

Evolutionary Multiobjective Optimization Software: NSGAII

Daniel Amadori

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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 minimum content of the report includes the problem definition and name, along with the mathematical equation of the assigned problem. 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.

1.3 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, 100, 200 individuals

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

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

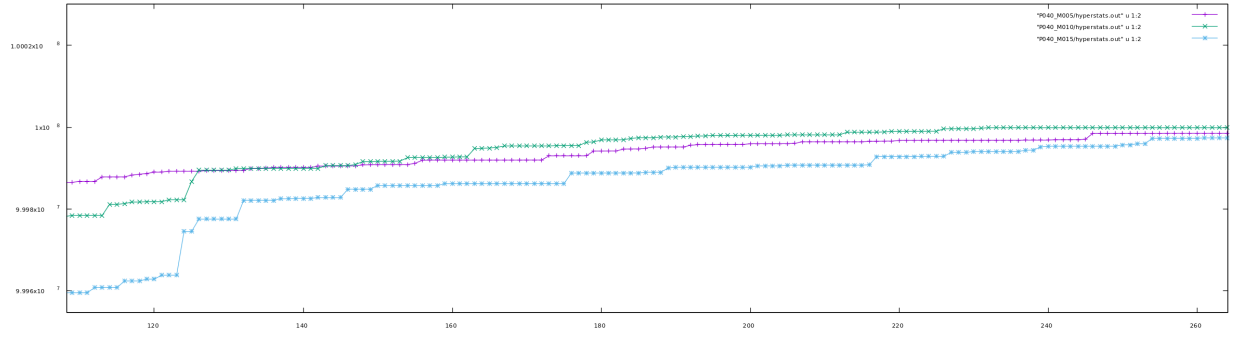


Figure 1: Population Size: 40

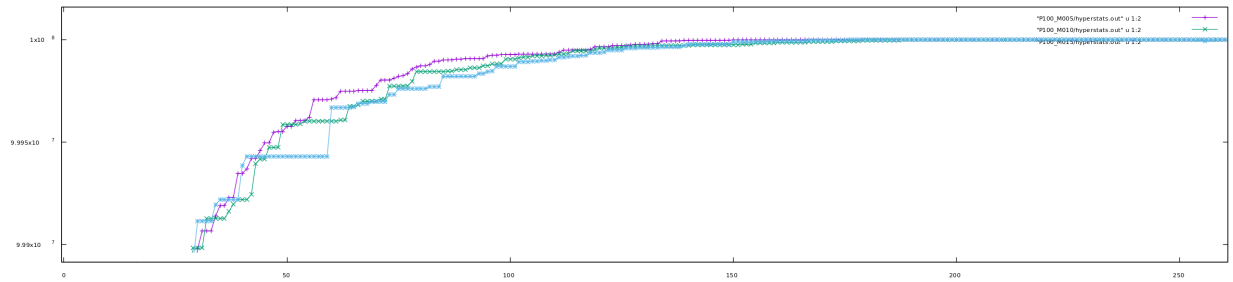


Figure 2: Population Size: 100

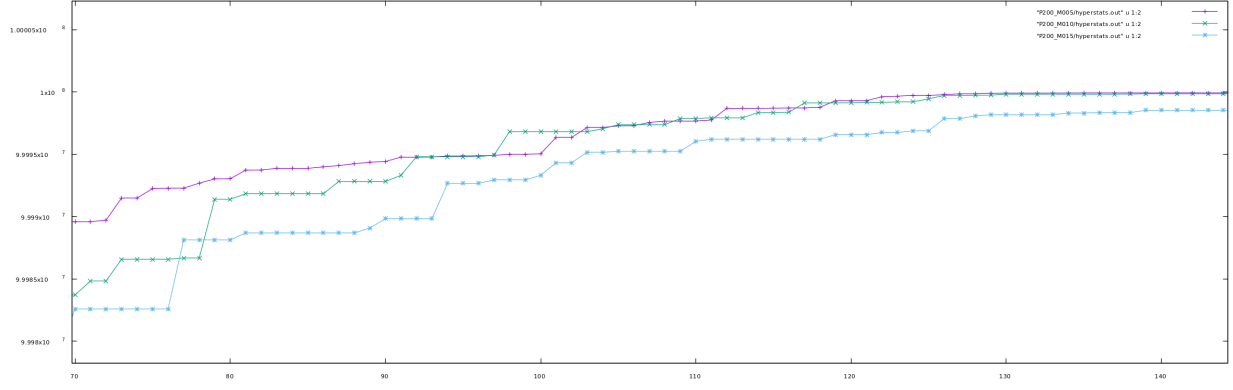


Figure 3: Population Size: 200

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

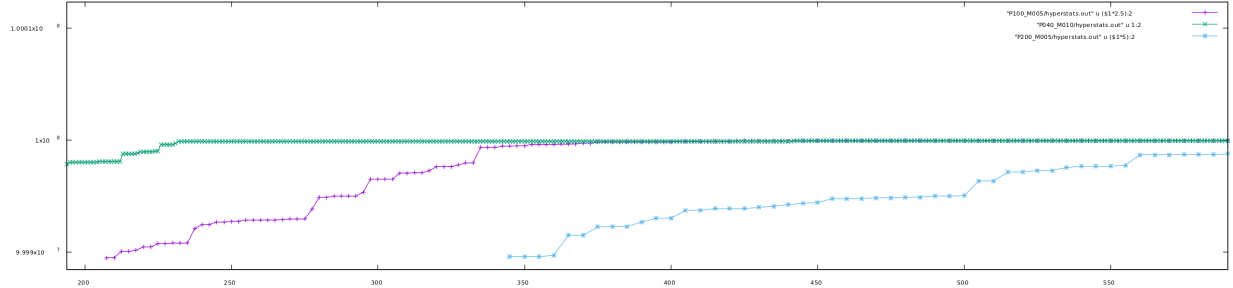


Figure 4: Best Mutation Rate per Population Size

Conclusion

In this study, the application of the nondominated sorting genetic algorithm (NSGA-II) to solve the ZD4 problem through multiobjective evolutionary optimization was thoroughly explored.

The investigation delved into 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. It was found that a population size of 40 individuals coupled with a mutation rate of 0.10 yielded the most favorable results. The choice of these parameters resulted in a convergence pattern that struck an effective balance between exploring the solution space and exploiting promising regions.