

Advance NSGA-II Algorithm for Solving MOO Problems

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Abstract: *Non-Dominated Sorting Genetic Algorithm (NSGA-II) is an algorithm known to resolve the Multi-Objective Optimization (MOO) problems. NSGA-II is one of the most extensively used algorithms for solving MOO problems. The present work is projected as expansion to the existing NSGA-II. In this method, different combination of crossover and mutation operator is used and the results are hence shown.*

Keywords: NSGA-II, Simulated Binary Crossover, Polynomial mutation, Parent-centric Blend Crossover, Power Mutation.

1. Introduction

The use of technology has increased rapidly over the years and so has increased the usage of software. This makes it important to maintain the quality of the software. Software testing is the most significant analytic quality assurance measure consuming at least 50% of software development cost [3]. The automation process of test data generation is a way that will reduce the time taken up by this task. Genetic Algorithm (GA) is used for this purpose.

A number of multi-objective evolutionary algorithms have been suggested earlier. Non-Dominated Sorting Genetic Algorithm (NSGA-II) is an algorithm given to solve the Multi-Objective Optimization (MOO) problems. It was proposed by Deb et.al in 2002 [4], advancing on the concept given by Goldberg 1989 [1]. NSGA-II is one of the most widely used algorithms for solving MOO problems. Rest of the paper is organized as follows: NSGA-II in second section, Proposed Methodology in third section, parameter setup and result in fourth section and conclusion in fifth section.

2. NSGA-II

2.1. NSGA-II

A number of multi-objective evolutionary algorithms have been suggested earlier such as Pareto Archived Evolution Strategy (PAES) & Strength Pareto Evolutionary Algorithm (SPEA), Non-Dominated Sorting GA (NSGA) etc. The Non-dominated Sorting Genetic Algorithm [4] NSGA-II uses a faster sorting procedure, an elitism preserving approach and a parameter less niching operator. The working is given as follows [6]:

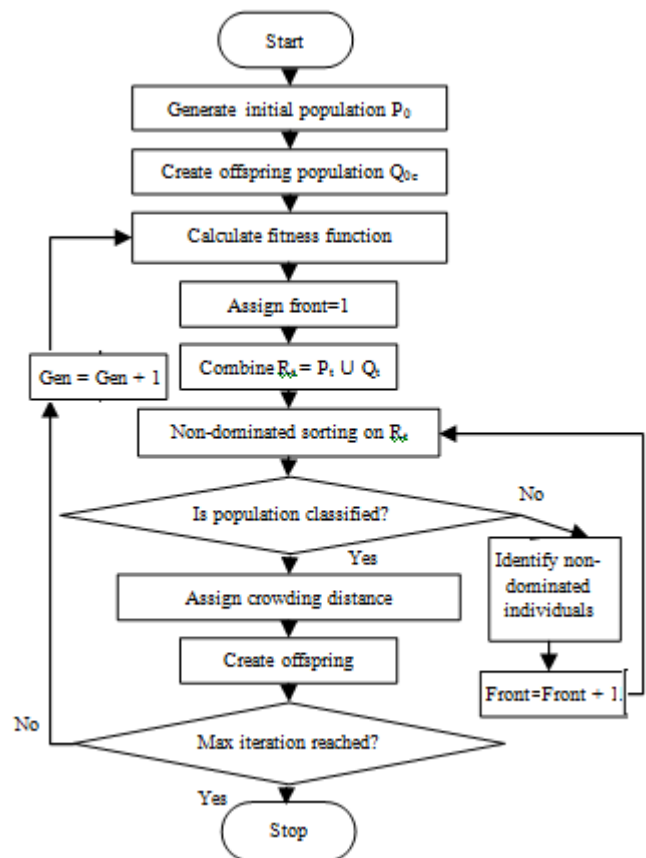


Figure 1: Working of NSGA-II

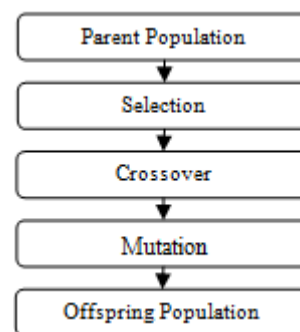


Figure 2: Creating offspring

2.2. Selection [7]

In original NSGA II *Binary tournament selection (BTS)* is used, where tournament is played between two solutions and better is selected and placed in mating pool. Two other solutions are again taken and another slot in mating pool is filled. It is carried in such a way that every solution can be made to participate in exactly 2 tournaments.

2.3. Crossover [8]

In NSGA II Simulated Binary Crossover (SBX) is used, which works with two parents solutions and create two offspring. The following step-by-step procedure is followed:

Step 1: Choose a random number $u_i \in [0, 1]$,

Step 2: Calculate using equation 1,

Step 3: Compute offspring using equation 2.

The mathematical formulation can be given as follows:

$$\beta_{q_i} = \begin{cases} (2u_i)^{\frac{1}{\eta_c+1}} & \text{if } u_i \leq 0.5; \\ \left(\frac{1}{2(1-u_i)}\right)^{\frac{1}{\eta_c+1}} & \text{otherwise.} \end{cases} \quad (1)$$

$$\begin{aligned} x_i^{(1,t+1)} &= 0.5[(1 + \beta_{q_i})x_i^{(1,t)} + (1 - \beta_{q_i})x_i^{(2,t)}], \\ x_i^{(2,t+1)} &= 0.5[(1 - \beta_{q_i})x_i^{(1,t)} + (1 + \beta_{q_i})x_i^{(2,t)}] \end{aligned} \quad (2)$$

Here,

u_i : Random number such that $u_i \in [0, 1]$,

η_c : Distribution index (Non-negative real number),

$x_i^{(1,t)}$ & $x_i^{(2,t)}$: Parent solutions,

$x_i^{(1,t+1)}$ & $x_i^{(2,t+1)}$: Offspring solutions.

2.4. Mutation [8]

In NSGA II Polynomial mutation is used, which mutates each solution separately, i.e. one parent solution gives one offspring after being mutated. The mathematical formulation can be given as:

$$y_i^{(1,t+1)} = x_i^{(1,t+1)} + (x_i^{(U)} - x_i^{(L)})\bar{\delta}_i \quad (3)$$

Where,

$$\bar{\delta}_i = \begin{cases} (2r_i)^{\frac{1}{(\eta_m+1)}} - 1 & \text{if } r_i < 0.5, \\ 1 - [2(1 - r_i)]^{\frac{1}{(\eta_m+1)}} & \text{if } r_i \geq 0.5. \end{cases} \quad (4)$$

Here,

r_i : Random number such that $u_i \in [0, 1]$,

η_m : Distribution index (Non-negative real number),

$x_i^{(1,t+1)}$: Parent solution,

$x_i^{(U)}$: Upper bound of parent solution,

$x_i^{(L)}$: Lower bound of parent solution,

$y_i^{(t+1)}$: Offspring solution.

2.5. Crowded Tournament Selection [6]

To get an estimation of the density of solutions close to a particular solution i in the population, we take the average of the two solutions on the either side of solution i along each of

the objective. This quantity d_i is the Crowding Distance. The following algorithm is used to calculate the crowding distance of each point in the set F .

Assignment procedure: Crowding-sort($F, <_c$)

Step 1: Call the number of solutions in F as $l = |F|$. For each i in the set, first assign $d_i = 0$.

Step 2: For each objective function $m = 1, 2, \dots, M$, sort the set in worse order of f_m . Find sorted indices vector $I_m = \text{sort}(f_m, >)$.

Step 3: For $m = 1, \dots, M$, assign a large distance to the edge solutions, $d_{I_1^m} = d_{I_l^m} = \infty$, and for all other solutions $j = 2$ to $(l - 1)$, assign:

$$d_{I_j^m} = d_{I_j^m} + \frac{f_m^{(I_{j+1}^m)} - f_m^{(I_{j-1}^m)}}{f_m^{\max} - f_m^{\min}} \quad (5)$$

3. Proposed Methodology

This section gives an overview of the proposed methodology. In the proposed work we replace the crossover and mutation used in original NSGA-II, Simulated Binary Crossover (SBX) and Polynomial Mutation (PM) are replaced by Parent-Centric Blend Crossover (PBX) [5] and Power Mutation (POM). Also the Binary tournament selection procedure is excluded in a hope to get better result.

3.1 Parent-Centric Blend Crossover

PBX or PBX- α is an extension to BLX- α [3] and is described as follows: Let us assume that $X = (x_1 \dots x_n)$ and $Y = (y_1 \dots y_n)$ ($x_i, y_i \in [a_i, b_i] \subset \mathfrak{R}, i = 1 \dots n$) are two real-coded variables that have been selected to apply the crossover operator to them. PBX- α generates (randomly) one of these two possible offspring:

$$Z_1 = (z_1^1 \dots z_n^1) \text{ or } Z_2 = (z_1^2 \dots z_n^2) \quad (6)$$

Where z_i^1 is a randomly (uniformly) chosen number from the interval $[l_i^1, u_i^1]$ with

$$l_i^1 = \max\{a_i, x_i - I * \alpha\} \text{ And } u_i^1 = \min\{b_i, x_i + I * \alpha\} \quad (7)$$

And z_i^2 is chosen from $[l_i^2, u_i^2]$ with

$$l_i^2 = \max\{a_i, y_i - I \text{ And } u_i^2 = \min\{b_i, y_i + I * \alpha\} \quad (8)$$

Where $I = |x_i - y_i|$.

3.2 Power Mutation

In [2] a new mutation operator called Power Mutation (POM) was introduced for real coded genetic algorithms. The following formula is used to form the mutated solution:

$$\hat{x} = \begin{cases} x - s(x - l), & \text{if } t < \alpha \\ x + s(u - x), & \text{if } t \geq \alpha \end{cases} \quad (9)$$

Where l and u are lower and upper bounds of the decision variable and α is a uniformly distributed random number between 0 and 1, and s is a random number.

3.3 Problem Statement

In [9] Schaffer gave two-objective problems:

$$SCH1 = \begin{cases} \text{Minimize } f_1(x) = x^2 \\ \text{Minimize } f_2(x) = (x - 2)^2 \end{cases} \quad (10) \quad -A \leq x \leq A.$$

Schaffer's second function, SCH2,

$$SCH2 = \begin{cases} \text{minimize } f_1(x) = \begin{cases} -x & \text{if } x \leq 1, \\ x - 2 & \text{if } 1 < x \leq 3, \\ 4 - x & \text{if } 3 < x \leq 4, \\ x - 4 & \text{if } x > 4, \end{cases} \\ \text{minimize } f_2(x) = (x - 5)^2 \\ -5 \leq x \leq 10 \end{cases} \quad (11)$$

4. Parameter Setup and Results

In this paper parameter settings are as; Population size = 20, Maximum number of cycles (MCN) = 100, $\alpha = 0$, $s = 0$.

Table 1: Time taken in milliseconds

Problem	Algorithm	With BTS	Without BTS
SCH1	PBX-POM	133	140
SCH2	PBX-POM	125	150

- With Binary Tournament Selection
 - Without Binary Tournament Selection
- Pareto-Optimal Set

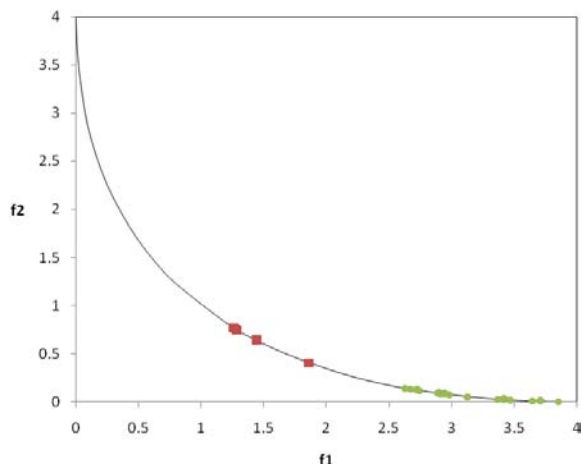


Figure 3: SCH2 Generation 100 PBX-POM

5. Other recommendations

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