MODELING AND OPTIMIZATION OF END MILLING MACHINING PROCESS

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Abstract

*Generally in any manufacturing industry, a human process planner selects the machining parameters based on his expertise or from data handbooks; they do not represent the optimal values. The optimization process involves the optimal selection of machining parameters such as cutting speed, feed and depth of cut, subjected to practical constraints of surface finish, tool wear, dimensional accuracy and machine tool capabilities. Several researches have used different techniques in literature to optimize machining process by considering a machining problem as single objective optimization problem. However a machining problem should be treated as a multi objective problem as it involves two conflicting objectives: machining time and production cost. In such problems there cannot be single optimal solution. To get all optimal solutions, a multi objective optimization method called Non-dominated Sorting Genetic Algorithm (NSGA) is proposed in the project work. In the first part of the present work, mathematical relationships between input and output parameters have been developed by Response Surface Methodology (RSM). Consequently there have been solved to get the optimal values. The general second order composite rotatable design is used in planning and modeling the experiments. The experiments were conducted on the general purpose milling machine using a 60mm*60mm*40mm block (AISI 1040steel).In the second part a multi optimization algorithm called non dominated sorting genetic algorithm was used to retrieve all set of optimum values. In NASA, the non-dominated sorting procedure is used to bring forth the good points of correct population and stable subpopulations of good points are maintained by Niche method. The present work enables the industries to have the optimum values of the milling process variables and conducting the process can be automated based on optimal values.*

Index Terms: *AISI 1040steel, Non-dominated Sorting Genetic Algorithm (NSGA), Optimization, Response Surface Methodology (RSM), and Multi Optimization Algorithm etc…*

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1. INTRODUCTION

Milling is the process of cutting away material by feeding a work piece past a rotating multiple tooth cutter. The cutting action of the many teeth around the milling cutter provides a fast method of machining. The machined surface may be flat, angular, or curved. The surface may also be milled to any combination of shapes. The machine for holding the work piece, rotating the cutter, and feeding it is known as the milling machine.

1.1 Methods Of Milling

1.1.1. Up Milling

Up milling is also referred to as conventional milling. The direction of the cutter rotation opposes the feed motion. For example, if the cutter rotates clockwise , the workpiece is fed to the right in up milling.

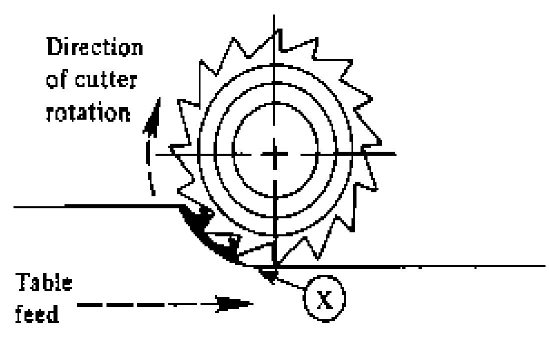


Fig.1.2. Up Milling machining process

1.1.2. Down Milling

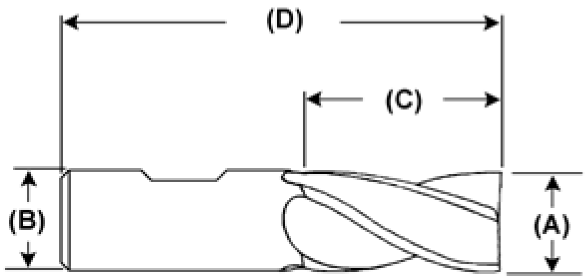
Down milling is also referred to as climb milling. The direction of cutter rotation is same as the feed motion. For example, if the cutter rotates counterclockwise , the workpiece is fed to the right in down milling.

1.1.3. End milling

An end mill is one of the indispensable tools in the milling processing. The end mill has edges in the side surface and the bottom surface. The fundamental usage is that the end mill is rotated, and makes a plane of a material in the right-and-left direction or a plane of a bottom side of the end mill. We can make various shapes of mechanical parts with the end mill.

An endmill is a type of milling cutter a cutting tool used in industrial milling applications. It is distinguished from the drill bit in its application, geometry, and manufacture. While a drill bit can only cut in the axial direction, a milling bit can generally cut in all directions, though some cannot cut axially.Endmills are used in milling applications such as profile milling, tracer milling, face milling, and plunging.

Design criteria



A-millsize or cutting diameter
B - shank diameter
C - length of cut or flute length
D - overall length

2. DESCRIPTION OF PRESENT PROBLEM

End milling hardened steel is an economical method to generate a high quality machined surface. Being a complex process, it is very difficult to determine the optimal parameters for improving cutting performance. A vast array of research is carried out to study the influence of the various factors effecting the machining performance and productivity. Surface finish and MT is the most important out put parameters in any machining process. These out put parameters are influenced numerous process parameters in endmilling . Form the literature survey it is found that the parameters such as depth of cut , feed rate , cutting speed and step over has considerable influence on surface roughness and machining time . To study the influence of these process parameters, an experiment is conducted using Response surface method (RSM). RSM comprises a group of statistical techniques for empirical model building and model exploration. The response surface methodology is practical, economical and relatively easy for use. The experimental data were utilized to build mathematical model for first and second order model, by regression method. A response or output function is related to a number of input variables that affect it. The variables studied will depend on the specific field of application. The response surface method can substantially reduce the total number of experiments often carried out randomly and it is an adequate and reliable method to measure the true mean response of interest.

The experimental study was carried out in wet cutting conditions on a DECKEL MAHO DMU 60 P five-axis,high-speed CNC milling machine equipped with a maximum spindle speed of 12,000 rpm, feed rate of 10 m/min and a 15-kW drive motor. CNC part programs for tool paths were created. The workpiece material used was AISI 1040 steel in the form of a 60mmX60mmX40mm block. A total of 30 experiments were conducted according to the central composite design developed by RSM. The corresponding surface roughness and machining time for each experiment is calculated and recorded.

The present optimization problem involves in two major objective functions. The first objective is to minimize Surface roughness (Ra) and the second objective is to minimize (MT). When the optimization problem involves in more than one objective function, the task of finding one or more optimum solutions is known as Multi-objective optimization.

The present problem involves in two major objectives. Optimization can not be done to only one objective, when another objective is also important. Different solutions may produce conflicting scenarios between the two objectives. A solution, which is excellent with respect to one objective, requires a compromise in the other objective. This prohibits one to choose a solution, which is optimal with respect to only one objective, which makes the two objectives conflicting. The surface roughness and machining time are proportional to each other. If surface roughness increases then machining time also increase and vice versa. Conventional optimization problem transforms a multi objective optimization problem into single objective optimization problem. A simple method of converting this multi-objective is to form a composite objective function as a weighted sum of the objectives, where a weight for an objective is assigned, which is proportional to the performance factor of that particular objective. When a composite function is optimized, in most cases it is possible to obtain only one optimal solution in a single simulation. Evolutionary algorithms (EA) are non-classical optimization methods, which mimic nature’s evolutionary principles to drive its search towards an optimal solution. One of the most striking differences to classical search and optimization algorithms is that EAs use population solutions in each in iteration, instead of single solution. Since population of solution is proposed in each iteration, the out come of EA is also a population of solutions. The ability of an EA to find multiple optimal solutions in one simulation run makes EAs unique in solving multi-objective optimization problems.

3. RESPONSE SURFACE METHODOLOGY

Response surface methodology or RSM is a collection of mathematical and statistical techniques that are useful for the modeling and analysis of problems in which response of interest is influenced by several variables and the objective is to optimize this response. For example, suppose that a chemical engineer wishes to find the levels of temperature (x1) and pressure (x2) that maximizes the yield (y) of a process. The process yield is a function of the levels of temperature and pressure, say

$$Y = f(x1, x2) + \varepsilon$$

Where ε represents the noise or error observed in the process y. if we denote the expected response by

$$E(y) = f\, f(x1, x2) = \eta,$$

then the surface is represented by

$$\eta = f(x1, x2)$$

is called response surface.We usually represent the response surface graphically, such as in fig 4.1, where η is plotted versus the levels of x1, x2. To help visualize the shape of a response surface, we often plot the contours of the response surface as shown in fig 4.2. in the contour plot, lines of constant response are drawn in the x1, x2 plane. Each contour corresponds to a particular height of the response surface.

In most RSM problems, the form of the relationship between the response and the independent variables is unknown. Thus, the first step in RSM is to find a suitable approximation for the true functional relationship between y and the set of independent variables is employed. If the response is well modeled by a linear function of the independent variables, then the approximating function is the first order model.

$$Y = \beta 0 + \beta 1x1 + \beta 2x2 + \text{----------------} + \beta kxk + \varepsilon$$

If there is curvature in the system, then a polynomial of higher degree must be used, such as the second order model.

$$Y = \beta_0 + \sum_{j=1}^{k} \beta_j x_j + \sum_{i<j} \sum \beta_{ij} x_i x_j + \sum_{j=1}^{k} \beta_{jj} x_j^2 + \varepsilon$$

Almost all RSM problems use one or both of these models. Of course it is unlikely that a polynomial model will be a reasonable approximation of the true function relationship over the entire space of the independent variables, but for a relatively small reason, they usually work quite well.The method of least squares is used to estimate the parameters in the approximating polynomials. The RSM is then performed using the fitted surface. If the fitted surface is the adequate approximation, of the true response function, then analysis of the fitted surface will be approximately equal to analysis of the actual system. The model parameters can be estimated most effectively if proper experimental design is used to collect the data. Designs for fitting response surfaces are called response surface results. RSM is a sequential procedure. Often, when we are at a point on the response surface that is remote from the optimum, such as the current operating condition in the fig 4.2, there is little curvature in the system and the first order model will be appropriate. Our objective here is to leave the experimenter rapidly and efficiently along the path of improvement towards the general vicinity of the optimum. Once the reason of the optimum has been found, a more elaborate model, such as second order model, may be employed, and an analysis will be performed to locate optimum. From the fig 4.3 we see that the analysis of response surface can be thought of as ‘climbing a hill’, where the top of the hill represents the point of maximum response. If the true optimum is a point of minimum response, then we think of ‘descending into a valley’.The eventual objective of RSM is to determine the optimum operating conditions for the system or to determine a region of the factor space in which operating requirements are satisfied.

3.1 Designs For Fitting First Order Model

Suppose we wish to fit the first order model in k variables

$$Y = \beta_0 + \sum_{i=1}^{k} \beta_i x_i + \varepsilon$$

There is a unique class of designs that minimize the variance of the regression coefficients (βi). These are the orthogonal first-order designs. A first- order design is orthogonal if the off-diagonal elements of the (X1X) matrix are all zero. This implies that the cross products of the columns of the X matrix sum to zero. The class of orthogonal first-order designs includes the 2k factorial and fractions of the 2k series in which main effects are not aliased with each other. In using these designs, we assume that the low and high levels of the k factors are coded to usual ±1 levels. The 2k designs do not afford an estimate of the experimental error unless some runs are replicated. A common method of including replication in the 2k designs is to augment the design with several observations at the center (the point xi=0, i=1, 2, 3, -----, k). The addition of center points to the designs does not influence the (βi) for i≥1, but the estimate of β0 becomes the grand average of all observations. Furthermore, the addition of center points does not alter the orthogonally property of the design.

3.2 Designs For Fitting Second Order Model

Central composite design is the most popular class of designs just for fitting second order models. Generally the CCD consists of a 2k factorial (or fractional factorial of resolution V) with nf runs, 2k axial or star runs and nc center runs. Figure 4.4 shows the CCD for k=2 and k=3 factors. The practical deployment of a CCD often arises through sequential experimentation. That is the 2k has been used to fit a first model, this model has exhibited lack of fit and the axial runs are then added to allow the quadratic terms to be incorporated in to the model. The CCD is a very efficient design for fitting the second order model. There are two parameters in the design that must be specified, the distance α of the axial runs from the design center and the number of center points nc. We now discuss the choice of these two parameters.

4. NONDOMINATED SORTING GENETIC ALGORITHEM

Many real-world design or decision making problems involve simultaneous optimization of multiple objectives. In principle, multi objective optimization is very different than the single objective optimization. In single objective optimization, one attempts to obtain the best design or decision, which is usually the global minimum or the global maximum depending on the optimization problem is that of minimization or maximization. In the case of multiple objectives, there may not exist one solution which is best (global minimum or maximum) with respect to all objectives. In a typical multi objective optimization problem, there exists a set of solutions which are superior to the rest of solutions in the search space when all objectives are considered but are inferior to other solutions in the space in one or more objectives. These solutions are known as Pareto-optimal solutions or non dominated solutions (ChankongandHaimes1983;Hans1988). The rest of the solutions are known as dominated solutions. Since none of the solutions in the non dominated set is absolutely better than any other, any one of them is an acceptable solution. The choice of one solution over the other requires problem knowledge and a number of problem related factors. Thus, one solution chosen by a designer may not be acceptable to another designer or in a changed environment. Therefore, in multi objective optimization problems, it may be useful to have a knowledge about alternative Pareto-optimal solutions.

One way to solve multi objective problems is to scalarize the vector of objectives into one objective by averaging the objectives with a weight vector. This process allows a simpler optimization algorithm to be used, but the obtained solution largely depends on the weight vector used in the scalarization process. Moreover, if available, a decision maker may be interested in knowing alternate solutions. Since genetic algorithms (GAs) work with a population of points, a number of Pareto-optimal solutions may be captured using GAs. A nearly GA application on multi objective optimization by Schaffer (1984) opened a new avenue of research in this field. Though his algorithm, VEGA, gave encouraging results, it suffered from biasness towards some Pareto- optimal solutions. A new algorithm, Non dominated Sorting Genetic Algorithm (NSGA), is presented in this paper based on Goldberg's suggestion (Goldberg1989). This algorithm eliminates the bias in VEGA and there by distributes the population over the entire Pareto- optimal regions. Although there exist two other implementations (Fonesca and Fleming 1993; Horn, Nafpliotis, and Goldberg 1994) based on this idea, NSGA is different from their working principles, as explained below.

In the remainder of the paper, we briefly describe difficulties of using three common classical methods to solve multi objective optimization problems. A brief introduction to Schaffer's VEGA and its problems are outlined. Thereafter, the non dominated sorting GA is described and applied to three two-objective test problems. Simulation results show that NSGA performs better than VEGA on these problems. A number of extensions to this work is also suggested.

4.1 Multi Objective Optimization Problem

A general multi objective optimization problem consists of a number of objectives and is associated With a number of in-equality and equality constraints. Mathematically, the problem can be written as follows (Rao1991):

Minimize / Maximize $f_i(x)$ $i= 1,2,\ldots\ldots N$

Subject to

$$g_j(x) <= 0 \quad j=1,2,\ldots J$$
$$h_k(x) = 0 \quad k=1,2,\ldots..K$$

4.2 GA Implementation

As early as in 1967, Rosenberg suggested, but did not simulate, a genetic search to the simulation of the genetics and the chemistry of a population of single- celled organisms with multiple properties or objectives (Rosenberg1967). The first practical algorithm, called Vector Evaluated Genetic Algorithm (VEGA), was developed by Schaffer in 1984 (Schaffer 1984). One of the problems with VEGA, as realized by Schaffer himself, is its bias towards some Pareto-optimal solutions.

Later, Goldberg suggested another non dominated sorting procedure to overcome this weakness of VEGA (Goldberg 1989). Our algorithm, Non dominated Sorting Genetic Algorithm (NSGA), is developed based on this idea. There exists atleast two other studies, different from our algorithm, based on Goldberg's idea. In the rest of this section, we discuss the merits and demerits of VEGA and NSGA, and the differences between NSGA and the two other recent implementations.

4.2.1. Schaffer's VEGA

Schaffer modified the simple tripartite genetic algorithm by performing independent selection cycles according to each objective. He modified Grefenstette's GENESIS program (Schaffer 1984) by creating a loop around the traditional selection procedure so that the selection method is repeated for each individual objective to fill up a portion of the mating pool. Then the entire population is thoroughly shuffled to apply cross over and mutation operators. This is performed to achieve the mating of individuals of different sub population groups. The algorithm worked efficiently for some generations but in some cases suffered from its bias towards some individuals or regions. The independent selection of specialists resulted in speciation in the population. The out come of this effect is the convergence of the entire population towards the individual optimum regions after a large number of generations. Being a decision maker, we may not like to have any bias towards such middling individuals, rather we may want to find as many non dominated points as possible.

Schaffer tried to minimize this speciation by developing two heuristics |the non dominated selection heuristic (a wealth re-distribution scheme), and the mate selection heuristic (across breeding scheme) (Schaffer 1984). In the non dominated selection heuristic, dominated individuals are penalized by subtracting a small fixed penalty from their expected number of copies during selection. Then the total penalty for dominated individuals was divided among the non dominated individuals and was added to their expected number of copies during selection. But this algorithm failed when the population has very few non dominated individuals, resulting in a large fitness value for those few non dominated points, eventually leading to a high selection pressure. The mate selection heuristic was intended to promote the cross breeding of specialists from different sub groups. This was implemented by selecting an individual, as a mate to a randomly selected individual, which has the maximum Euclidean distance in the performance space from its mate. But it failed too to prevent the participation of poorer individuals in the mate selection. This is because of random selection of the rest mate and the possibility of a large Euclidean distance between a champion and a mediocre. Schaffer concluded that the random mate selection is far superior than this heuristic.

One method to minimize speciation is through a nondominated sorting procedure in conjunction with a sharing technique, as suggested by Goldberg (1989). Recently Fonesca and Fleming (1993) and Horn, Nafpliotis, and Goldberg (1994) implemented that suggestion, and successfully applied to some problems. These methods are briefly discussed later. But before that, we discuss our algorithm NSGA which is also developed based on Goldberg's suggestions.

4.3. Non-Dominating set

If S is the non dominating set then following two condition must hold

• Any two solutions of S must be non dominated with respect to each other.

• Any solution not belonging to S is dominated by at least one member of S.

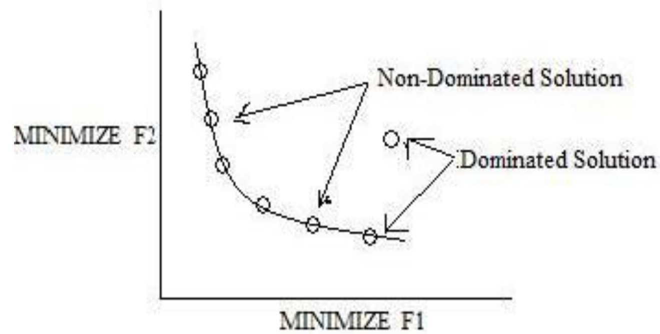


Figure 4.1.Concept of Dominance

4.4 Identifying Non Dominating set

There are several approaches proposed in the literature[?]like Naive and Slow approach,Continuously update,Kung et al.s Efficient Method etc.We use continuously update approach to compute non-dominating set of solution.

Identifying Non Dominating set

Step1: Initialize P^{I}= {1}.Set solution counter i = 2.

Step2: Set j = 1.

Step3: Compare solution i with j from P0 for domination.

Step4: If i dominates j ,delete the j^{th} member from P^{I} or update P^{I} = P^{I} \{ $P^{I\ (j)}$}.If j < | P^{I} |, increment j by one and then go to step3.Otherwise go to step5.Alternatively ,if the j^{th} member if P0 dominates i,increment i by one and then go to step2.

Step5: Insert i in P^{I} or Update P^{I} = P^{I} [{i}.If i < N, increment i by one and go to step2.Otherwise ,Stop and declare P^{I} as the non dominated set.

4.5 Non-Dominated sorting

In MOO there are sets of optimal solutions which are Non-Dominated with respected to each other. Such solutions are arranged in the ascending level of non domination. Procedure to find various level of domination is as follows:

Non-Dominated Sorting Algorithm
Step1: Set all non dominated sets P_j ,(j = 1, 2..J) as empty sets. Set non
domination level counter j = 1.
Step2: Use any approach to find the non-dominated set P0 of population
P.
Step3: Update P_j = P0 and P = P\P0.
Step4: If P $\neq$ Φ ;,increment j by one and go to step2.Otherwise,stop and
declare all non-dominated sets P_i ,for i = 1, 2..j.

5.6 Pareto Optimality

All non dominated solutions are important in the context of Multi Objective Optimization. All these solution are called pareto optimal solution and curve joining such points is called pareto optimal front.

5.7 Non-Dominated Sorting Genetic Algorithm

The multi-objective genetic algorithm used in our work is a hybrid genetic algorithm, where the initial population is formed as a combination of first fit (80% of initial population size) and random (20% of initial population size) instead of entirely random manner. We shall try to find a set of solution as close as possible to the pareto optimal front and as diverse as possible. We have implemented multi-objective genetic algorithm for traffic grooming problem using Non-dominating Sorting Genetic Algorithm (NSGA). The first step of an NSGA is to sort the population P according to non domination. This classifies the population into a number of mutually exclusive equivalent classes (or non dominated sets) Pj , i.e.,

$$P = \bigcup_{j=1}^{\rho} P_j$$

Where ρ is the number of non-domination levels.

The fitness assignment procedure begins from the first non-dominated set and successively proceeds to dominated sets. Any solution i of the first (or best) non-dominated set is assigned a fitness equal to Fi = |P| (population size). This specific value of |P| is used for a particular purpose. Since all solutions in the first non-dominated set are equally important in terms of their closeness to the pareto optimal front relative to the current population, we assign the same fitness to all of them. Assigning more fitness to a solution belonging to a better non-dominated set ensures a selection pressure toward the pareto optimal front. However, in order to achieve the second goal, diversity among the solutions in a front must also be maintained.The sharing function method is used front-wise. That is, for each solution i in the front F, the normalized euclidian distance dij from another solution j in the same front is calculated as follows:

$$d_{ij} = \sqrt{\sum_{k=1}^{\eta} \left(\frac{x_k^{\{i\}} - x_k^{\{j\}}}{x_k^{max} - x_k^{min}} \right)^2}$$

where η is the number of objectives

$$Sh(d) = \begin{cases} 1 - \left(\frac{d}{\sigma_{share}} \right)^{\alpha}, & \text{if } d \leq \sigma_{share}; \\ 0 & otherwise \end{cases}$$

The above function takes value between [0,1],depending on the values of d(euclidean distance) and σshare.If d is zero(means two solutions are identical or their distance is zero),

Sh(d) = 1.On the other hand, if d $\geq \sigma$share (meaning that two solutions are at least a distance of σshare away from each other),Sh(d) = 0.This means that two solutions which are a distance of

σshare away from each other do not have any sharing effect on each other.Any other distance will have partial effect on each.Hence,we compute niche count (assuming _ = 2) as:

$$nc_i = \sum_{j=1}^{|P|} Sh(d_{ij})$$

Niche count of i(nci) is an estimate measure of crowding around a solution i.

The steps of NSGA as given in is as follows
NSGA Fitness Assignment
Step1: Choose the sharing parameter σshare and a small positive number ϵ
and initialize $F_{min} = |P| + \epsilon$. Set front counter j = 1.
Step2: Classify population P according to non-domination:
$\{P_1, P_2, P\rho\} = Sort(P, \preceq)$
Step3: For each $q \in P_j$
Step3.1: Assign Fitness $F_j^{(q)} = Fmin - \epsilon$.
Step3.2: Calculate niche count nc_q using the above equation among solutions of P_j only.
Step3.3: Calculate shared fitness $F_j^{/(q)}=F_j^{(q)}/ncq$
Step4: $F_{min} = \min(F_j^{/(q)} : q \in P_j)$ and set j = j + 1.
Step5: If $j \leq \rho$, to go Step3. Otherwise, the process is complete

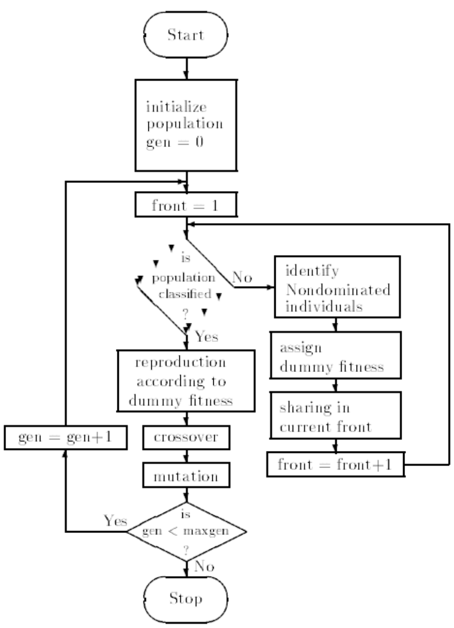


Fig.4.2. NSGA Flow chart

5. IMPLEMENTATION OF PROPOSED METHODOLOGY

5.1. EXPERIMENTAL DETAILS

5.1.1. Work piece material, cutting tools and equipment

The experimental study was carried out in wet cutting conditions on a DECKEL MAHO DMU 60 P five-axis,high-speed CNC milling machine equipped with a maximum spindle speed of 12,000 rpm, feed rate of 10 m/min and a 15-kW drive motor. CNC part programs for tool paths were created. The workpiece material used was AISI 1040 steel in the form of a 60mmX60mmX40mm block. Tables 1 and 2 provide detailed information on chemical composition and mechanical properties of this AISI 1040 steel. A flat end mill (10mm diameter, 451 helix angle, TiAlN coated solid carbide, 4-flutes) produced by Sandvik(R216.34-10045-AC22N 1620) was used in the tests. The up milling cutting method and compressed cooling oil as the cutting environment were used. The same tool was used until maximum flank wear reached VBmax _0.1 mm.The setup of the workpiece and flat end mill is shown in Fig. 6.1.

5.1.2. Surface roughness measurement

Surface roughness Ra was measured using a portable Mitutoyo Surf Test 301. A minimum of 10 measurement in the traverse direction were taken, the highest and lowest values were discarded and the average value was recorded. In this study, Ra values were measured between 0.55 and 2.74 mm. The repeatability of the measurements was found to be in the range of 2–5%, which was considered satisfactory for generating empirical models.

5.1.3. Experimental design

In this study, the experimental plan has four controllable variables namely, spindle speed, feed rate, depth of cut and step over. Thus, a minimum of 16 runs is required to develop a full second-order model. Meanwhile, plans with some highly desirable properties such as rotatability, orthogonal or uniform precision require more runs. Among various designs, the rotatable central composite design has the most popular promising outstanding benefits. In this study, a rotatable central composite (uniform precision) design with six central replicates was selected, with five different levels for each variable, as shown in Table 3. Variable ranges were determined on the basis of a cutting tool catalog. As presented in Table 4, the experimental plan was composed of a full 24 factorial with four central replicates (runs 1–20), augmented by eight axial runs with two central replicates (runs 21–30) to estimate second-order effects.

For the selection of the best model, the adjusted coefficient of multiple correlations.

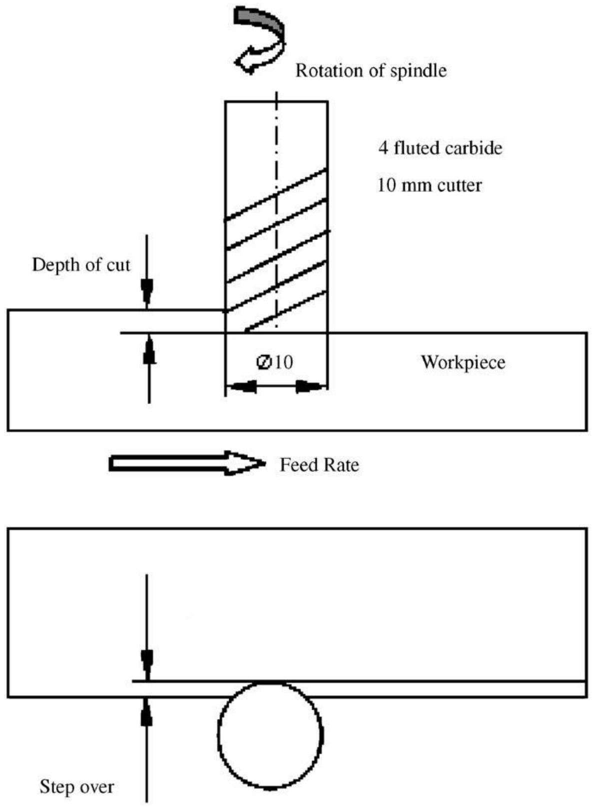


Fig.5.1. Schematic representation of workpiece and flat end mill

The machining conditions at which the experiments were conducted are listed in Table 5.1.

Table 5.1 Machining conditions

1	Work piece	En-24 (SAE 4340)
2	Chemical	C-0.39%, Si-0.24%, Mn-0.71%,P-
3	Work piece size	60mmX60mmX40mm
4	Surface	Portable Mitutoyo Surf Test 301

5.2. IDENTIFYING PROCESS PARAMETERS

Optimal performance of any machining process is based on choosing the right combination of input parameters. End milling process is so stochastic in nature that the selection of optimal parameters is not possible by trial and error method. Research has been carried out to study the effect of several process parameters on Ra and . Based on some literature survey and preliminary investigations, the following four parameters are chosen as input parameters.

1. Spindle speed (rpm)
2. Feed Rate (mm/min)
3. Depth of cut (mm)
4. Step over(mm)

5.3. FINDING THE UPPER AND LOWER LIMITS OF THE CONTROL VARIABLES

The upper and lower limits of the process variables are identified. The upper limit of a factor was coded +2 and lower limit as -2. The selected process parameters with their limit values are given in the Table 5.2

Table 5.2 Control factors and their levels

S.no	parameter	Notation	-2	-1	0	1	2
1	Spindle speed	X1	4000	5500	7000	8500	10000
2	Feed Rate	X2	640	1320	2240	3400	4800
3	Depth of cut	X3	0.1	0.3	0.5	0.7	0.9
4	Step over	X4	1	2	3	4	5

5.4 DEVELOPING THE DESIGN MATRIX

In this work Design Expert 7.1.4 was used to obtain the central composite second order rotatable design. The selected design matrix, is a three-level, four factor central composite rotatable factorial design (CCD) consisting of 30 sets of coded conditions. It comprises a half replication of 23 factorial design plus three center points and eight star points. CCD is a very efficient design for fitting the second-order model [18]. The machining time and the surface roughness (Ra) are considered as the output responses.

5.5 CONDUCTING THE EXPERIMENTS AS PER THE DESIGN MATRIX AND RECORDING THE RESPONSES

Experiments were conducted according to the design matrix that has been developed by Design Expert 8.0.1 and the corresponding surface roughness (Ra) and Machining time(MT) are tabulated in the Table 6.3.The MRR is calculated as the ratio of volume of material removed from work piece to the machining time. The Ra was measured in perpendicular to the cutting direction using Surtronic (surface roughness tester) at a 0.8 mm cut-off value. For each sample, three readings of surface roughness are taken and an average of three measurements taken at three different places is recorded as the final reading.

Table 5.3 Central composite design with corresponding output values of R_a and MT(Parent population P_t)

S.no.	X_1 (mm)	X_2 (deg.)	X_3 (mm/rev)	X (m/min)	Roughness (µm)	MT (min)
1	8500	1320	0.7	4	0.76	1.30
2	5500	1320	0.3	4	0.86	1.30
3	7000	2240	0.5	3	1.26	1.28
4	5500	3400	0.7	4	2.57	0.72
5	5500	1320	0.7	2	1.09	2.45
6	7000	2240	0.5	3	1.20	1.28
7	8500	1320	0.3	2	0.55	2.45
8	8500	3400	0.7	2	0.68	1.53
9	5500	3400	0.3	2	0.70	1.53
10	8500	3400	0.3	4	1.04	0.72
11	5500	3400	0.7	2	2.74	1.53
12	5500	3400	0.3	4	1.13	0.72
13	5500	1320	0.3	2	0.73	2.45
14	7000	2240	0.5	3	1.30	1.28
15	8500	3400	0.7	4	1.75	0.72
16	8500	1320	0.3	4	0.66	1.30
17	7000	2240	0.5	3	1.23	1.28
18	8500	3400	0.3	2	0.57	1.53
19	5500	1320	0.7	4	1.43	1.30
20	8500	1320	0.7	2	0.83	2.45
21	7000	2240	0.5	3	1.27	1.28
22	10000	2240	0.5	3	0.91	1.28
23	7000	4800	0.5	3	2.10	1.00
24	7000	2240	0.5	1	0.87	3.68
25	7000	2240	0.9	3	1.81	1.28
26	7000	2240	0.1	3	0.74	1.28
27	7000	2240	0.5	3	1.29	1.28
28	4000	2240	0.5	3	2.08	1.28
29	7000	2240	0.5	5	1.32	0.83
30	7000	640	0.5	3	1.32	2.92

5.6 DEVELOPMENT OF MATHEMATICAL MODELS USING DESIGN EXPERT 8.0.1

In the present study, mathematical relationships between the control variables and the output responses were developed using the RSM. The need in developing the mathematical relationships is to relate the machining responses to the cutting parameters thereby facilitating the optimization of the machining process. Design Expert-8.0.1 statistical analysis software, was used to compute the regression coefficients of the proposed models. Because of the lower predictability of the first-order models for the present problem, the second-order models were postulated. The analysis of variance (ANOVA) was used to check the adequacy of the developed models.

5.7. FORMULATION OF OPTIMIZATION PROBLEM

In the process of optimization, the aim is to minimam the MT and minimize the Ra, which forms the multi-objective optimization problem. Equations (5.1) and (5.2) represent the Ra and the MT respectively. The complexities of the models were reduced by applying the back elimination procedure. The final equations, after eliminating the insignificant terms, are as follows:

SR=+2.26873-(0.00069186*A)-(0.000317182*B)+(0.040858*C)+(0.72572*D)+(0.00000000724712*A*B)-(0.000114881*A*C)-(0.0000531375*A*D)+(0.000882196*B*C)+(0.00000263901*B*D)+(0.27752*C*D)+(0.0000000581981*A*A)+(0.00000000286653*B*B)-(0.39175*C*C)-(0.06067*D*D);

--(5.1)

MT=+5.05321+(0.000488891*A)-(0.00137808*B)+(0.83823*C)-(1.76017*D)-(0.0000000359534*A*B)+(0.0000582352*A*C)-(0.0000213060*A*D)+(0.0000197961*B*C)+(0.0000605759*B*D)-(0.019818*C*D)-(0.0000000284298*A*A)+(0.000000216738*B*B)-(1.16075*C*C)+(0.19732*D*D);

----------------------------------(5.2)

In the above equations , A , B, C and D represent the logarithmic transformations of depth of cut, horizontal inclination angle, feed and cutting speed respectively and are given below:

$$A_1 = \frac{\ln(X_0) - \ln(0.4)}{\ln(0.6) - \ln(0.4)}.$$

$$A_2 = \frac{\ln(X_1) - \ln(30)}{\ln(50) - \ln(30)}.$$

$$A_3 = \frac{\ln(X_2) - \ln(0.96)}{\ln(1.36) - \ln(0.96)}.$$

$$A_4 = \frac{\ln(X_3) - \ln(200)}{\ln(250) - \ln(200)} \quad \text{-- (5)}$$

The above relations were obtained from the following transformation equation:

$$A = \frac{\ln(X_n) - \ln(X_{n0})}{\ln(X_{n1}) - \ln(X_{n0})} \quad \text{-- (6)}$$

where A is the coded value of any factor corresponding to its natural value Xn; Xn1 is the natural value of the factor at the + 1 level, and Xn0 is the natural value of the factor corresponding to the base level or zero level. The objective functions were optimized subject to the feasible bounds of the control variables. Table 5.4 exhibits the feasible bounds for each variable.

Variable	lower limit	upper limit
Spindle speed(A) in rpm	4000	10000
Feed rate(B) in mm/min	640	4800
Depth of cut(C) in mm	0.1	0.9
Step over(D) in mm	1	5

5.8 SIGNIFICANCE OF REGRESSION COEFFICIENTS

In statistics, the coefficient of determination R2 (R-Sq) is the proportion of variability in a data set that is accounted for by a statistical model. In this definition, the term variability" is defined as the sum of squares. R2 is a statistic that will give some information about the goodness of fit of a model. In regression, the R2 coefficient of determination is a statistical measure of how well the regression line approximates the real data points.The value of R2 in quadratic model for MT is 0.9510 which means that the regression model provides an excellent explanation of the relationship between the independent variables (factors) and the response (MT). The value of R2 in quadratic model for the surface roughness is 0.8812 which means that the regression model provides an excellent explanation of the relationship between the independent variables (factors) and the response (Ra) which indicates that the model is considered statistically significant.

5.9 ANALYSIS OF PROCESS PARAMETERS ON OUTPUTS (Ra AND MT)

Table 6.5 shows the ANOVA for the Ra. The P-value for the model is lower than 0.05 (i.e. at 95% confidence level) indicates that the model is considered to be statistically significant [22]. Similar analysis was carried out for the MT and is given in Table 5.6.

Table 5.5 Analysis of variance for R_a:\

Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F
Model	8.234	14	0.59	7.95	0.0001 significant
A-A	2.06	1	2.06	27.86	<0.0001
B-B	1.49	1	1.49	20.13	0.0004
C-C	3.08	1	3.08	41.60	<0.0001
D-D	0.54	1	0.54	7.24	0.0168
AB	0.20	1	0.20	2.66	0.1235
AC	0.64	1	0.64	8.70	0.0099
AD	0.045	1	0.045	0.61	0.4468
BC	0.58	1	0.58	7.78	0.0138
BD	0.11	1	0.11	1.44	0.2484
CD	5.625E-005	1	5.625E-005	7.603-004	0.9784
A^2	5.382E-003	1	5.382E-003	0.073	0.7911
B^2	0.027	1	0.027	0.37	0.5532
C^2	0.046	1	0.046	0.62	0.4423
D^2	0.20	1	0.20	2.74	0.1185
Residual	1.11	15	0.074		
Lack of Fit	1.10	10	0.11	77.84	<0.0001 not significant
Pure Error	7.083E-003	5	1.417E-003		
Cor Total	9.34	29			

Response 1 R_a
ANOVA for Response Surface Quadratic Model
Analysis of variance table [Partial sum of squares - Type III]

The Model F-value of 7.95 implies the model is significant. There is onlya 0.01% chance that a "Model F-Value" this large could occur due to noise.Values of "Prob > F" less than 0.0500 indicate model terms are significant. In this case A, B, C, D, AC, BC are significant model terms. Values greater than 0.1000 indicate the model terms are not significant. If there are many insignificant model terms (not counting those required to supporthierarchy), model reduction may improve your model.The "Lack of Fit F-value" of 77.84 implies the Lack of Fit is significant. There is only a0.01% chance that a "Lack of Fit F-value" this large could occur due to noise.Significant lack of fit is bad -- we want the model to fit.

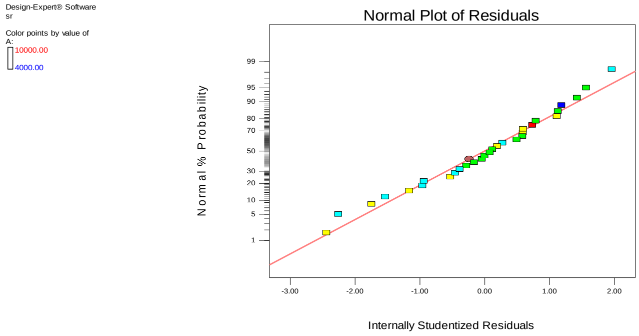


Fig 5.2 normal probability plot of the residuals for surface roughness

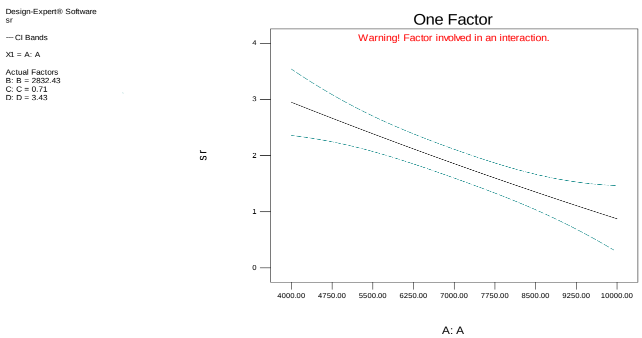


Fig 5.3 effect of spindle speed on surface roughness

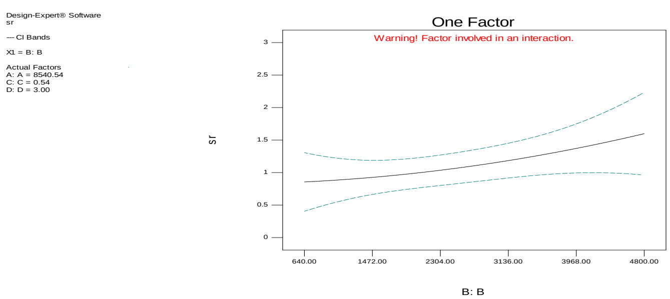


Fig 5.4 effcect of feed rate on surface roughness

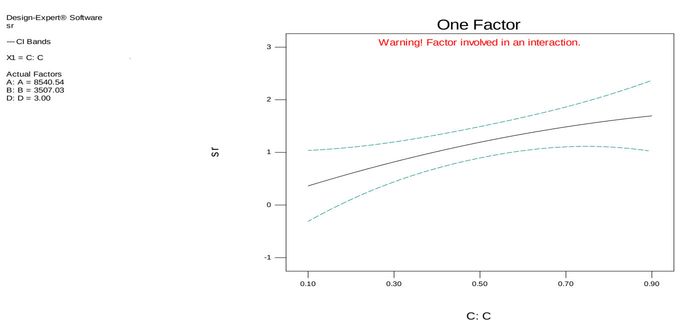


Fig 5.5 effect of depth of cut on surface roughness

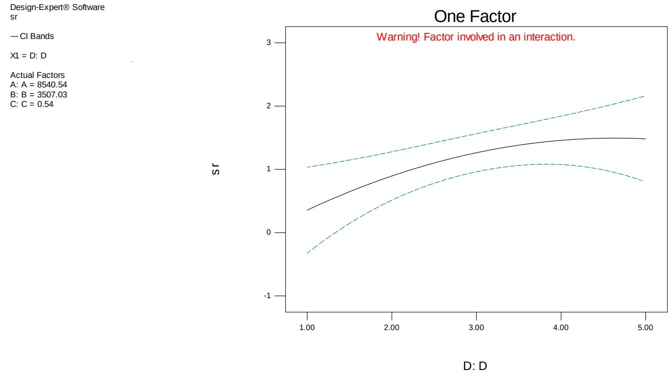


Fig 5.6 effect of step over on surface roughness

Table. 5.7. varience for MT:Response2mtANOVAfor Response Surface Quadratic ModelAnalysis of variance table [Partial sum of squares - Type III]

Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F
Model	13.46	14	0.96	20.79	<0.0001 significant
A-A	0.000	1	0.000	0.000	1.0000
B-B	2.62	1	2.62	56.62	<0.0001
C-C	0.000	1	0.000	0.00	1.0000
D-D	5.62	1	5.62	121.55	<0.0001
AB	0.000	1	0.000	0.000	1.0000
AC	0.000	1	0.000	0.000	1.0000
AD	0.000	1	0.000	0.000	1.0000
BC	0.000	1	0.000	0.000	1.0000
BD	0.14	1	0.14	3.01	1.1031
CD	0.000	1	0.000	0.000	1.0000
A^2	0.034	1	0.034	0.73	0.4051
B^2	0.73	1	0.73	15.78	0.0012
C^2	0.034	1	0.034	0.73	0.4051
D^2	1.19	1	1.19	25.79	0.0001
Residual	0.69	15	0.046		
Lack of Fit	0.69	10	0.069	11.98	0.075 not significant
Pure Error	0.000	5	0.000		
Cor Total	14.16	29			

The Model F-value of 20.79 implies the model is significant.There is onlya 0.01% chance that a "Model F-Value" this large could occur due to noise. Values of "Prob > F" less than 0.0500 indicate model terms are significant.In this case B, D, B2, D2 are significant model terms.Values greater than 0.1000 indicate the model terms are not significant. If there are many insignificant model terms (not counting those required to support hierarchy), model reduction may improve your model.

Std. Dev.	0.22	R-Squared	0.9510
Mean	1.51	Adj R-Squared	0.9052
C.V. %	14.27	Pred R-Squared	0.7681
PRESS	3.28	Adeq Precision	17.385

The "Pred R-Squared" of 0.7681 is in reasonable agreement with the "Adj R-Squared" of 0.9052."Adeq Precision" measures the signal to noise ratio. A ratio greater than 4 is desirable. Your ratio of 17.385 indicates an adequate signal. This model can be used to navigate the design space.

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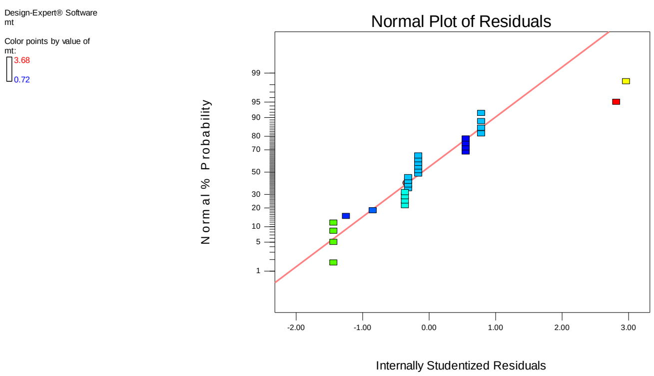

Fig5.7 Normal probability plot of the residual for machining time

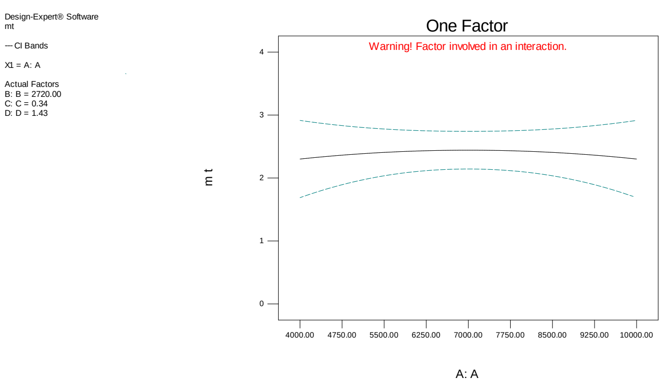

Fig 5.8 effect of spindle speed on machining time

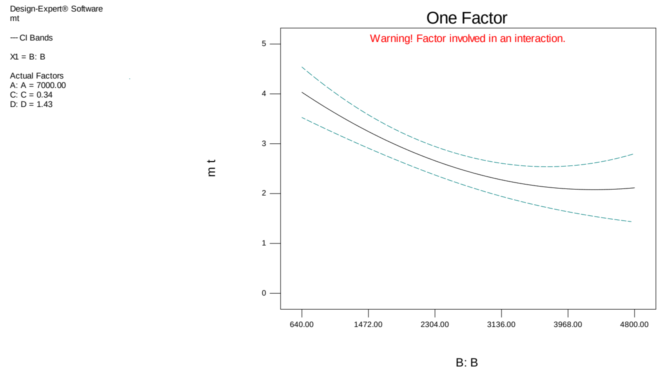

Fig 5.9 effect of feed rate on machining time

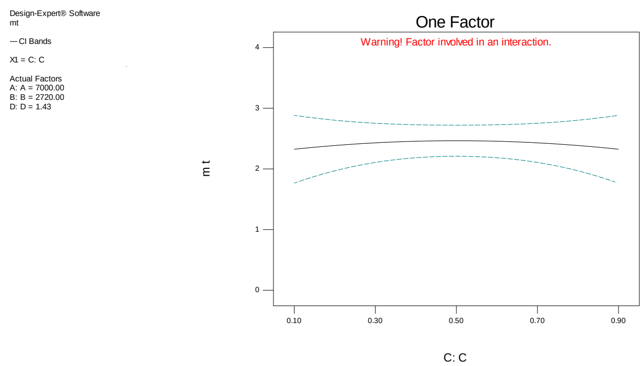

Fig 5.10 effect of depth of cut on aching time

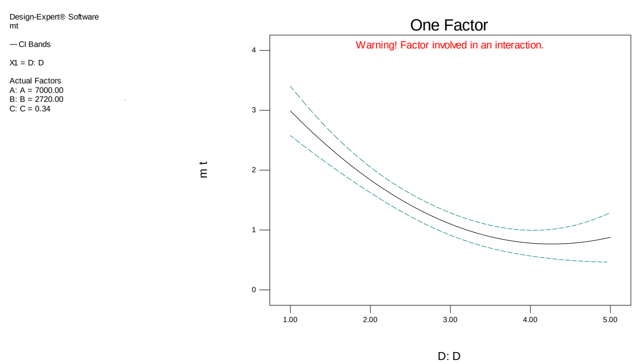

Fig 5.11 effect of step over on machining time

The following equations were obtained for the Ra and MT in terms of the coded factors:

R_a =-0.83990+1.18148E-004 * A-9.81121E-005 * B+5.18185 * C+0.21532 * D-7.09837E
-008 * A * B-6.68750E-00 * A * C+3.54167E-005* A * D+9.09771E-004 * B * C

$+7.83551E-005 * B * D+9.37500E-003 * C * D+6.22563E-009* A^2+2.82176E-008 * B^2$
$-1.02481* C^2-0.085992* D^2$-----------------------(3)

$MT =+6.28404+2.18906E-004 * A-1.38423E-003* B+0.87953 * C-2.02336* D$
$-2.88481E-022* A * B+1.18539E-018 * A * C+4.34837E-019* A * D$
$-2.84598E-018* B * C+8.95619E-005* B * D+3.66027E-015* C * D$
$-1.56361E-008* A^2+1.46131E-007* B^2-0.87953* C^2+0.20857* D^2$------------------------------------(4)

5.10 IMPLEMENTATION

Tables 5.7 to 5.9 display the implementation of NSGA for the present problem. Sample calculations are shown for one iteration of the algorithm. The bit lengths chosen for X1, X2, X3 and X4 are 4, 5, 4, and 3 respectively. It refers to the number of binary digits chosen for an individual control variable. As a first step, in the algorithm, an initial population of 27 chromosomes was generated randomly.

Table 5.7. Lower and upper bounds and bit length for all variables

Sr. No	Input parameter	Upper limit	Lower limit	Bit length
1	Spindle speed	4000	10000	4
2	Feed rate	640	4800	5
3	Depth of cut	0.1	0.9	4
4	Step over	1	5	3

S.NO	CHROMOSOME	X1	X2	X3	X4	Ra (µm)	MT (min)	RANK
1	0000 11000 1010 000	4000	3860.64	0.63	1.00	1.7265	2.7444	7
2	1010 10000 0110 011	8000	2787.10	0.42	2.71	1.0580	1.2042	4
3	0001 11000 1000 111	9400	3860.64	0.53	5.00	2.4706	1.0280	4
4	0011 00000 0100 011	5200	640.00	0.31	2.71	1.0419	2.6272	5
5	1011 00101 0111 110	8400	1310.97	0.47	4.43	0.8953	1.2960	4
6	1110 11000 1001 110	9600	3860.64	0.58	1.00	1.6309	2.6233	6
7	1100 00110 0011 100	8800	1445.16	0.26	3.28	0.8228	1.4426	4
8	1111 11011 0000 010	10000	4263.22	0.10	2.14	0.6617	0.9988	1
9	1100 00001 1010 011	8800	714.19	0.63	2.71	0.8708	2.7077	4
10	1110 01001 0101 011	9600	1847.74	0.37	2.71	1.2943	1.4622	5
11	0110 10001 1010 110	6400	3994.84	0.63	4.43	2.1548	0.8915	2
12	1001 01000 0010 101	7600	1713.55	0.21	3.85	0.6385	1.0667	1
13	0100 11110 1010 101	5600	4665.81	0.63	3.85	2.5190	1.3084	5
14	1001 11010 0011 010	7600	4129.03	0.26	2.14	0.7162	0.9585	2
15	1101 01000 0011 100	9200	1713.55	0.26	3.28	0.8867	1.1706	3
16	1010 10010 1000 000	8000	3055.48	0.53	1.00	0.9415	2.9172	5
17	1010 00011 0101 111	8000	1042.58	0.37	5.00	0.6667	1.5341	2
18	1100 01101 0010 001	8800	2384.52	0.21	1.57	0.6771	2.2369	3
19	0110 10010 1100 110	6400	3055.48	0.74	5.00	2.1689	0.7350	1
20	0011 10000 1000 010	5200	2787.10	0.53	3.14	1.6840	1.0242	3
21	1011 11000 1110 011	8400	3860.64	0.79	2.71	2.2661	1.0680	4
22	0000 10101 1000 111	4000	3458.06	0.53	5.00	2.5852	0.8617	3
23	0100 11111 1000 110	5600	4800.00	0.53	4.43	2.1865	1.4411	6
24	0001 11111 0001 111	4400	4800.00	0.15	5.00	0.8189	1.5281	3
25	0011 10100 1011 100	5200	3323.87	0.69	3.28	2.2784	0.9010	3
26	0100 10011 0010 111	5600	3188.68	0.21	5.00	0.7709	0.7541	1
27	0101 11001 1100 001	6000	3994.84	0.74	1.57	1.9069	2.2358	6
28	1111 00110 0011 000	10000	1445.16	0.26	1.00	1.0488	3.6455	6
29	1111 10001 1001 010	10000	2921.29	0.58	2.14	1.6989	1.3747	5
30	1010 11100 1100 110	8000	4397.42	0.74	4.43	2.4828	0.8398	2

Then the population was classified into different levels of non-domination sets. In this approach, each solution has to be compared with every other solution in the population. For example, the objective function values of the first chromosome for the Ra and the MRR are 1.6261 and 2.3288 respectively. They were then compared with the corresponding objective function values of the second chromosome and subsequently with the values of other chromosomes in the population. The values of objective 1 and objective 2 are greater for the first chromosome when compared to the second chromosome. Therefore, it can be said that the first chromosome is non-dominating with respect to second one. The comparison was continued for all other chromosomes in the population and as the first chromosome is still non-dominant, it was ranked as 1. Similarly, each non-dominant chromosome obtained in first sorting was given as rank 1. Then disregarding these chromosomes temporarily again sorting was done for the remaining chromosomes. All non-dominant chromosomes obtained in second sorting were given as rank 2. This procedure was repeated till all chromosomes in the population were sorted and ranked. Eventually, the members of the population were classified into four distinct non-dominated sets as shown in Table 5.8.

To preserve the diversity among the chromosomes of the populations, sharing function method as explained in section 3 was used. In this method, initially, the Euclidean distances between the chromosomes of first front were computed. The distance values of 0.0000, 0.1149, 0.2970, 0.6089, 0.9286, 0.3383, 0.0042, 1.0879, 0.7523 and 0.3288 were obtained for the first chromosome with reference to the chromosomes 1, 3, 4, 5, 9, 13, 19, 21, 22 and 23 respectively. The sharing function values were subsequently computed using equation (7) by choosing σshare value as 0.35. Then the niche count for the first front was computed based on equation (8). Similar procedure was applied to calculate the niche count values for the other fronts. The niche count values obtained for each chromosome are listed in Table 6.9.

A dummy fitness (Fi) equal to the population size (27) was assigned to all chromosomes of the first front. Then the shared fitness (F') value of each chromosome in the first front was obtained using equation (5). This process of degrading the fitness of a solution which is crowded by many solutions helps to emphasize the solutions residing in less crowded regions. Similarly, the shared fitness values for other chromosomes were computed. Dummy fitness for chromosomes in the second front is obtained as 5.8816 by subtracting a small value of 0.12 from the minimum shared fitness value of the first front. This makes sure that no solution in the first front has shared fitness worse than the assigned fitness of any solution in the second front. This procedure was continued until all the solutions are assigned a shared fitness value. Table 6.9 illustrates the above procedure.

Roulette-wheel selection operator was used to pick-up the good solutions from the population. This operator assigns number of copies in the mating pool proportional to the shared fitness. In this process, initially, the probability of selecting each chromosome (pi) was calculated by dividing the individual shared fitness value with the sum of fitness values of all chromosomes in the population. Thereafter, the cumulative probability (Pi) of each chromosome was calculated by adding the individual probabilities from the top of the Table. In order to choose n strings, n random numbers between zero and one were created at random. Thus, a string that represents the chosen random number in the cumulative probability range (calculated from the fitness values) for the chromosome was copied to the mating pool. For example, random number (0.884) was created for the first chromosome; the twenty third chromosome got a copy in the mating pool, because that string occupies the interval (0.8716, 0.9524) as shown in the Table 6.9. Chromosomes with a higher fitness value represent a larger range in the cumulative probability values and therefore they have greater probability of being copied into the mating pool. On the other hand, a chromosome with a smaller fitness value represents a smaller range in cumulative probability value and has a smaller probability of being copied into the mating pool.

Table 5.9 Selection of chromosomes

S.NO	Shared Fitness (F)	Probability (P)	Cumulative probability of selection	Random Number	Selected Chromosome Number
1	5.0000	0.0245	0.0245	0.337	12
2	4.2661	0.0209	0.0454	0.770	24
3	7.0395	0.0344	0.0798	0.724	22
4	4.9659	0.0242	0.1040	0.671	20
5	4.9980	0.0244	0.1248	0.434	14
6	3.5100	0.0172	0.1456	0.555	17
7	5.1305	0.0251	0.1707	0.073	03
8	7.1655	0.0350	0.2057	0.697	21
9	6.9557	0.0340	0.2397	0.041	02
10	4.6889	0.0229	0.2626	0.945	30
11	11.8946	0.0582	0.3208	0.747	22
12	9.7752	0.0478	0.3686	0.186	08
13	7.0675	0.0346	0.4032	0.297	11
14	11.4207	0.0559	0.4591	0.836	26
15	5.6944	0.0278	0.4869	0.228	09
16	4.9898	0.0244	0.5113	0.252	10
17	12.0592	0.0589	0.5702	0.816	25
18	7.3083	0.0357	0.6059	0.769	24
19	11.5052	0.0563	0.6622	0.774	22
20	5.3953	0.0264	0.6886	0.833	26
21	5.5079	0.0269	0.7155	0.162	07
22	7.2579	0.0355	0.7510	0.735	22
23	3.4125	0.0166	0.7676	0.906	28
24	5.7850	0.0283	0.7959	0.849	26
25	6.1003	0.0298	0.8257	0.533	17
26	10.5917	0.0518	0.8775	0.260	10
27	3.1609	0.0155	0.8930	0.989	30
28	3.3521	0.0164	0.9094	0.766	23
29	4.3162	0.0211	0.9305	0.636	19
30	14.0900	0.0689	1.0000	0.647	19

The chromosomes selected in the mating pool were used in the crossover operation. In this work, two-point crossover was adopted, in which, the portions of the strings between the randomly selected crossover sites were swapped to create the new intermediate population as shown in Table 6.10. However, with the random sites, the offspring produced may or may not have a combination of good substrings from parent strings, depending on whether or not the crossing sites fall in the appropriate locations. If good strings are not created by crossover, they will not survive too long, because reproduction will select against those chromosomes in subsequent generations. In order to preserve some of the good chromosomes that are already present in the mating pool, not all chromosomes in the mating pool are used in crossover. When a crossover probability of pc is used, the expected number of strings that will be subjected to crossover is only 100 pc percent and the remaining percent of the population remains as they are in the current population. In this work, pc was chosen as 0.85 and the calculations are shown in Table 5.10.

S.NO	Selected Chromosome Number	Crossover	Crossover sites	Offspring	Mutation site	Mutated chromosome
1	12	YES	12,11	1001010000000101	---	1001010000000101
2	24	YES	12,11	0001111110011111	---	0001111110011111
3	22	NO	---	0000101011000111	---	0000101011000111
4	20	NO	---	0011100001000010	5,11	0011100001100010
5	14	YES	4,10	1000000110011010	---	1000000110011010
6	17	YES	4,10	1011110100101111	---	1011110100101111
7	03	NO	---	0001110001000111	---	0001110001000111
8	21	YES	7,11	1011100000110011	8,16	1011100100110011
9	02	YES	7,11	1010100001110011	---	1010100001110011
10	30	YES	14,11	1010111001000110	9	1010111001000110
11	22	YES	14,11	0000101011100111	---	0000101011100111
12	08	YES	5,6	1111100110000010	---	1111100110000010
13	11	YES	5,6	0110110011010110	10	0110110011010110
14	26	YES	2,4	0100100110010111	---	0100100110010111
15	09	YES	2,4	1100000011010011	2,11	1100000011110011
16	10	NO	---	1110010010101011	---	1110010010101011
17	25	YES	8,11	0011101010011100	---	0011101010011100
18	24	YES	8,11	0001111101001111	---	0001111101001111
19	22	NO	---	0000101011000111	---	0000101011000111
20	26	NO	---	0100100110010111	---	0100100110010111
21	07	YES	5,1	0000101100011100	---	0000101100011100
22	22	YES	5,1	1100001011000111	15	1100001011000111
23	28	YES	7,15	1111000110010110	---	1111000110010110
24	26	YES	7,15	0100101100011001	1	1100101100011001
25	17	YES	9,6	1010010010101111	---	1010010010101111
26	10	YES	9,6	1110000110101011	---	1110000110101011
27	30	NO	---	1010111001100110	---	1010111001100110
28	23	YES	8,10	0100111101000110	12,13	0100111101011110
29	19	YES	8,10	0110100111100110	6,12	0110110111110110
30	19	NO	---	0110100101100110	---	0110100101100110

The third operator, mutation, was then applied on the intermediate population. Bit-wise mutation was performed. The mutation operator changes 1 to 0 and vice versa based on a small mutation probability, pm. Mutation was implemented with the probability of 0.1 as shown in Table 6.10. Mutation is basically intended for local search around the current solution. Implementation of mutation completes one iteration of the algorithm. The above procedure was epeated until the maximum number of generations was completed. For better convergence, the algorithm was run for the maximum of 200 generations. Hence from the usual binary tournament selection, recombination, and mutation operators are used to create a child population Qt of size 30. This population is shown in table 5.11.

Table.5.11.NEW POPULATION

S.NO	X1	X2	X3	X4	Ra (µm)	MT (min)
1	7600	1713.55	0.10	3.86	0.4585	0.9670
2	4400	4800.00	0.26	5.00	1.3685	1.5957
3	4000	3458.06	0.53	5.00	2.5852	0.8617
4	5200	2787.09	0.74	2.14	1.8202	1.6277
5	7200	1042.58	0.26	2.14	0.6562	2.8170
6	8800	4129.03	0.37	5.00	0.9667	0.6322
7	4400	3864.64	0.53	5.00	2.4706	1.0280
8	8800	3055.48	0.42	2.71	1.1869	1.0378
9	8000	2787.09	0.85	2.71	1.8471	1.1317
10	8000	4397.41	0.53	4.43	1.6988	0.8757
11	4000	3458.06	0.74	5.00	3.3248	0.7707
12	10000	3189.67	0.10	2.14	0.8006	0.9887
13	6400	3994.84	0.63	4.43	2.1548	0.8915
14	5600	3189.68	0.31	5.00	1.1104	0.8066
15	8800	774.19	0.85	2.71	0.8643	2.5468
16	9600	1847.74	0.37	2.71	1.1294	1.4622
17	5200	3458.06	0.26	3.28	1.0224	0.8988
18	4400	4665.81	0.58	5.00	2.8778	1.5213
19	4000	3458.06	0.53	5.00	2.5852	0.8617
20	5600	3189.68	0.31	5.00	1.1104	0.8066
21	4000	3592.26	0.26	3.28	1.4210	0.0690
22	8800	1310.97	0.53	5.00	0.8752	1.2477
23	10000	1042.58	0.21	4.43	0.8018	1.1669
24	8800	3592.26	0.26	1.57	0.7430	1.9170
25	8000	1847.74	0.37	5.00	0.7381	0.9465
26	9600	1042.58	0.37	2.71	1.0535	2.2070
27	8000	4397.42	0.74	4.43	2.4828	0.8398
28	5600	4665.81	0.69	4.43	2.8381	1.3008
29	6400	4263.22	0.85	4.43	3.0584	0.9034
30	6400	3055.48	0.74	4.43	2.1535	0.6583

Now, we combined the parent population P t and child population Q t to get R t (asR t = Pt □ Qt). The population Rt will be of size 60. Then, the population Rt is sorted according to non-domination as discussed above. Since all previous and current population members are included in Rt, the elitism is ensured. Now, solutions belonging to the best non-dominated first set F1 are 9,11,13,14,15,16,28,41, 48,52 of best solutions in the combined population and must be emphasized more than any other solution in the combined population. Here the size of F1 is 10, which is smaller than 27, we definitely choose all members of the set F1 for the new population Pt+1. The remaining members of the population Pt+1 are chosen from subsequent non-dominated fronts in the order of their ranking. Thus, solutions from the second set F2 are 19, 34, 35, 36, 38, 42, 45, 47 and 53 of size 9 chosen. Next, followed by solutions from the third set F3 are 10, 22, 24, 26, 29, 30, 32, 43, 50 and 51 of size 10.Now, the count of solutions in all sets from F1 to F3 of 29 would be larger than the population size of 27. To choose exactly 27 population members, we sort the solutions of the last front i.e., from F3 using the crowded comparison operator □ n , in the descending order and choose the best solutions needed to fill all population slots as shown in Table 5.11.

6. RESU LTS

S.NO	X1	X2	X3	X4	Ra (µm)	MT (min)
1	6533.187	2439.51	0.100076	1.000004	0.084051	2.931112
2	6508.645	2002.209	0.100049	1.000017	0.156272	3.183431
3	6466.435	1249.54	0.100004	1.000011	0.283715	3.811783
4	6448.678	2192.7	0.10002	1.000007	0.123591	3.062107
5	6480.476	2174.824	0.100132	1.000008	0.127108	3.073385
6	6406.645	2138.849	0.100017	1.000019	0.132289	3.093435
7	6447.739	1011.441	0.100512	1.000018	0.325055	4.06183
8	6430.935	1069.701	0.100062	1.000005	0.31475	3.996808
9	6485.049	1004.334	0.100026	1.000016	0.326229	4.071477
10	6466.309	926.4827	0.100079	1.000058	0.339711	4.157937
11	6442.314	1738.919	0.100273	1.000044	0.200194	3.37376
12	6413.774	1657.177	0.100011	1.00001	0.213694	3.438123
13	6435.172	1385.096	0.100049	1	0.260304	3.678696
14	6402.46	2756.851	0.100018	1.000004	0.029757	2.800237
15	6403.286	1974.26	0.100053	1.000015	0.159988	3.199643
16	6436.883	1465.12	0.100004	1.000014	0.246556	3.604857
17	6450.108	1631.655	0.10046	1.000047	0.218621	3.461059
18	6468.069	1541.808	0.100008	1.000053	0.233632	3.537966
19	6442.314	1910.555	0.100304	1.000074	0.171245	3.24531
20	6445.05	775.8321	0.100009	1.000004	0.365961	4.333501
21	6520.837	808.4053	0.100053	1.000008	0.360569	4.2995
22	6461.528	2725.998	0.100282	1.000042	0.03604	2.811168
23	6435.23	1653.275	0.100132	1.00001	0.214545	3.442301
24	6278.611	1086.794	0.10006	1.000115	0.313179	3.968506
25	6627.468	1277.514	0.100155	1.000004	0.281372	3.791542
26	6528.329	2666.577	0.100061	1.000001	0.046609	2.832798
27	6459.948	1373.888	0.100104	1.000001	0.262365	3.690516
28	6407.653	910.4003	0.100011	1.00001	0.342515	4.172511
29	6393.539	1184.624	0.100077	1.000005	0.294911	3.873653
30	6455.599	1229.08	0.100051	1.000028	0.287225	3.8318
31	6481.824	1122.661	0.100121	1.000041	0.305767	3.943221
32	6410.315	2399.466	0.100071	1.000013	0.088912	2.949524
33	6475.282	1686.096	0.100248	1.000049	0.209375	3.417055
34	6474.423	2881.491	0.100021	1.000001	0.010346	2.760996
35	6464.141	1346.06	0.100015	1.000027	0.267111	3.717097
36	6482.078	2018.12	0.100133	1.00003	0.15334	3.172246
37	6457.564	2694.278	0.100155	1.00003	0.040934	2.822527
38	6443.678	2467.46	0.100024	1.000015	0.077872	2.917122
39	6528.329	828.7814	0.10002	1.000015	0.357079	4.273658
40	6432.301	1714.678	0.100023	1.000015	0.203989	3.392362
41	6473.885	2356.301	0.100334	1.000016	0.097162	2.972445
42	6476.37	1168.119	0.100066	1.000016	0.297848	3.895317
43	6479.401	2464.509	0.10024	1.000018	0.079202	2.919017
44	6440.688	1045.052	0.100053	1.000006	0.319028	4.024101
45	6420.888	715.6952	0.100013	1.000002	0.376566	4.405141

46	6417.316	2059.24	0.100008	1.000005	0.145687	3.14364
47	6436.601	1425.448	0.100133	1.000018	0.253453	3.641231
48	6466.104	751.5437	0.1	1.000019	0.370228	4.364404
49	6482.078	1962.534	0.100213	1.00003	0.162766	3.209974
50	6466.151	1601.873	0.100054	1.000057	0.223422	3.486283
51	6406.645	2079.996	0.100017	1.000019	0.142164	3.130072
52	6383.798	2279.854	0.100008	1.000005	0.108594	3.011401
53	6431.76	1496.802	0.10002	1.000006	0.241126	3.576187
54	6468.34	817.7863	0.10007	1.000008	0.358655	4.28487
55	6627.339	885.2525	0.100063	1.000027	0.348804	4.215125
56	6448.678	2327.431	0.10002	1.000066	0.10116	2.98683
57	6402.46	2782.552	0.10016	1.000017	0.025824	2.791793
58	6430.935	1810.744	0.100062	1.000005	0.187731	3.317908
59	6468.34	2903.07	0.100038	1.000004	0.006761	2.754963
60	6463.568	1412.593	0.10002	1.000007	0.25569	3.654298
61	6441.079	1849.989	0.100126	1.00009	0.181251	3.288922
62	6407.021	2111.907	0.100017	1.000013	0.136808	3.110036
63	6304.319	2162.031	0.100239	1.000005	0.128827	3.077055
64	6465.309	984.3735	0.100055	1.000008	0.329617	4.092536
65	6427.13	1582.654	0.10009	1.000017	0.226507	3.501128
66	6537.083	2240.459	0.100092	1.000001	0.117094	3.035917
67	6377.428	1702.305	0.10009	1.000008	0.206082	3.400176
68	6413.774	1396.08	0.100003	1.00001	0.258357	3.667285
69	6505.752	2832.963	0.100221	1.000042	0.019278	2.775395
70	6466.151	2095.057	0.100054	1.000057	0.140164	3.121915
71	6424.593	2645.315	0.100002	1.000004	0.04827	2.840871
72	6530.755	711.3897	0.100013	1.000002	0.37759	4.41821
73	6414.89	1634.362	0.100011	1.00001	0.217584	3.457004
74	6370.479	2517.116	0.100097	1.000002	0.069235	2.893842
75	6419.938	961.4498	0.100012	1.000009	0.33357	4.115325
76	6392.535	1097.991	0.100118	1.000013	0.309958	3.964201
77	6442.314	1775.824	0.100304	1.000004	0.193967	3.345141
78	6481.824	855.8771	0.100014	1.000003	0.352035	4.240701
79	6458.705	1036.191	0.100095	1.00004	0.320625	4.034852
80	6452.106	1136.049	0.100008	1.000004	0.303254	3.927393
81	6468.069	1563.753	0.100025	1.000053	0.229904	3.51893
82	6442.314	1945.871	0.100276	1.000044	0.165258	3.220494
83	6461.528	2562.579	0.100176	1.000042	0.06267	2.874874
84	6442.097	1932.713	0.100304	1.000016	0.167497	3.229741
85	6463.089	936.9364	0.100004	1.000003	0.337842	4.145823
86	6398.68	2915.108	0.100112	1.000008	0.004018	2.752153
86	6398.68	2915.108	0.100112	1.000008	0.004018	2.752153
87	6431.76	1758.918	0.100224	1.000006	0.196686	3.357763
88	6462.436	1226.263	0.10002	1.000007	0.287716	3.835008
89	6463.089	1203.677	0.100008	1.000003	0.291606	3.857981
90	6440.692	1285.667	0.100017	1.000013	0.2774	3.774602
91	6403.145	1477.991	0.100004	1.000054	0.244314	3.591619
92	6450.854	1820.891	0.100142	1.000037	0.186238	3.310966
93	6450.854	2504.056	0.100248	1.000037	0.072296	2.900568
94	6464.211	1337.285	0.100101	1	0.268669	3.725651
95	5549.974	4799.965	0.147509	1	0.08998	3.118402
96	5551.665	4799.954	0.188925	1.000034	0.066586	3.156852
97	5649.898	4799.998	0.212056	1	0.145376	3.174862
98	5584.014	4799.995	0.203744	1	0.119541	3.169178
99	5585.436	4799.991	0.185838	1	0.052121	3.153552
100	5539.064	4799.998	0.173789	1	0.010529	3.14352

The algorithm can be run for a few more times to get more number of optimal values. It can be observed from the table 7, that no solution in the front is better than any other as they are non-dominated solutions. The choice of a solution has to be made based on the production requirements. Table 7 enables to choose the optimal machining parameters for a fixed combination of the metal removal rate and the surface roughness. The obtained values by the algorithm are better than the experimentally observed values shown in Table 6.3. For example, the 23rd experiment in Table 6.3 leads to the Ra value of 2.25µm and the MRR value of 4.242 gm/min. By optimization using the proposed algorithm, for the same value of Ra, the MRR was increased to 7.6807 gm/min (S. No. 44, Table 7). Similarly, the 11th experiment from Table 6.3 corresponds to the Ra value of 1.65 µm and the MRR of 3.088 gm/min. After optimization, the Ra was reduced to 1.49µm, for approximately the same value of the MRR of 3.0883 gm/min (S. No.40, from Table 7). In the above cases, improvement in the output responses was made possible by the selection of the different set of machining parameters.

CONCLUSIONS

Optimization of end milling parameters is very much essential as this is a highly stochastic process. Optimization helps in determining the parameters that result in both improved production rate and enhanced surface quality. In the present work influences of end milling parameters namely Spindle speed, Feed Rate, Depth of cut , Step over on Surface roughness (Ra) and Machining time (MT) are studied. Analytical models are developed based on experimental results for Ra and MT using Response Surface Methodology (RSM). The present problem has been modeled as a multi-objective problem as Ra and MT are conflicting in nature. Increasing an input parameter in end milling results in improved production rate and increased tool wear as well. Excessive tool wear leads to poor surface quality. The optimization of these models is carried out using Non-dominated Sorting Genetic Algorithm (NSGA). Unlike the conventional methods like Classical weighted approach and Goal programming method, NSGA retrieves all the Pareto-sets irrespective of the indicated weights of the objective functions. It is useful for the manufacturing industrie to select the values of input parameters at the desired levels of Ra and MT. Different sets of optimal process parameters are found out and represented in the form known as the Pareto-optimal set. Totally 100 such optimal parametric combinations are identified. The NSGA algorithm is implemented using Visual C++.

In the Pareto-optimal set, the outcome is a group of non-dominated solutions and none of the solution is better than any other solution in that set. Hence, a process engineer can select optimal combination of parameters from that set, depending upon the requirements. Once the optimal values have been determined the process can be automated based on those values.

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