

# Studies on Modified Genetic Algorithm (NSGA-II) in Predicting Pareto Optimal Solutions

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**Abstract**— The paper described the contribution of various researchers in the field of genetic algorithm for predicting optimum combination of input parameters. It is observed that modified genetic algorithm programming based tool is better than other statistical methods like taguchi, RSM etc. Also multiple solutions are obtained simultaneously for various output parameters.

**Key words:** Modified Genetic Algorithm, Response Surface Methodology, Optimum Conditions

## I. INTRODUCTION

Non-dominated sorting genetic algorithm-II (NSGA-II) is a fast elitist multi-objective optimization algorithm proposed by Deb et al. (2002). It is a modified version of NSGA-II proposed by Srinivasan and Deb (1994). NSGA was criticized for its computational complexity and lack of elitism. Also to ensure diversity in population so as to get a wide variety of equivalent solutions, NSGA relied on the concept of sharing which required specification of a sharing parameter. NSGA-II has a better sorting algorithm, incorporates elitism and sharing parameter need not to be chosen as priori [Deb et al., 2002]. The mathematical models of responses predicted from RSM are coupled with NSGA-II code and the technique is called as hybrid RSM-NSGA-II. Few researchers have been used statistical and computation techniques for the production of biodiesel [Dhingra et al., 2013a; Dhingra et al., 2013b; Dhingra et al., 2014a; Dhingra et al., 2014b; Dhingra et al., 2014c; Dhingra et al., 2014d; Dhingra et al., 2016a; Dhingra et al., 2016b]. The major steps/functions utilized in the NSGA-II program are as follows researchers [Beyer and Deb, 2001; Srinivas and Deb, 1994; Garg et al., 2012]:

### A. Step I. Population Initialization:

Initially, a random population P is created which depends upon the constraints and problem range, if any.

### B. Step II. Non-Dominated Sorting:

Once the population is initialized and the fitness functions (taken from RSM) are evaluated, the population is sorted based upon the non-domination into different fronts. Two entities are calculated for each solution: (a) Number of solutions that dominate the solution p i.e.  $n_p$  and (b) a set of solutions that dominate p. When the value of  $n_p$  is zero, it means no solution dominates p and p belongs to first front F1. Rank 1 is assigned to individual p i.e.. This is repeated for all individuals in the population P. For each solution p with, visit each member q of its set  $S_p$  and reduce its domination count by 1. If for any member of q,  $n_q$  becomes zero, it must be put in a separate list Q. Members listed in Q denote second non-dominated front. This procedure is continued till all the fronts are identified.

### C. Step III. Crowding Distance:

An evolutionary algorithm must have a good spread among the set of solutions obtained. There is no need of any user defined parameter for maintaining diversity among population members in NSGA-II approach. It evaluates crowding distance based upon density of solutions surrounding a particular solution in the population. For estimating the solutions surrounding a particular solution, average distance of two solutions on either side of current solution is computed for each objective function. It is called crowding distance  $(CD)$ . The computation of crowding distance requires sorting the population according to each objective function value in ascending order of magnitude for each front. The solutions with largest and smallest function values are assigned infinite distance values, for each objective function. All other intermediate solutions are given a distance values equal to absolute normalized difference in the function values of two adjacent solutions. The overall crowding distance value is calculated as sum of individual distance values, corresponding to each objective.

### D. Step IV. Selection:

Selection is the exploitation phase of search which ensures that good and fit individuals remain in the population. Numbers of operators such as tournament selection, roulette wheel selection and truncation selection are available for propagating the influence of best individual. Each operator has its own advantages and applications. For obtaining a uniformly spread out pareto optimum front, Crowding comparison operator is used which takes into account non-domination rank (irank) and crowding distance  $(CD)$ . An individual 'i' is selected if  $irank_i < irank_j$  or  $CD_i < CD_j$  or AND. It reveals that between two solutions having different ranks the solution having better rank (front) is preferred. If both the solutions are having same rank then solution lying in the less crowded region is selected.

### E. Step V. Genetic Operators:

In crossover operator, two of the fittest individuals are selected as the parents to produce better offspring. Simulate Binary Crossover (SBX) is utilized for reproduction. It works with two parent solutions and creates two offspring. It also simulates the binary crossover observed in the nature and is given as:

$$c_{1,k} = \frac{1}{2} [(1 - \beta_k) p_{1,k} + (1 + \beta_k) p_{2,k}] \quad \dots (1)$$

$$c_{2,k} = \frac{1}{2} [(1 + \beta_k) p_{1,k} + (1 - \beta_k) p_{2,k}] \quad \dots (2)$$

Where  $c_{i,k}$  is the  $i$ th child with  $k$ th component,  $p_{i,k}$  is the selected parent and  $\beta_k$  is a sample from a random number generated having the density as given below:

$$p(\beta) = \frac{1}{2}(\eta_c + 1)\beta^{\eta_c}, \quad \text{If } 0 \leq \beta \leq 1 \quad \dots (3)$$

$$p(\beta) = \frac{1}{2}(\eta_c + 1)\frac{1}{\beta^{\eta_c+2}}, \quad \text{If } \beta > 1 \quad \dots (4)$$

This distribution is obtained from a uniformly sampled random number  $u$  between 0-1,  $\eta_c$  refers to the distribution index for crossover. Hence  $\beta(u)$  is defined as:

$$\beta(u) = (2u)^{\frac{1}{\eta_c+1}} \quad \dots (5)$$

$$\beta(u) = \frac{1}{[2(1-u)]^{\frac{1}{\eta_c+1}}} \quad \dots (6)$$

The mutation is needed to keep diversity in the population and prevent the solution to strike to a local minima. A polynomial mutation is utilized in the algorithm which uses a random number generated based upon the small mutation probability  $p_m$  is computed as  $1/n$ , where  $n$  shows the number of process variables.

$$c_k = p_k + (p_k^u - p_k^l)\delta_k \quad \dots (7)$$

Where  $c_k$  is the child,  $p_k$  is the parent and  $p_k^u$  is the upper bound on the parent component,  $p_k^l$  is the lower bound and  $\delta_k$  is small variation calculated from a polynomial distribution using the following equations:

$$\delta_k = (2r_k)^{\frac{1}{\eta_m+1}} - 1, \quad \text{If } r_k < 0.5 \quad \dots (8)$$

$$\delta_k = 1 - [2(1-r_k)]^{\frac{1}{\eta_m+1}}, \quad \text{If } r_k > 0.5 \quad \dots (9)$$

Where  $r_k$  is the mutation distribution index and  $\eta_m$  is a uniformly sampled random number between 0-1.

Initially, all the GA operators (population size, maximum number of generations, crossover probability and mutation probability) are selected based upon the feasible ranges and constraints. An initial population of  $n$  chromosomes is generated randomly. The population is then sorted depending upon non domination. Each solution is given a rank equal to its non-domination level i.e. each non dominant chromosome obtained in the first sorting is assigned rank 1 and included in the set F1. These non-dominant chromosomes having rank 1 are disregarded temporarily and sorting is again performed for remaining chromosomes. All non-dominant chromosomes obtained in the sorting are assigned rank 2 and so on till all the chromosomes are ranked. Selection is then done on the basis of the rank and the crowding distance. Then Simulated Binary Crossover and polynomial mutation are applied to create an offspring population of size  $N$ . A combined population having size  $2N$  is created. Finally population is sorted based upon non-domination. The solutions belonging to F1 are the best solutions in the current population. If size of F1  $< N$ , all the members of set F1 are selected for the new population. Subsequently, remaining members of population are selected from subsequent fronts on the basis of ranking and the crowding distance. The new population of size  $N$  is utilized for selection, crossover and mutation to create a new population of size  $N$ . This continues till sorting criteria is achieved. Figure 1 shows the flow chart of NSGA-II.

In the biodiesel engine work, performance of various biodiesels produced was evaluated in a single

cylinder, direct injection diesel engine using hybrid RSM-NSGA-II technique. The pareto optimum sets of solution were generated (depending upon the GA operators chosen). From these solutions, few solutions were selected based on rank and crowding distance. The performance (BSFC and BTE), combustion (Pmax) and emission (CO, NOx, HC and smoke opacity) parameters were the responses while engine input parameters were: Blending ratio, load torque and compression ratio of an engine running on biodiesel. The non-linear regression models were first created by applying RSM based on CCRD at optimum ranges of engine input parameters. The responses were then measured at suggested experiments.

The predicted regression models (BSFC, BTE, Pmax, CO, NOx, HC and smoke opacity) of each biodiesel fuelled engine were coupled with NSGA-II program and hybrid RSM-NSGA-II program was developed. Thus desired solutions were predicted by running this program by changing the GA operators until a pareto front is developed for various responses of the engine. Further confirmation experiments were conducted at few optimum solutions to check the authenticity of the predicted results.

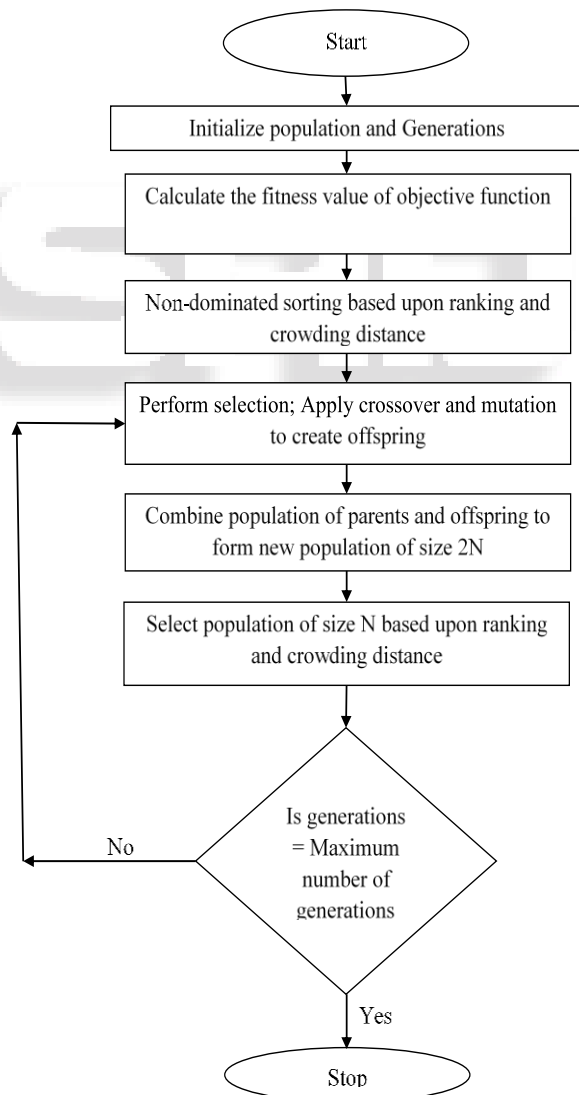


Fig. 1: NSGA-II flowchart

## II. CONCLUSION

- 1) NSGA-II helps in predicting many pareto optimal solutions so that end users can select any one of these solutions suggested depending upon their requirements.
- 2) NSGA-II is modified genetic algorithm and hence is better than other GA techniques applied in the various fields.

## REFERENCES

- [1] Deb, K., Pratap, A., Agarwal, S., & Meyarivan, T. (2002). A fast and elitist multiobjective genetic algorithm: NSGA-II. *Evolutionary Computation, IEEE Transactions on*, 6(2), 182-197.
- [2] Dhingra, S., Bhushan G., & Dubey, K. K. (2013a). Development of a combined approach for improvement and optimization of karanja biodiesel using response surface methodology and genetic algorithm. *Frontiers in Energy*, 7(5), 495–505
- [3] Dhingra, S., Bhushan G., & Dubey, K. K. (2013b). Performance and emission parameters optimization of mahua (madhuca indica) based biodiesel in direct injection diesel engine using response surface methodology. *Journal of Renewable and Sustainable Energy*, 5, 063117, DOI: 10.1063/1.4840155.
- [4] Dhingra, S., Bhushan G., & Dubey, K. K. (2014a). Understanding the interactions and evaluation of process factors for biodiesel production from waste cooking cottonseed oil by design of experiments through statistical approach. *Frontiers in Energy* (in press).
- [5] Dhingra, S., Bhushan G., & Dubey, K. K. (2014b). Multi-objective optimization of combustion, performance and emission parameters in a jatropha biodiesel engine using Non-dominated sorting genetic algorithm-II. *Frontiers of Mechanical Engineering*, 9(1), 81-94
- [6] Dhingra, S., Bhushan G., & Dubey, K. K. (2016a). Comparative performance analysis of jatropha, karanja, mahua and polanga based biodiesel engine using hybrid genetic algorithm. *Journal of Renewable and Sustainable Energy*, 8, 013103 , DOI:10.1063/1.4939513.
- [7] Dhingra, S., Bhushan G., & Dubey, K. K. (2016b). Validation and enhancement of waste cooking sunflower oil based biodiesel production by the trans-esterification process. *Energy Sources, part A*, 38(10), 1448-1454.
- [8] Dhingra, S., Dubey, K. K., & Bhushan, G. (2014c). A Polymath Approach for the Prediction of Optimized Transesterification Process Variables of Polanga Biodiesel. *Journal of the American oil Chemist's Society*, 91(4), 641-653
- [9] Dhingra, S., Dubey, K. K., & Bhushan, G. (2014d). Enhancement in Jatropha-based biodiesel yield by process optimization using design of experiment approach. *International Journal of Sustainable Energy*, 33 (4), 842-853.
- [10] Garg, M. P., Jain, A., & Bhushan, G. (2012). Modelling and multi objective optimization of process parameters of wire electrical discharge machining using non-dominated sorting genetic algorithm-II. *Proceedings of the Institution of Mechanical Engineers, Part B: Journal of Engineering Manufacture*.
- [11] Srinivas, N., & Deb, K. (1994). Multiobjective optimization using nondominated sorting in genetic algorithms. *Evol. Comput.*, 2(3), 221-248.