 Object definition	15
4.3 Definitions	16
4.4 Assumption.....	18
4.5 Mapping to GA	19
4.6 Conclusion	21
Chapter 5 SIMULATION FRAMEWORK	22
5.1 Simulation Framework	23
5.2 Simulation software	24
Chapter 6 OPTIMIZATION	26
6.1 Introduction	27
6.2 Optimization	27
6.3 Performance	29
6.4 Conclusion	30
Chapter 7 RESULTS	31
7.1 Introduction	32
7.2 Effect of mutation-probability	33
7.3 Effect of Number of Generation	34
7.4 Effect of Initial Population Size.....	36
7.5 Conclusion	37
Chapter 8 CONCLUSION	38
8.1 Conclusion	39

LIST OF FIGURES

<i>Number</i>	<i>Page</i>
Figure 2.1: NFP (No Fit Polygon)	8
Figure 2.3: Gravity Center NFP	9
Figure 3.1: 8-Queen Problem. String representation for this configuration will be [1,5,8,4,2,6,1,3]	11
Figure 3.2: Mating process	12
Figure 3.3: Genetic Algorithm	13
Figure 4.1: A Polygon	15
Figure 4.2: Examples of Front Facing Lines	16
Figure 4.3: Examples of Back-Facing lines	16
Figure 4.4: Incoming-line and Outgoing-line	17
Figure 4.5: Start-point and End-point	17
Figure 4.6: Apex Point	17
Figure 4.7: Crevice-Point	18
Figure 4.8: Edge Points	18
Figure 4.9: An example chromosome with 3 genes for 3 polygons.	19
Figure 4.10: Demonstrating the fitness evaluation process	20
Figure 5.1: Screenshot of the simulation software	24
Figure 5.2: Software Data Flow	25
Figure 6.1: Polygon Hit	27
Figure 6.2: Performance Curve	29
Figure 7.1: Polygons used in experiment	32
Figure 7.2: Mutation probability Vs Average fitness	33
Figure 7.3: Mutation Probability Vs Average Best Fitness	33
Figure 7.4: No. of Generations Vs Average fit of population	34
Figure 7.5: No. of generation Vs Average Best Fit	35
Figure 7.6: Initial population size Vs Average Best Fitness	36
Figure 7.7: No. of initial population size Vs Average fitness of the population	37

Chapter 1 INTRODUCTION

1.1 Introduction

Cutting and packing problems arise in many fields and situation. For example a garment industry might need to cut shapes out of a long strip of fabric in an optimized fashion so that minimum amount of cloth is wasted. Unfortunately this class of problems, known as Bin-packing problems, is known to be **NP-Hard**[1] problems in computer science.

Bin-packing problems can be classified in several categories, e.g. 1D bin-packing problems, 2D Strip-packing packing problems and 3D Bin-packing problems. In this thesis we have dealt with a 2D Strip-packing problem with arbitrary shapes. Most of the previous work dealt with packing rectangular shapes or some composition of rectangular shapes within a finite 2D space. Researchers have found some heuristics to find solutions for the bin packing problems, but some others have also used approximation algorithms like **Genetic Algorithm**[1] and **Neural Networks**[2] as an approach to solve these problems.

1.2 Objective

2D Strip-Packing problem is that a strip of 2D space is given with fixed width but variable length. A set of arbitrary polygon are also given which need to be fit in the 2D strip in such a way that minimum length is required. The objectives of this thesis are :

- Study existing solutions, if there is any
- Defining how shapes are to be represented.
- Deciding on an efficient algorithm.

1.3 Motivation

Garments industry is one of the biggest export industries of Bangladesh. Lots of clothe shapes have to be cut out of long sheets of cloth but the whole process is done manually and hence minimally optimized. Clothes are wasted in the process of this manual placement of shapes on long cloth strips. It can be easily speculated that even a save of 1 inch while cutting shapes out of cloth strip can save hundreds of thousands of worth. Placing arbitrary shapes on cloth strip and then cutting them my means of automated machine such that minimum length of cloth is required to fit the given number of shapes easily translates into a Strip-Packing problem. Whatever algorithm is developed, no one can claim about absolute optimality due to the NP-

Hard nature of the problem, but even near optimal solution to this problem has been speculated to save hundreds of thousands of worth on daily basis.

1.4 Problem Formulation

The problem consists of the following input:

- A rectangular bin with fixed width w and a variable height h which can be stretched infinitely.
- A set of arbitrary shapes $\{S_1, S_2, \dots, S_n\}$.

And we are to fit the arbitrary shapes in such a way that the following conditions are met:[6][7]

- No shape has any of its part outside the bound of the bin.
- No two shapes overlap
- All the shapes are packed in such a way that the height required h for the bin is minimized.

The final solution may have shapes with orientation different from their original input however the basic dimension must remain the same, i.e. the shape cannot be stretched, sheared or distorted by any means but only rotated around some fixed point.

1.5 Optimality of the solution

Being an **NP-Hard** problem there is no way to claim that a particular solution is the most optimal which poses as one of the major constraints in evaluating an instance of solution. However, the “goodness” of the solution can be compared between different instances of solution.

1.6 Genetic Algorithm

Genetic Algorithm (GA) is a pseudo-random search technique inspired from natural evolution theory. The parallel-search nature of **GA** and its ability to avoid local minima in the search space combined with the fact that the solution relies on proper combination of several parameters that describes the position and orientation of the arbitrary shapes makes it a good candidate to generate approximate results for Bin-packing problems.

In this thesis we fit a given number of arbitrary shapes within a rectangular bin of fixed width and infinite height and we aim to minimize the height required. We chose to use **GA** as our tool to address the problem.

1.7 Methodology of the thesis

To do this thesis a structural procedures will be followed. The step by step procedure is mentioned below

1.7.1 Literature survey

Not many books are available that has solutions for such problem hence most of the literature to be read will be gathered from internet.

1.7.2 Deciding on a algorithm

After enough literature survey, we will decide/devise an efficient algorithm that suits our need as well as solve our specific problem.

1.7.3 Finding out bottlenecks and decide on optimization techniques

We will find out the major bottlenecks of the algorithm and try to develop highly optimized modules that will be used by our new algorithms.

1.7.4 Compilation of the necessary tools and materials

Due to the graphical nature of the problem the final result must be presented graphically to the user hence a good GUI must be used. For that purpose we will decide on which GUI libraries to use to develop the simulation software. As well as we will decide which platform to use to develop the software.

1.7.5 Implement the algorithm and develop the softare

In this phase the actual software will be develop which will be as flexible as taking all possible inputs and parameters from the user through a good looking UI.

1.7.6 Performance evaluation

Finally the output of the new algorithm will be analyzed and the effect of various parameter will be studied.

1.8 Conclusion

In this report we will first define and formulate the problem at hand. We will then explore what has been done so far to address such problems and other similar or related problems. Next we present our new approach with detailed description of Genetic Algorithms. We then present several result outputs and interpretation of each output generated. While interpreting we will try to show how the results are dependant on each of the input parameters of problem.

Chapter 2 CANDIDATE APPROACHES

2.1 Introduction

Nesting problem is interesting to many industries like garment, paper, ship building, and sheet metal industries since small improvements of the layout can result in a large saving of material. In some cases both the pieces and the containing region are rectangular, and a considerable amount of effective solutions have been proposed for rectangular nesting problems in the past decades. However, there are also many other cases where either the pieces or the containing region is irregular in shape, due to the geometrical complexity introduced by irregular shapes, such problems are not studied as well as rectangular nesting problem. Today even a purely automatic algorithm is still difficult to outperform an experienced operator, hence irregular nesting problem is still an attractive research topic.

2.2 Rectangular Bounding-Box Approach

In this approach a set of rectangular boxes are fit inside the strip. In case of arbitrary polygon, the bounding boxes are found out and used in the algorithm.

It is quite discernible that this approach for arbitrary polygon is very naïve and inefficient as too much space would be wasted.

2.3 Positional and Rotational Encoding of Polygon Placement Method, using GA [5]

In this method, the 2D coordinates and the orientation angle is encoded in the chromosome of Genetic Algorithm. The evaluation of a particular chromosome is calculated using two basic parameters, awards are given for better fit and penalties are given for overlap and other violations. The genetic algorithm then converges the population with more awards.

Though the algorithm is simple but the final result may have overlaps.

2.4 NFP Method [4]

The concept of NFP (No Fit Polygon) was proposed by Art [7], Adamowicz and Albano [8]. No Fit Polygon (NFP) is the fundamental geometric tool for 2D irregular nesting problems. It gives the set of non-overlapping placements for polygons. NFP can be defined as below:

Given two polygons A and B, A is fixed, and B slides around A without overlapping and B keeps not rotating. During this tracing movement, the locus of the reference point on B forms a closed path denoted as NFP_{AB}

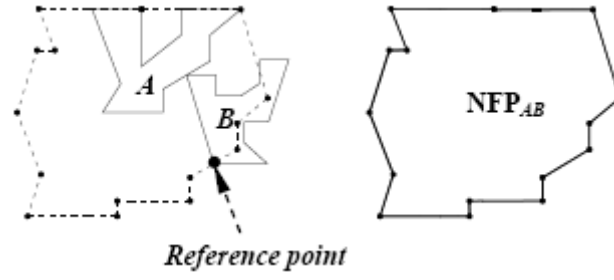


Figure 2.1:NFP (No Fit Polygon)

The relevant property of NFP regarding the interaction between A and B is as follows: if B is positioned with its reference point on the boundary of NFP then A and B will touch; if B is positioned with its reference point inside the boundary of NFP then the A and B will overlap. Thus, the boundary of NFP represents all touching positions. In the nesting procedure, pieces are arranged in pattern of touching each other for saving materials, therefore, based on the NFP, the problem of nesting one piece can be simplified to select the optimal position on NFP.

The basic approach of this algorithm is to find an optimal position in the NFP.

However, existing NFP algorithms have some common drawbacks, such as high time-complexity and difficult to implement and not robust enough. The lowest average complexity of the existing NFP algorithms is $O(lmn)$ (l presents the number of edges of NFP, and m and n present the numbers of edges of A and B respectively).

2.5 Gravity Center NFP [4]

The basic NFP based algorithm is further enhanced with Gravity Center NFP. In this approach the reference of the given polygon is taken as the center of gravity of the polygon instead of any arbitrary vertex. This gives better results compared to the traditional NFP algorithm. In this approach the polygon is also rotated in a discrete fashion, i.e. 360° is divided into n parts and then the polygon is rotated and for each orientation an NFP is calculated. Later the NFP having the lowest gravity center is chosen and the polygon is placed.

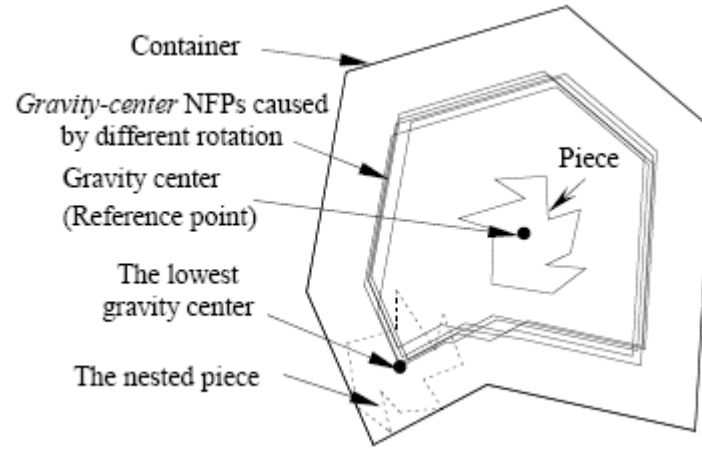


Figure 2.2: Gravity Center NFP

This method suffers from the same problem of time complexity and computational complexity as the traditional NFP method.

2.6 Conclusion

The problem that we have in our hand is much simpler in the sense that the orientation of the polygon remains static. Hence the time and computational complexity that the above methods suffer can be easily avoided and a much simpler technique could be employed to solve the problem. This led us to design and implement a new algorithm which is much simpler and produces good results much quicker than the above methods.

The following section discusses shortly about Genetic Algorithm which will be extensively used in our new algorithm. The genetic coding has been designed in such a way that even a randomly generated population of polygon arrangement will never have overlaps.

Chapter 3 GENETIC ALGORITHM

3.1 Genetic Algorithm (GA)

Genetic algorithm (GA) is based on the natural evolution theory. GA begins with a set of k randomly generated states, called **population**. Each state, or **individual**, is represented as a string over a finite alphabet, most commonly a string of 0s and 1s. Each state must be one candidate solution or an acceptable configuration of the problem which may or may not be optimal. For example, in 8-queens-problem, which asks to arrange 8 chess queens on a chess board in such a way that no queen can attack another queen, a state must specify positions of 8 queens. A common representation of the state can be a string of 8 numbers. Each number will be associated with a queen in one particular column of the chess board, and the number it self will represent the row that queen belongs to. This representation is illustrated in **Figure 3.1** below. 8 such numbers can fully represent the positions of all 8 queens on the chess board. Randomly generating one such state may have queens attacking another queen.

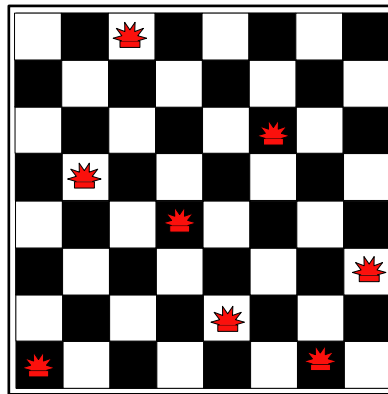


Figure 3.1: 8-Queen Problem. String representation for this configuration will be [1,5,8,4,2,6,1,3]

3.2 Fitness

Each state is rated by the evaluation function called **fitness function**. A fitness function should return higher values for better states, so, for the 8-queens problem we use the number of non-attacking pairs of queens, which has a value of 28 for a solution.

The population is allowed to mate within it self and produce next generation, very much like natural processes. In this particular variant of the genetic algorithm, the probability of being chosen for reproducing is directly proportional to the fitness score.

3.3 Cross-over

For each pair to be mated a **crossover** point is randomly chosen from the positions in the string, e.g. in **Figure 3.2** the crossover point is selected after the 3rd number.

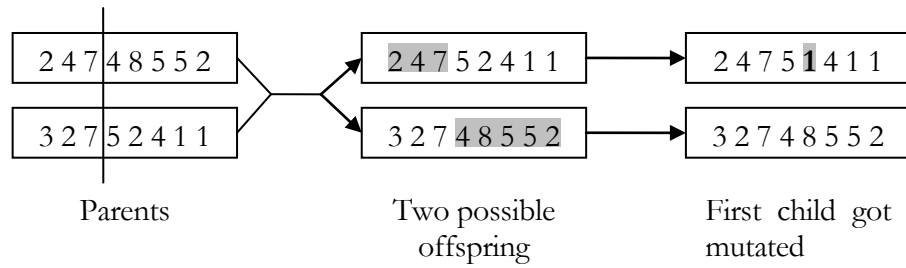


Figure 3.2: Mating process

Offspring are created crossing over the parent strings at the crossover point. For example, in **Figure 3.2**, the first child got its first 3 numbers from 1st parent and the rest numbers from the 2nd parent.

3.4 Mutation

Finally offspring are subjected to random mutation with very small independent probability. In our example in **Figure 3.2**, the 1st child got mutated in its 5th number while the 2nd child remained unchanged. Mutation enables the algorithm to pop out of local minima in the search space.

Genetic algorithm combines an uphill tendency with random exploration and exchange of information among parallel search threads. Genetic algorithm is suitable in places where some part of string representation, called schema, may contribute to the optimal solution.

```

function GENETIC-ALGORITHM(population, FITNESS-FN) returns an
individual
  inputs: population, a set of individuals
  FITNESS-FN, a function that measures the fitness of an individual

  repeat
    new_population  $\leftarrow$  empty set
    loop for i from 1 to SIZE( population ) do
      x  $\leftarrow$  RANDOM-SELECTION( population, FITNESS-FN)
      y  $\leftarrow$  RANDOM-SELECTION( population, FITNESS-FN)
      child  $\leftarrow$  REPRODUCE(x,y)
      if ( small random probability) then child  $\leftarrow$  MUTATE(child)
      add child to new_population
    population  $\leftarrow$  new_population
  until some individual is fit enough , or enough time has elapsed
  return the best individual in population, according to FITNESS-FN

```

```

function REPRODUCE(x,y) returns an individual
  inputs: x,y, parent individuals

  n  $\leftarrow$  LENGTH(x)
  c  $\leftarrow$  random number from 1 to n
  return APPEND( SUBSTRING(x,1,c) , SUBSTRING(y,c+1,n) )

```

Figure 3.3: Genetic Algorithm

3.5 Conclusion

The problem being an NP-Hard problem, the optimality of the any solution cannot be claimed to the best, and there is no deterministic algorithm to solve it. Genetic algorithm has been chosen to solve the problem for its inherent feature of parallel search and the ability to get out of local minima/maxima though the process of mutation. Genetic algorithm is also chosen because in this problem because a good schema of the chromosome can actually lead to many offspring of good fitness.

Chapter 4 DEVELOPED ALGORITHM

4.1 Developed Algorithm

The approach that has been taken to solve the given Strip-Packing problem was based on Genetic Algorithm. The first issue was to represent the arbitrary shapes into some geometric form.

4.2 Object definition

Each arbitrary shape was represented by an n -sided polygon. Each side of the polygon was a straight line. Curves and other smoother shapes were approximated by sampling a curve at many points and joining them with small lines. Therefore an arbitrary shape was represented by

- A set of points $P=\{P_0, P_1 \dots P_n\}$
- A set of lines $L=\{L_0, L_1 \dots L_n\}$

Where $n+1$ is the order of polygon. The polygon could be of both convex¹ and non-convex¹ type. Each line in the L , is directed and is described by a vector. Every polygon was oriented in anti-clockwise direction as shown below:

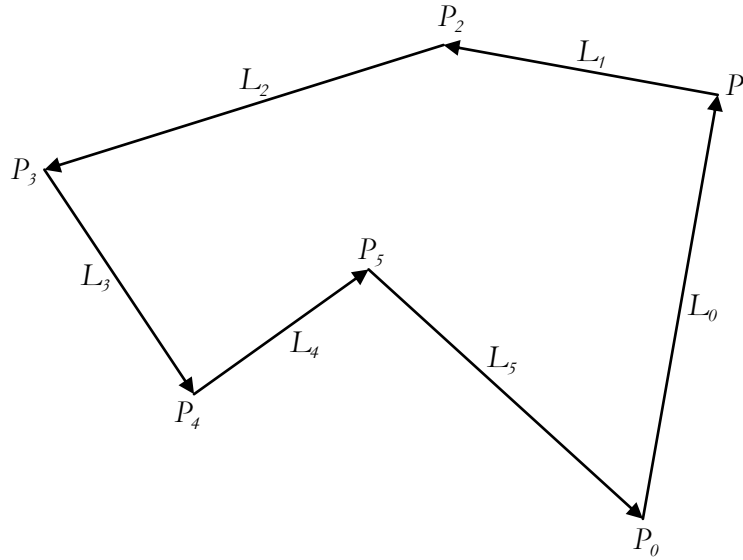


Figure 4.1: A Polygon

¹ A polygon is said to be convex if for every point inside the polygon a line is drawn in any direction it only intersects the polygon itself at one single point. Otherwise the polygon is said to be non-convex.

4.3 Definitions

4.3.1 Front-Facing Lines:

Front-Facing lines are defined to be those lines which, looking from bottom appears to have some component of it point towards right, as shown below:

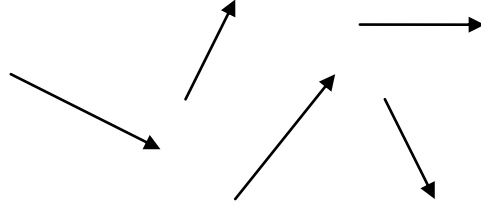


Figure 4.2: Examples of Front Facing Lines

Mathematically, a vector v is said to be Front-Facing if the z ordinate of

$$r = v \times (0,1,0)$$

r is positive, i.e. $r.z > 0$. Informally if v is “cross-product-ed” with Y -Axis and if the z ordinate of the resultant vector is positive, we defined that vector v as Front-Facing vector.

4.3.2 Back-Facing Line:

This is just the opposite of Front-Facing line. Looking from bottom if any component of a line appears to point towards left then we define that as Back-Facing line.

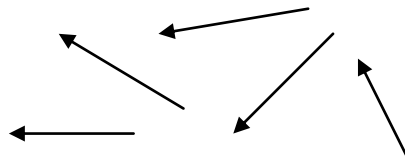


Figure 4.3: Examples of Back-Facing lines

If the mathematical test for the Front-Facing fails then the line must be a Back-Facing line.

4.3.3 Incoming-Line And Outgoing-Line of a Point

In a polygon a point has two lines associated with it. One is Incoming-Line and the other one is Outgoing-Line. Incoming-Line is the one that points towards the point, while Outgoing-Line is the line that points away from the point.

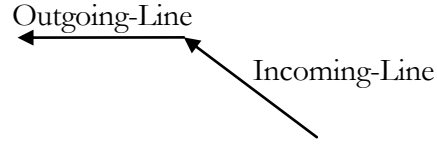


Figure 4.4: Incoming-line and Outgoing-line

4.3.4 Start-Point and End-Point

Each line has two points associated with, Start-Point and End-Point. Start-Point is the point that the vector v of the line starts from and End-Point is the point the vector v ends at.



Figure 4.5: Start-point and End-point

4.3.5 Apex-Point

A point is said to be Apex-Point if its Incoming-Line and Outgoing-Lines are oriented in such a way that looking from bottom the point seems to be “pointing” downwards, as shown below:

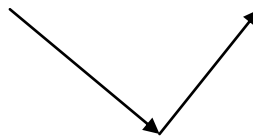


Figure 4.6: Apex Point

Mathematically, a point P is said to be an Apex-Point if the following condition is true

$$(P.IncomingLine \cdot (0,1,0)) < (P.OutgoingLine \cdot (0,1,0))$$

4.3.6 Crevice-Point

A point is said to be Crevice-Point if its Incoming-Line and Outgoing-Lines are oriented in such a way that looking from bottom the point seems to be “pointing” upward, as shown below:

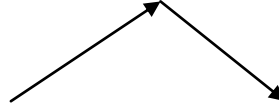


Figure 4.7: Crevice-Point

Mathematically, if the condition of the Apex-Point fails, then the point must be a crevice point.

4.3.7 Edge-Point

Edge point are those points whose either Incoming-Line or the Out-Going line is a Back-Facing line while the other one is a Front-Facing line. For example:



Figure 4.8: Edge Points

4.4 Assumption

For our algorithm we ignored orientation, i.e. the orientation of the polygon will not be changed and the same orientation will be used all through-out the algorithm and simulation process. This types of requirement as usually posed in garments industry where cloth have a particular type of “run” and all clothe pattern to be cut out must also align themselves in certain orientation to match with that run. However, polygons can be translated (moved).

4.5 Mapping to GA

The first and the most important step in solving a problem using GA is to design/encode the string representation (chromosome²). The given strip packing problem is such that there can be no overlap between two polygons whatsoever. This restriction requires the chromosome to be designed in such ways that even random generation of chromosomes guarantees that there will not be any overlap between polygons.

4.5.1 Chromosome representation

Keeping that in mind, we designed our chromosome such that it has n number of genes (We define **chromosome** as the string/array representation of a single state in GA. We also define each basic element of that string/array as **gene**) where n is the number of total polygon to be fit in the strip. Each gene has two information: “Sequence-Number” and “X-Position” and associated with a particular polygon, which will be discussed shortly.

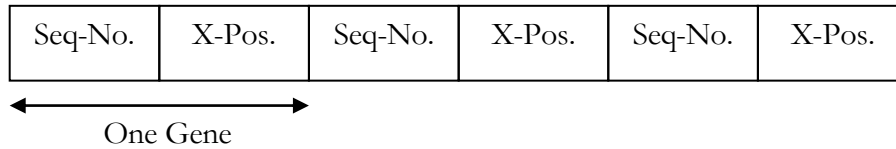


Figure 4.9: An example chromosome with 3 genes for 3 polygons.

4.5.2 Evaluating fitness value

The fitness of a particular chromosome is determined by traversing through all its genes according to the Sequence-Number (which has a range of 0 to $n-1$) in ascending order, i.e. the gene having the lowest Sequence-Number will be visited first and the highest Sequence-Number will be visited last. For each gene visited, the corresponding polygon is allowed to drop freely from a height which is the atleast equal to the worst possible height (h_w) that could be generated using all the polygon. This worst possible height can be found out once and very easily by stacking all the polygon's bounding box one over another and taking the total height (h_w). With y-ordinate set to h_w , the polygon is dropped with x-ordinate set to X-Position information stored in the gene. However, before dropping the polygon, the gene is checked if, with the given X-Position, the polygon bound stays within the strip. In case the polygon bound doesn't remain within the strip, the X-Position information in the gene is modified so as to bring the polygon bound within the strip. The process is illustrated in **Figure 4.10**.

As the polygon is dropped, collision detection tests are

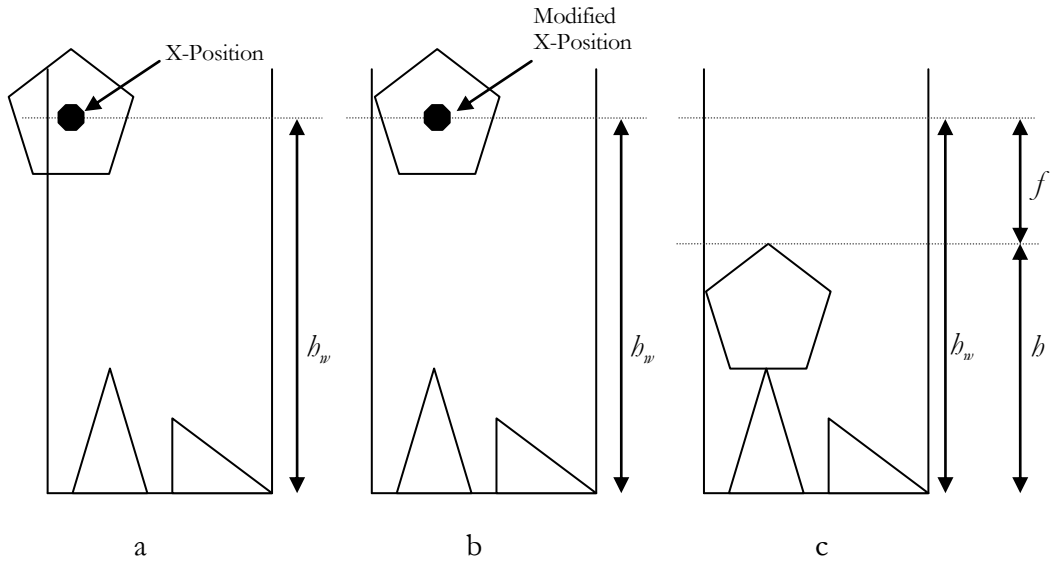


Figure 4.10: Demonstrating the fitness evaluation process

- a) The X-Position of the polygon is such that it made the polygon hang outside the strip bound.
- b) The X-Position of the polygon is modified to bring the polygon bound inside the strip bound..
- c) Finally the polygon is allowed to drop freely and collision detection tests are performed.

performed to find if the polygon in question collides with polygons that had already been dropped. If it collides, the collision points are calculated and the maximum distance the polygon can move downward is also calculated and the polygon is allowed to fall that much distance downward. This causes all the polygons to stack at the bottom of the strip according to the information stored in all the genes and hence the chromosome. The maximum height required (h) for all the polygons is noted and then the fitness value is calculated as follows

$$f = h_w - h \dots\dots\dots(4.1)$$

More the value of fitness f is, the lesser is the height (h) required to fit all the polygons and thus represents a better solution.

4.5.3 Mating

Once the fitness value of all the chromosomes are found out, the population is allowed to mate according to the standard GA algorithm, which was discussed earlier. However, instead of

replacing the current generation with the new generation, we added the new generation of chromosome to the old generation of chromosomes, thus increasing the population size. In the process, we “killed” chromosome which had fitness value under a certain threshold. This “killing” process kept the population size under some sort of check and allowed only the better chromosomes to live through generations.

After running the above process for a certain number of generations, we would stop the algorithm and output the best chromosome found so far.

4.6 Conclusion

Due to the inherent quality of GA to search for a solution in parallel fashion, combined with the ability to pop out of local minima/maxima makes it a very suitable tool to generate a near optimal solution. However, the biggest challenge of solving this particular problem with the discussed scheme, the collision detection routine becomes the biggest bottleneck as far run-time is concerned. Hence the collision detection routines need to be optimized.

Chapter 5 SIMULATION FRAMEWORK

5.1 Simulation Framework

Our simulation framework is basically a stand-alone software that was built with a GUI support. There are basically 3 modules, polygon input module, output module and GA-parameter input module.

5.1.1 *Our simulation framework consists of the following parameters*

5.1.1.1 *n number of arbitrary polygons.*

Polygons are stored in simple text files which are read in by the simulation program.

5.1.1.2 *Initial Population, k*

Initially k number of chromosomes/individuals are created randomly. These k chromosomes act as the first generation.

5.1.1.3 *Number of Generations*

This is basically the number of iterations or generations to be simulated for. Since the problem is a NP-Hard problem, there is no particular sentinel condition so we need to set this parameter manually.

5.1.1.4 *Mutation probability μ such that $0 \leq \mu \leq 1$*

This is the probability that determines if a new born chromosome is mutated in some gene location. If mutation has to be performed, a gene location is selected in random and then either of the “Sequence-Number” or the “X-Pos” would be mutated, i.e. changed randomly. Changing “X-Pos” might render the polygon invalid because some part of the polygon might hang outside the strip-bound. So after every mutation process, the chromosome needs to be validated. Usually μ is set to very low probability and in our simulation framework, we used a default value of 0.1.

5.1.1.5 *Cull-Threshold τ such that $0 \leq \tau \leq 1$*

This is the parameter that decides if a chromosome should be “killed” or kept alive through generations. This is a normalized parameter and for every chromosome the fitness value is also normalized between worst chromosome’s fitness value and the best chromosome’s fitness value. For every chromosome, the normalized fitness NF is calculated using the following formula:

$$NF = \frac{\text{Chromosome.fitness} - \text{WorstChromosome.fitness}}{\text{BestChromosome.fitness} - \text{WorstChromosome.fitness}}$$

if $NF < \tau$ then the chromosome is “killed.”

5.2 Simulation software

The simulation software provides the user to input and change all the parameters that were discussed in the previous section. The user can run the algorithm and watch how the average fitness value of the population changes as well the plot of the best chromosome found so far. The software also plots the population size. The user may also stop the simulation anytime he/she feels like and see the output of the best result found so far.

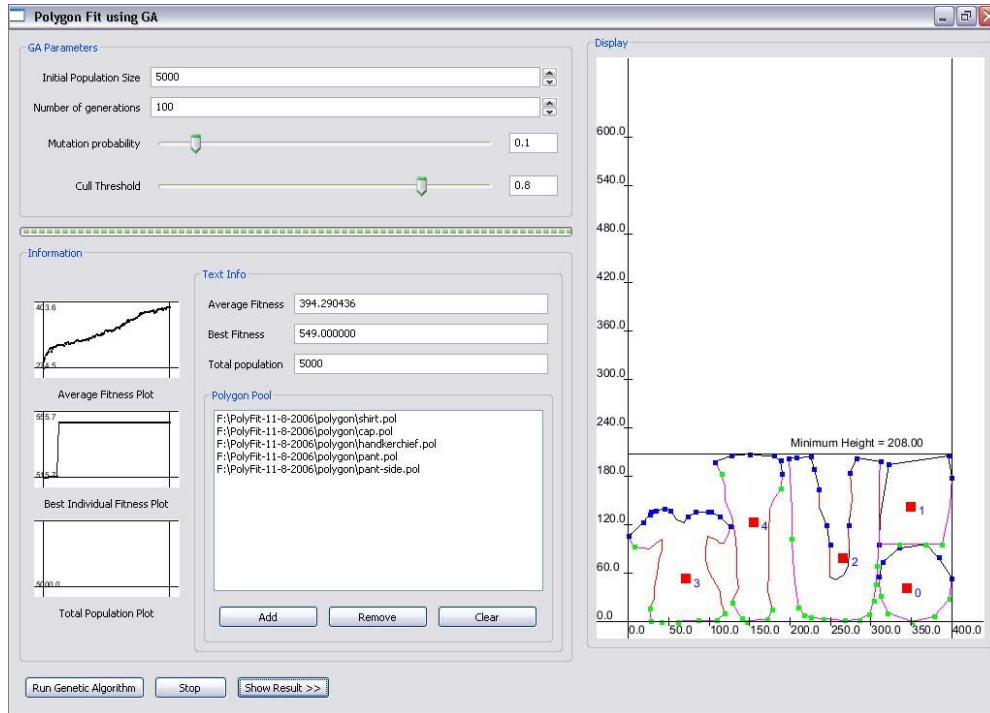


Figure 5.1: Screenshot of the simulation software

The software takes polygon data as input in form of files which contains polygon vertices information in textual format. It then provides the user to change several GA parameters like initial population, mutation probability, number of generations etc.

The algorithm is run in a different thread so that the user interface can be interacted with while the algorithm is running and user can cancel the operation at any time. The user can view the best result produced so far graphically.

Since the software demanded graphical representation of the final result as well as ability to graphically take input from user, a good GUI has been designed. For this GUI to be developed a well renowned cross-platform GUI SDK has been used called wxWidget[10] which has built in features for OpenGL.

The basic software operation can be summarized as follows.

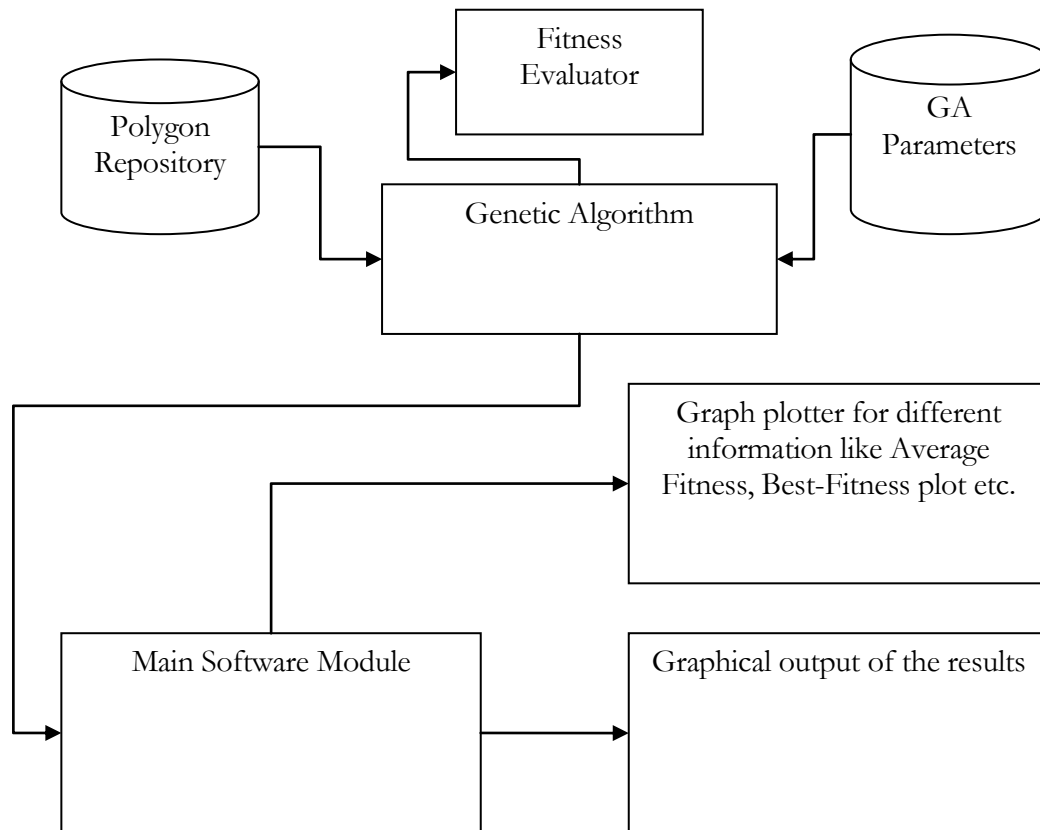


Figure 5.2: Software Data Flow

Chapter 6 OPTIMIZATION

6.1 Introduction

Since we relaxed ourselves from rotating the polygons, their orientation becomes static. As polygons would be dropped from the top of the strip with fixed/static orientation we can pre-calculate lots of collision data beforehand while loading the polygons.

6.2 Optimization

It can be noted that when a polygon is to be dropped from the top of the trip, only the points/vertices of the front-facing lines can collide with the back-facing lines of the polygons that had already been dropped. On the other hand, only the points/vertices of the back-facing lines of the polygon already dropped in the strip can collide with the front facing lines of the polygon to be dropped. This prunes out half of the vertices and lines to be tested for collision on average and reduces the collision test to $1/4$. The fact is demonstrated below.

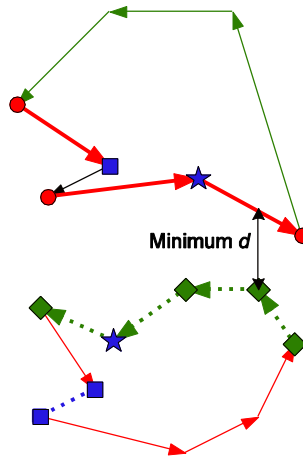


Figure 6.1: Polygon Hit

In the above Figure 6.1, the bold lines of the top polygon are the front facing lines. The stripped lines of the bottom polygon are the back-facing lines. All the points that belongs to the front-facing lines of the top polygon are “collidable” points with the back-facing lines of the bottom polygon. However, points marked with “stars” are crevice points with respect to the other polygon. Crevice points can never contribute to collision, hence they are pruned. Points marked with “box” are positioned in such way that they cannot contribute to any collision because the polygon it belongs to has at least one line that blocks the point from colliding. Hence, these points are also pruned. Lines that have both its point marked with “box” are pruned because such line cannot contribute to a collision.

All the points marked with “circles” are front-collidable points of the top polygon which are tested for collision with all the stripped lines (back-facing lines) of the bottom polygon. When collision test is performed, an imaginary line is produced from the point to the given line and tested if the following are true

- If the imaginary line intersects with the other line
- If the y-intercept of the intersection is lower or equal to the y-ordinate of the point.

If the point is found to collide with the line, the distance d between the point and the intersection point is calculated. The same procedure is carried for all the back-facing points of the bottom polygon with all the front-facing lines of the top. The minimum of all d is then used to translate the top polygon downward.

All the back-facing lines, front-facing lines, front-collidable-points, back-collidable-points are pre-calculated once the polygons are loaded and the results are simply used while finding the fitness during GA. This roughly reduces the collision detection calculation for each pair of polygon to almost $1/4$.

Two more optimization operations are also performed.

6.2.1 Potential Collidable Polygons

Before a polygon is dropped from the top, the lower end of the bounding box of the polygon is extended till the bottom of the containing strip and then the resultant bounding box is tested for overlap with all the bounding boxes of the polygons which had already been dropped. Only those polygons that overlap with the extended bounding box may collide with the polygon about to be dropped, and this set of polygons is termed as “Potential Collidable Polygons” (PCP). This allows many polygons not to be tested for collision at all thus increasing performance.

6.2.2 Height Pruning

Within the “PCP” if a collision is detected, and after translating the polygon, about to be dropped, its y-ordinate of the lower corner of the bounding box is saved. When another polygon of PCP has to be tested; if its y-ordinate of the top corner of the bounding box is less than the y-ordinate already saved then the polygon is not tested at all. This prunes away all the

polygons that are far below in the stack of dropped polygon, thus increasing performance even further.

6.3 Performance

Total number of collision test performed to run GA for a certain number of generations is taken as a performance metric. Collision detection routine is the heart of finding the fitness value of a given chromosome. Due the mathematical complexity of the collision detection routine the overall performance of the simulation depends largely on the performance of the collision detection routine. However, since the problem is a NP-Hard problem combined with the fact that GA is used it is not guaranteed that a “good” solution will be found within the given number of generations.

Generation	Mean Collision Test x 1000	Theoretical total collision test x 1000	Ratio (Theoretical Collision/Actual Collision)
20	9805.55	259160	26.42992999
30	14120.736	388740	27.5297265
40	18120.414	518320	28.60420297
50	22285.156	647900	29.07316422
60	25974.20667	777480	29.93277177
70	29731.31433	907060	30.50857388
80	32989.97533	1036640	31.42287891
90	36492.47967	1166220	31.95781735
100	37793.90467	1295800	34.28595197

Table 1: Performance Sheet

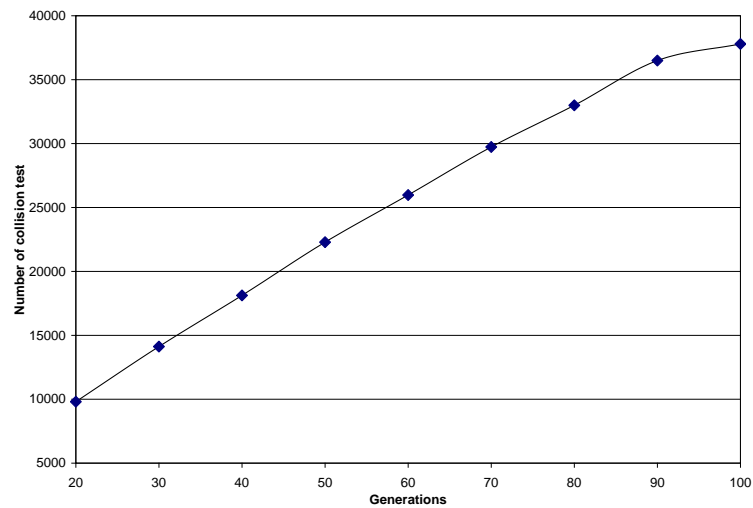


Figure 6.2: Performance Curve

The relationship between no. of generation and total number of collision test is fairly linear.

The “Theoretical” number of collision test is the number of collision test we would need to perform if there weren’t any optimization. Table 1 tells that the optimization that we applied to solve the problem reduced the execution time by almost 30 times. Moreover this improvement over “Theoretical” number seems to be getting better as the number of generation is increasing.

6.4 Conclusion

Optimization in the collision detection algorithm is very important as it happens to the major bottleneck of the whole system. Table 1 clearly shows the almost 30 times less operations are performed due the optimization performed.

Chapter 7 RESULTS

7.1 Introduction

The current system has several input parameters, they are as follows:

- Initial Population Size
- Number of Generations
- Mutation Probability
- Set of Polygons

In this section we will study the effect of various parameters on the output of the algorithm. While studying one parameter we will keep other parameters constant and observe the output. For all the experiment conducted below, 7 polygons were used with a total vertex count of 191.

Following are the polygons that were used in the experiment.

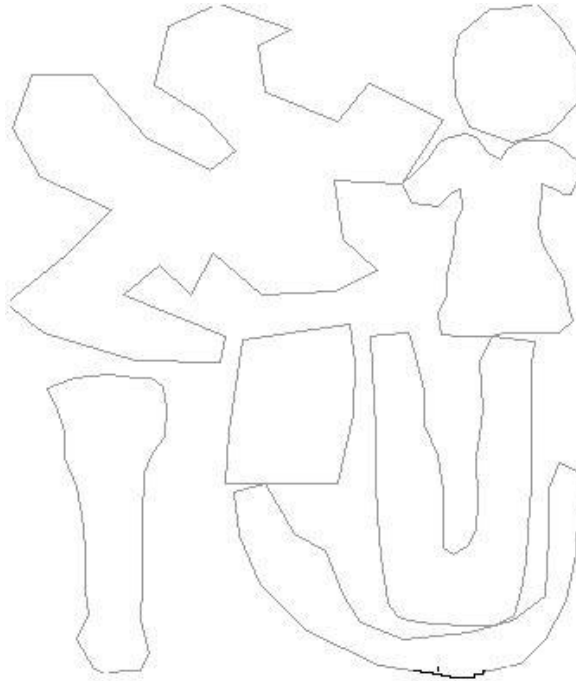


Figure 7.1: Polygons used in experiment

7.2 Effect of mutation-probability

This experiment was conducted to test the effect of mutation probability on the final output. Number of generations was set to 100, while initial population size was set to 1000 for this experiment.

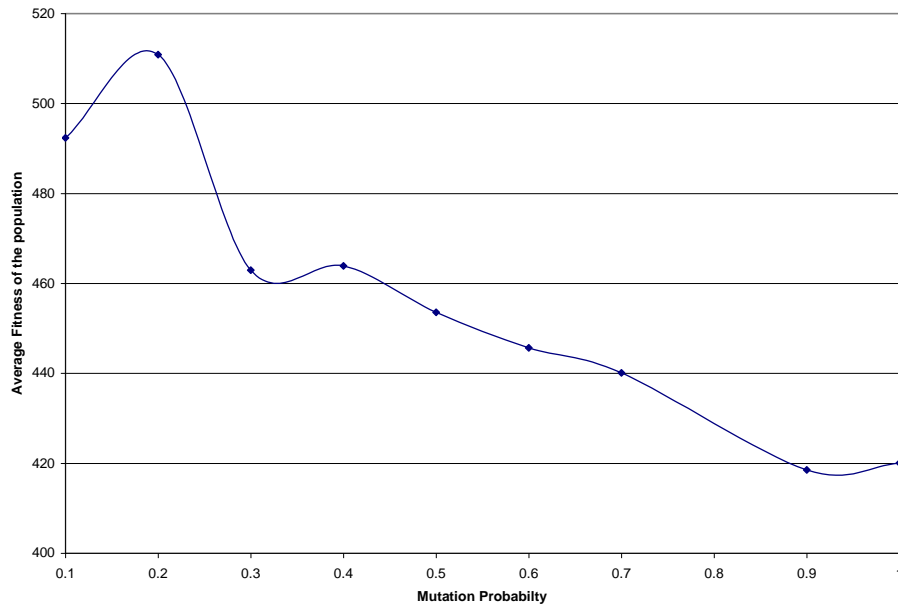


Figure 7.2: Mutation probability Vs Average fitness

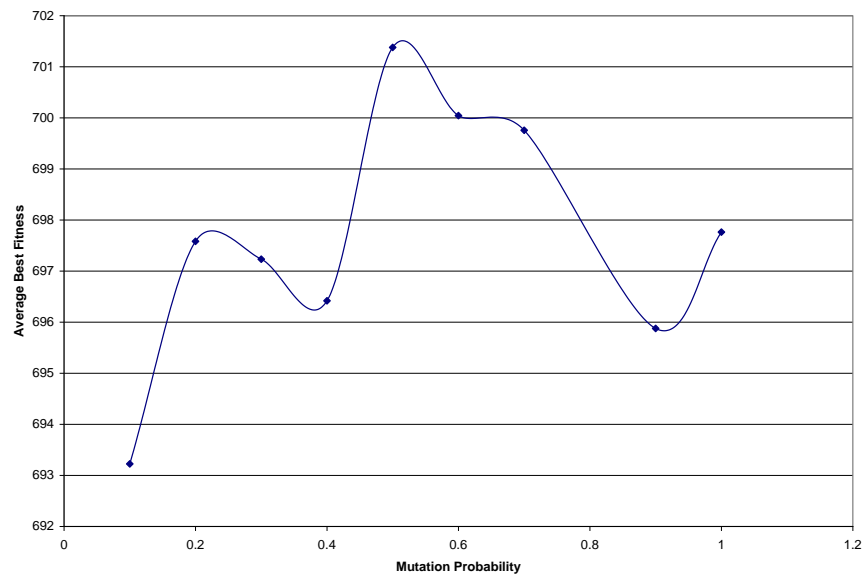


Figure 7.3: Mutation Probability Vs Average Best Fitness

The mutation probability was changed and the corresponding average fitness of the population was observed.

7.2.1 Interpretation

Mutation was introduced in Genetic Algorithm to let GA pop out of local minima and maxima. However, this mutation probability needs to be set to very small value. As mutation probability increases, more individual get mutated and the algorithm converges to “blind” random search. As the algorithm becomes more “blindly” random, the average fitness value decreases. However, setting the mutation probability to too low will make the algorithm unable to pop out of local minima or maxima. This also makes the average fitness of the population go low. In the experiment it can be seen that mutation probability of around ~ 0.2 produces the best result. Although **Figure 7.3** shows that mutation probability of around ~ 0.5 gives the best result but this might have happened due to shortage of data in our test cases. Usually the better picture is grasped in the average fitness curve.

7.3 Effect of Number of Generation

This experiment was conducted with the mutation probability set to 0.2 and the initial population set to 1000. The number of generations was increased and each time the average fitness of the population as well as the best fitness was observed.

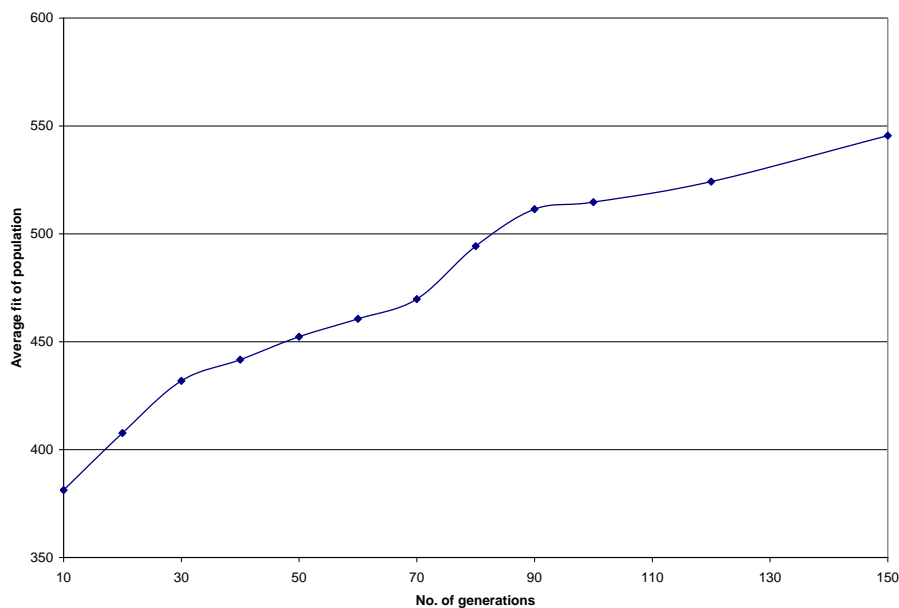


Figure 7.4: No. of Generations Vs Average fit of population

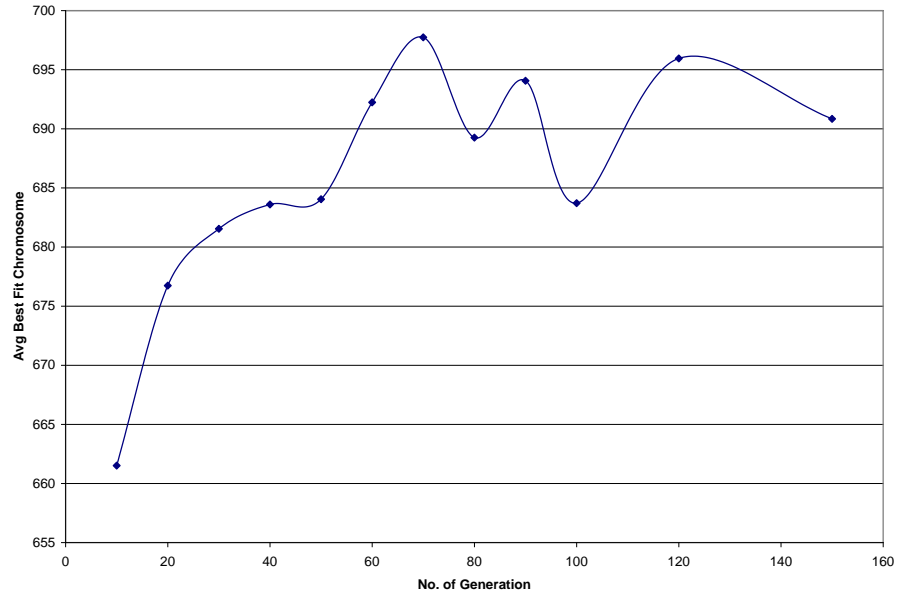


Figure 7.5: No. of generation Vs Average Best Fit

7.3.1 Interpretation

It can be noted that as the number of generation is increased the average fitness of the population increases. This is explained by the fact that mutation probability is set to 0.2 (low) and since good individual has the greater probability to mate, the average fitness of the population approaches the best fitness.

However, increasing the number of generations doesn't monotonically increase the fitness of the best individual found so far. This can be explained by the fact that once a good individual is found, it becomes extremely hard to beat that individual any by the grace of GA we happened to find the good solutions by 100 generations.

7.4 Effect of Initial Population Size

This experiment was conducted to test the effect of initial population size on the final result. For this experiment, the mutation probability was set to 0.2, and number of generation was set to 100.

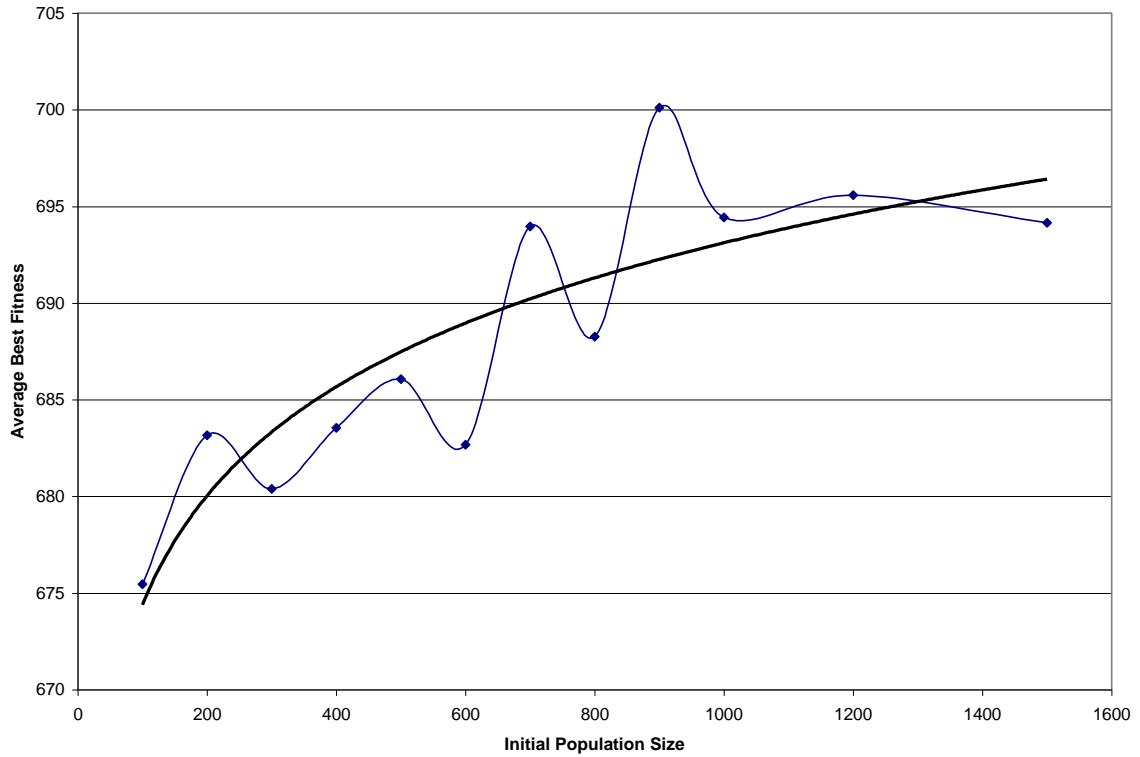


Figure 7.6: Initial population size Vs Average Best Fitness

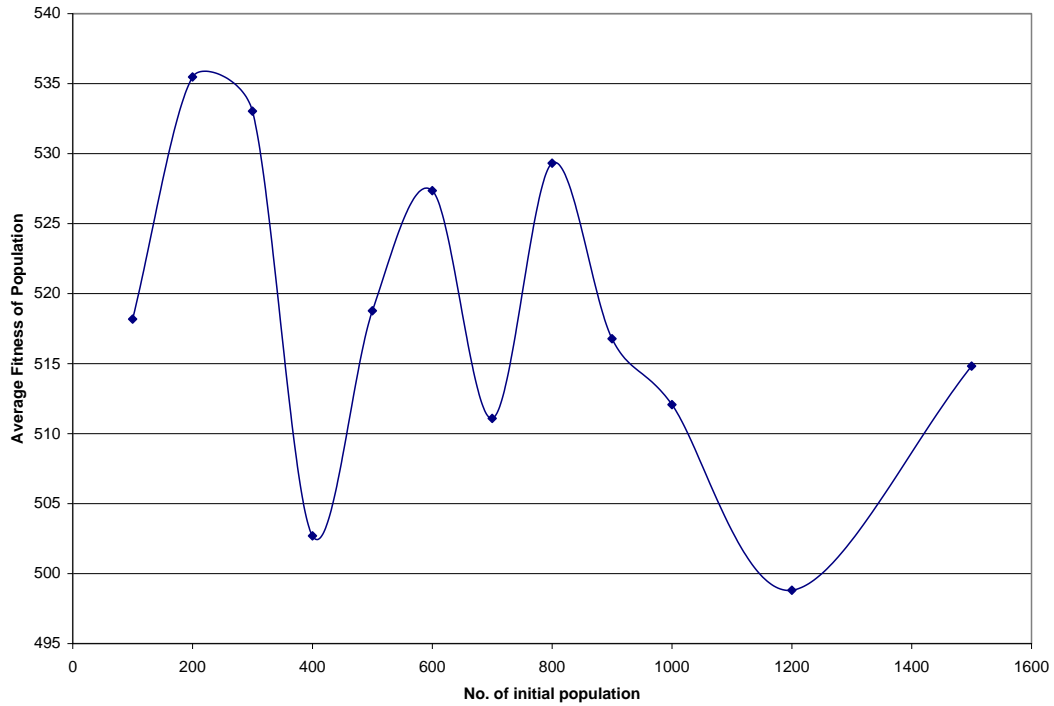


Figure 7.7: No. of initial population size Vs Average fitness of the population

7.4.1 Interpretation

The role of initial population size is very mysterious. The **Figure 7.7: No. of initial population size Vs Average fitness of the population** shows that the final average fitness value behaves erratically as the initial population size increases. However **Figure 7.6: Initial population size Vs Average Best Fitness** curve tells us that as the initial population size increases the final best chromosome also gets better however too much initial population size does not help much.

Still it is recommendable that the initial population size is taken big enough so as to increase the probability of having many good chromosomes.

7.5 Conclusion

The experiments gave us some light on how to adjust parameters while running the GA algorithm. It has been shown that too big mutation probability may make the algorithm converge to random search and thus reduce the performance. The number of initial population size and number of generation is related to the number of polygons fed into the system. The more polygon is fed it is recommendable to increase both these parameters to allow the GA to try out more combinations of polygon placements.

Chapter 8 CONCLUSION

8.1 Conclusion

This thesis proposed a very simple algorithm to solve the specific problem of garments industry. In the garments industry clothes shapes are needed to be cut out of long running strip of cloth but the orientation of the shapes need not to be changed. This is because every cloth has a particular “run” and when cloth shapes are cut its orientation has to conform to that run.

There are many algorithms which solves the problem of packing arbitrary shapes. However, the orientation posed a big problem and introduced both run-time and computational complexity which we could easily avoid in our thesis.

We first surveyed all the available related algorithms; there are only a few of them. Then we first defined and formulated the problem at hand. The nature of the problem made us chose Genetic Algorithm as the major tool to solve the problem. We presented our new approach with detailed description of Genetic Algorithms. We then presented several result outputs and interpretation of each output generated. While interpreting we tried to show how the results are dependant on each of the input parameters of problem. We also showed all the possible areas where we optimized the algorithm.

We hope we have been able to propose a new and good approach, based wholly on Genetic Algorithm, to find out a near-optimal solution for packing a set of arbitrary polygon with fixed orientation in a strip with an aim to minimize the total height required.

We also showed how various GA parameters and other parameters can be find tuned to generate much better results.

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