

Evolutionary Multiobjective Optimization Software: NSGAII

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January 10, 2024

Abstract

This report investigates the application of the nondominated sorting genetic algorithm (NSGA-II) to solve the ZD4 problem using multiobjective evolutionary optimization. The study explores various combinations of parameters, specifically population size and mutation rate, to analyze their impact on algorithm convergence. The evaluation is based on the hypervolume metric, providing insights into the balance between exploration and exploitation in the optimization process.

1 Introduction

Multiobjective evolutionary algorithms (MOEAs) play a crucial role in solving complex optimization problems with multiple conflicting objectives. This report focuses on the NSGA-II, a nondominated sorting-based MOEA that addresses computational complexity, nonelitism, and sharing parameter issues commonly associated with such algorithms.

1.1 Problem Definition

The NSGA-II algorithm will be employed to tackle the ZD4 problem, and for each combination of parameters tested, figures depicting the non-dominated final front and convergence curves of the hypervolume indicator will be presented.

n	Variable Bounds	Objective Functions	Optimal Solutions
10	$x_1 \in [0, 1],$ $\forall i \in \{2, \dots, n\} : x_i \in [-5, 5]$	$f_1(x) = x_1,$ $f_2(x) = g(x) \left(1 - \sqrt{\frac{x_1}{g(x)}}\right),$ $g(x) = 1 + 10(n - 1) + \sum_{i=2}^n (x_i^2 - 10 \cos(4\pi x_i))$	$x_1 \in [0, 1],$ $\forall i \in \{2, \dots, n\} : x_i = 0$

Table 1: Problem definition

1.2 Experimental Setup

The NSGA-II evolutionary multiobjective optimization software will be employed to solve the ZD4 problem. The execution will involve the testing of different parameters, ensuring the same number of fitness function evaluations in each execution (47,000 evaluations). The random seed for reproducibility will be set to 0.92.

1.2.1 Input File definition

In this file, which is provided as input, it is possible to see all the parameters that define the previously explained problem and the modes of execution. Of all these parameters, only the parameters: popsize, ngen, pmut have been modified.

Line	Value	Parameter
1	100	popsize: Population size (appropriate multiple)
2	200	ngen: Number of generations
3	2	nobj: Number of objectives
4	0	ncon: Number of constraints
5	10	nvar: Number of real variables
6	[0, 1]	min-max_realvar[0]: Range of the value of the first variable
7-15	[-5, 5]	min-max_realvar[1-9]: Range of the value for variables 1 to 9
16	0.9	pcross: Probability of crossover
17	0.1	pmut: Probability of mutation
18	15	eta_c: distribution index for real variable SBX crossover
19	20	eta_m: distribution index for real variable polynomial mutation
20	0	nbin: number of binary variables
21	1	choice: option to display the data realtime using gnuplot
22	1	obj1, obj2, obj3: index of objectives to be shown on x, y and z axes respectively
23	2	angle1, angle2: polar and azimuthal angle required for location of eye

Table 2: Input file

1.3 Parameter Exploration

The study will explore variations in population size and mutation rate to find optimal combinations that yield good results in terms of hypervolume convergence.

To determine the probability of mutations, it is advisable to use $1/\text{number of variables}$, in this case $1/10$.

Mutation Rate: 0.05, 0.10, 0.15

Population Size:

- 40 individuals, 235 generations
- 100 individuals, 470 generations
- 200 individuals, 1175 generations

2 Results and Discussion

Figures detailing the comparison of hypervolume convergence will be presented, accompanied by an explanation and justification of the best parameter sets. The focus will be on achieving a balance between exploration and exploitation.

The following table shows the results of comparing various parameters. They are represented as rating pairs with values between 1 and 3, where 1 indicates the best. The first value corresponds to **Population Size**, while the second value corresponds to **Mutation Rate**.

Parameters	Population Size				
Mutation Rate	PS°, MR°	40	100	200	Best PS
	0.05	1°, 2°	2°, 1°	3°, 1°	40
	0.10	1°, 1°	2°, 3°	3°, 2°	40
	0.15	1°, 3°	2°, 2°	3°, 3°	40
	Best MR	0.10	0.05	0.05	40, 0.10

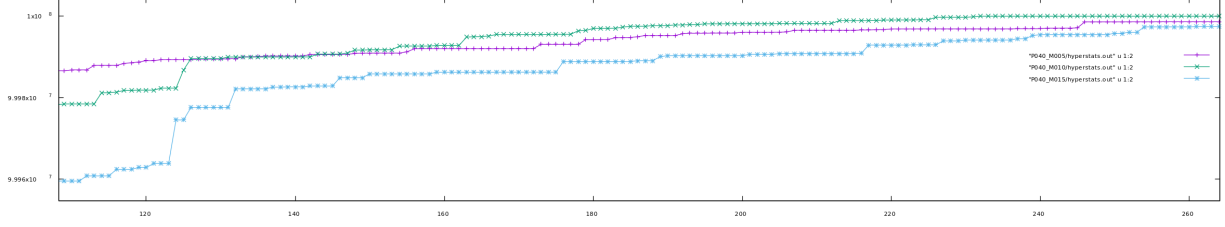


Figure 1: Population Size: 40

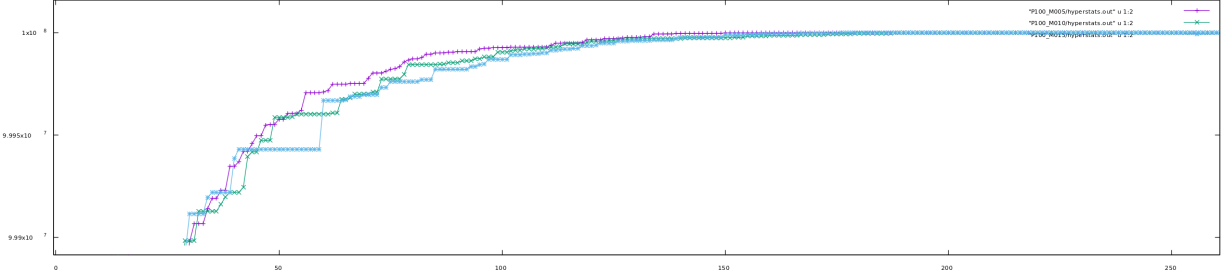


Figure 2: Population Size: 100

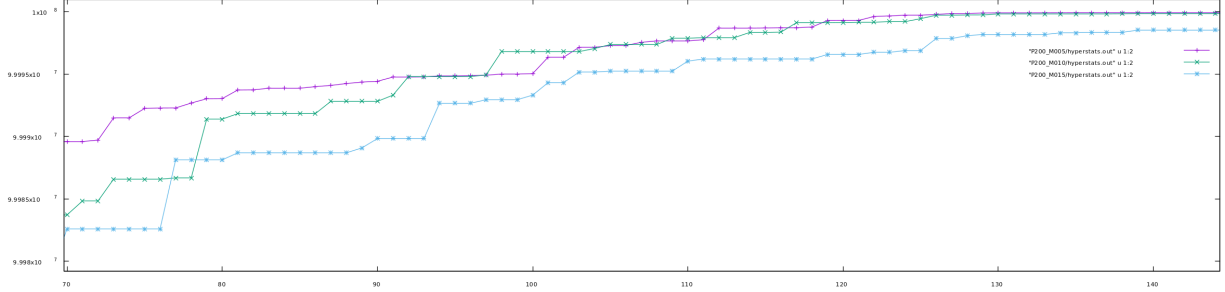


Figure 3: Population Size: 200

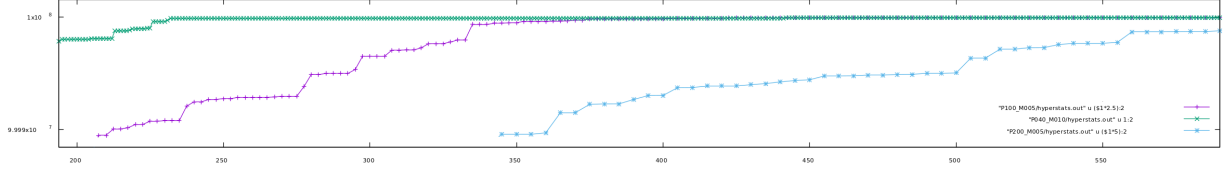


Figure 4: Best Mutation Rate per Population Size

In Figure 4, the comparison is shown for the best **Mutation Rate** for each **Population Size**.

- PS: 40, MR: 0.10
- PS: 100, MR: 0.05
- PS: 200, MR: 0.05

The combination of a **Population Size** of 40 individuals and a **Mutation Rate** of 0.10 turns out to be the best.

2.1 Final generation's non-dominated solution sets

For each Population Size is possible to see 3 different Figure (for each Mutation Rate) of the final generation's non-dominated solution set. It's an approximate finite representation of the optimal solutions forming the Pareto frontier.

The quantity of points depicted is influenced by the population size, meaning that experiments with larger populations yield a denser and more continuous non-dominated frontier.

Population Size of 40 individuals

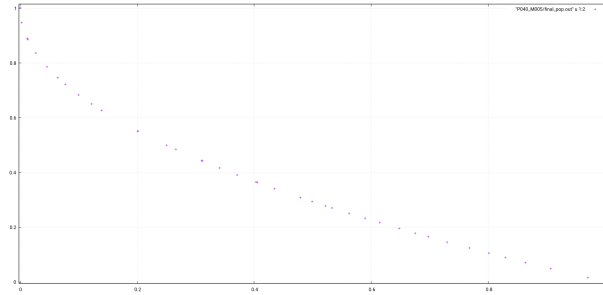


Figure 5: Mutation Rate: 0.05

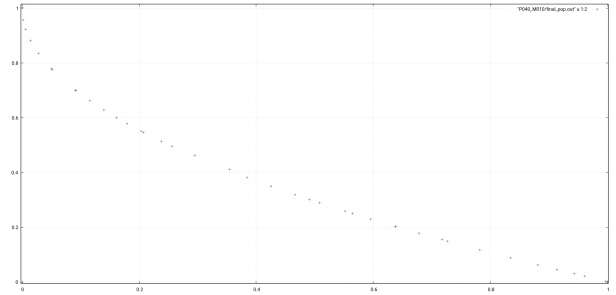


Figure 6: Mutation Rate: 0.10

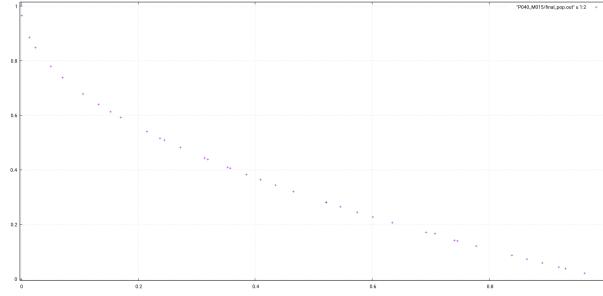


Figure 7: Mutation Rate: 0.15

Population Size of 100 individuals

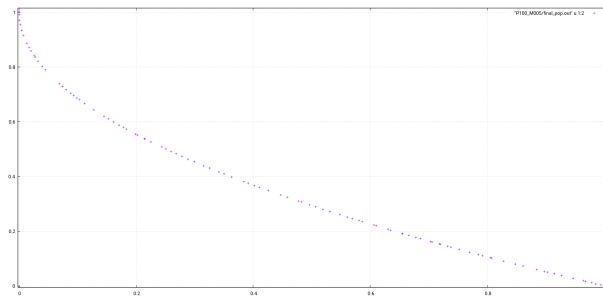


Figure 8: Mutation Rate: 0.05

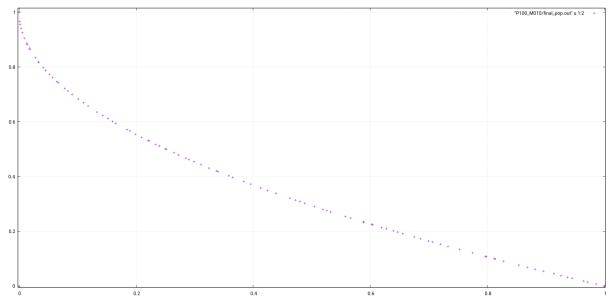


Figure 9: Mutation Rate: 0.10

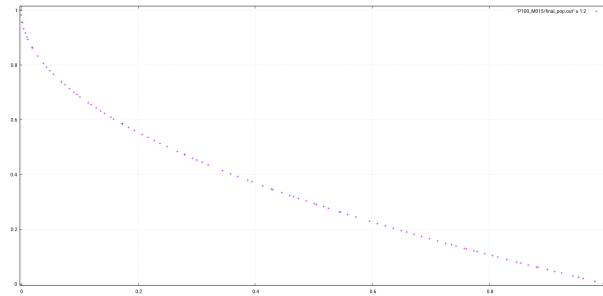


Figure 10: Mutation Rate: 0.15

Population Size of 200 individuals

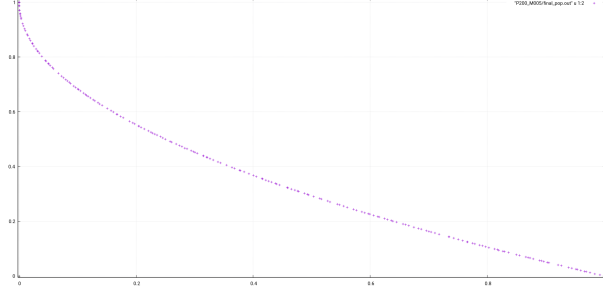


Figure 11: Mutation Rate: 0.05

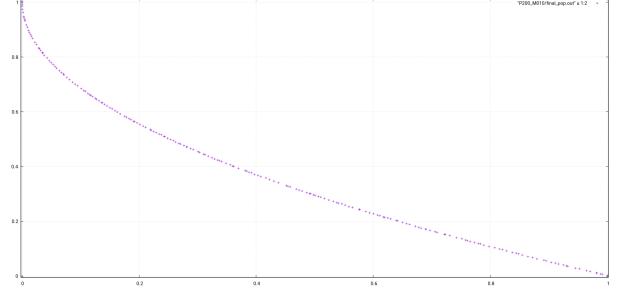


Figure 12: Mutation Rate: 0.10

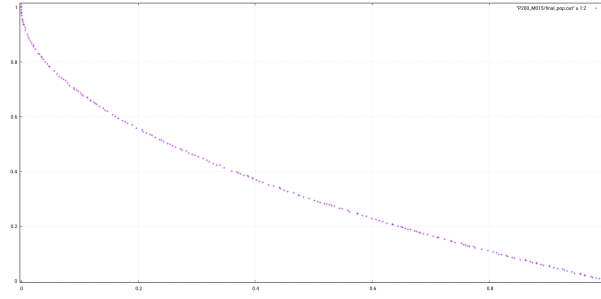


Figure 13: Mutation Rate: 0.15

Conclusion

In this report, the application of the nondominated sorting genetic algorithm (NSGA-II) to solve the ZD4 problem through multiobjective evolutionary optimization was thoroughly explored. The impact of varying population sizes and mutation rates on the algorithm's convergence performance, with a specific focus on achieving a balance between exploration and exploitation, was examined.

A population size of 40 individuals coupled with a mutation rate of 0.10 yielded the most favorable results. These parameters resulted in a convergence pattern that effectively balanced exploring the solution space and exploiting promising regions.