LABORATORY 3
GROUP 5

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INTRODUCTION

In this laboratory, we implemented a genetic algorithm to optimize the **Styblinski–Tang function**, a well-known test function in continuous optimization. It is characterized by a **non-convex landscape** and **multiple local minima**, making it a suitable benchmark for evaluating the performance of global optimization techniques.

The goal was to find the global minimum of the Styblinski–Tang function in two dimensions:

$$f(x,y) = \frac{1}{2}\left(\frac{x^4}{2} - 16x^2 + 5x + \frac{y^4}{2} - 16y^2 + 5y\right)$$

The known global minimum of the function is at (x,y)≈(−2.903,−2.903)(x, y), where the function value is approximately f(x,y)≈−78.332

We applied a genetic algorithm using **Rank Selection** to choose parents, **Gaussian mutation**, and **random interpolation-based crossover**. Importantly, mutation and crossover were applied only to a portion of the population, while the rest was preserved. The population was initialized with values x,y∈[−5,5]x, y \in [-5, 5]x,y∈[−5,5].

IMPLEMENTATION

The genetic algorithm was implemented in Python, using a modular structure in genetic_algorithm.py. The algorithm follows the classic structure: initialize → evaluate → select → crossover → mutate → replace.

Below is a breakdown of the key components with relevant code snippets and explanations.

1. **Population Initialization:** The population is initialized randomly within the specified range (in this case, [−5,5][-5, 5][−5,5] for both x and y):

```
population = [
    (random.uniform(*x_range), random.uniform(*y_range))
    for x in range(self.population_size)
]
```

This generates a list of individuals (2D vectors) with uniformly distributed random values.

2. **Evaluate the Population:** Each individual's fitness is determined by the function value (lower is better).

```python
def evaluate_population(self, population):
    fitness = []
    for x in population:
        fitness.append(styblinski_tang_2d(*x))
    return fitness
```

3. **Selection:** We use fitness-proportional selection, where better individuals (lower values) get higher selection weights.

```python
def selection(self, population, fitness_values):
    # sort indices of the population by fitness (lowest fitness is best)
    sorted_indices = np.argsort(fitness_values)
    max_weight = len(population)
    #creating array of length max weights
    weights = [0] * max_weight
    for rank, idx in enumerate(sorted_indices):
        weights[idx] = max_weight - rank
    # normalize
    weights = np.array(weights)
    probabilities = weights / np.sum(weights)
    # how many are selected for reproduction
    num_selected = int(self.population_size * self.crossover_rate)
    # randomly select
    selected_indices = np.random.choice(max_weight, size=num_selected, replace=True, p=probabilities)
    return [population[i] for i in selected_indices]
```

4. **Crossover:** Pair parents to create children by blending their coordinates using a random mixing factor α.

```python
def crossover(self, parents):
    np.random.shuffle(parents)
    children = []
    num_parents = len(parents)
    # if there are odd parents, duplicate the random parent
    if num_parents % 2:
        random_index = np.random.randint(num_parents)
        random_parent = parents[random_index]
        parents = np.concatenate([parents, [random_parent]])
        num_parents += 1
    for i in range(0, num_parents, 2):
        p1 = np.array(parents[i])
        p2 =  np.array(parents[i + 1])
        alpha = np.random.rand()
        # child = parent1 * random(x) + parent2 * (1-random(x))
        child = alpha * p1 + (1 - alpha) * p2
        children.append(child)
    return np.array(children)
```

5. **Mutation:** With a certain chance, we randomly tweak each coordinate with Gaussian noise.

```python
def mutate(self, individuals):
    for i in range(len(individuals)):
        #for each x and y
        for j in range(2):
            # decide by random if a child is mutated
            if np.random.rand() < self.mutation_rate:
                # a random gaussian mutation to a child
                individuals[i, j] += np.random.normal(0, self.mutation_strength)
                # don't let the values out of range
                x_range, y_range = init_ranges[styblinski_tang_2d]
                if j == 0:
                    individuals[i, j] = np.clip(individuals[i, j], x_range[0], x_range[1])
                elif j == 1:
                    individuals[i, j] = np.clip(individuals[i, j], y_range[0], y_range[1])
    return individuals
```

6. **Evolution loop:** Each generation, we: Evaluate current population, Select parents, Generate and mutate children, Replace part of the population with children

```
for generation in range(self.num_generations):
    fitness_values = self.evaluate_population(population)

    best_idx = np.argmin(fitness_values)
    best_solutions.append(population[best_idx])
    best_fitness_values.append(fitness_values[best_idx])
    average_fitness_values.append(np.average(fitness_values))

    parents_for_reproduction = self.selection(population, fitness_values)
    children = self.crossover(parents_for_reproduction)
    children = self.mutate(children)

    # MODIFY THIS
    # make is so that each children is replacing a random individual in a population
    indices = np.random.choice(range(len(population)), size=len(children), replace=False)
    for i, child in zip(indices, children):
        population[i] = child
```

Results

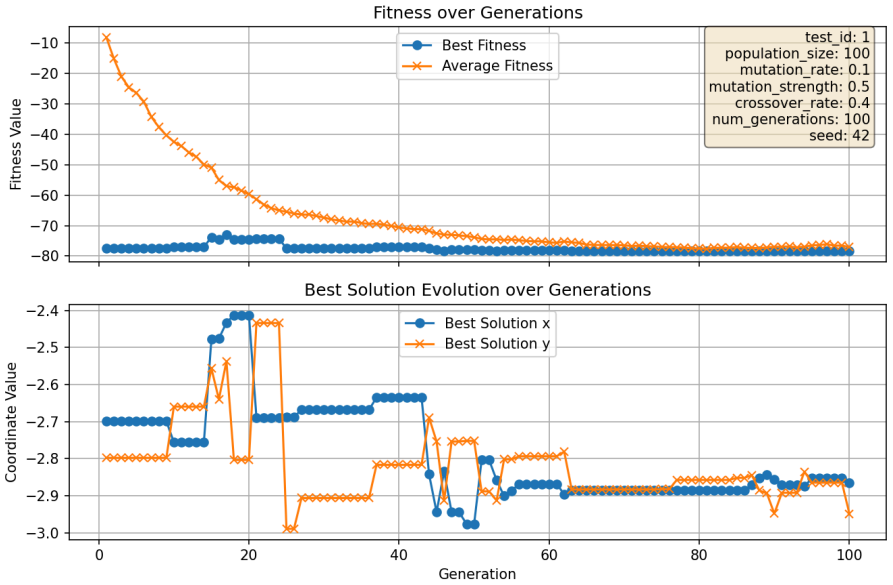
Finding the best parameters:
We needed to create a metric of how well the algorithm converged, and how fast. We check if the average fitness value of a given generation is close enough to the real global minimum of Styblinski-Tang function in 2D. We decided on those values:

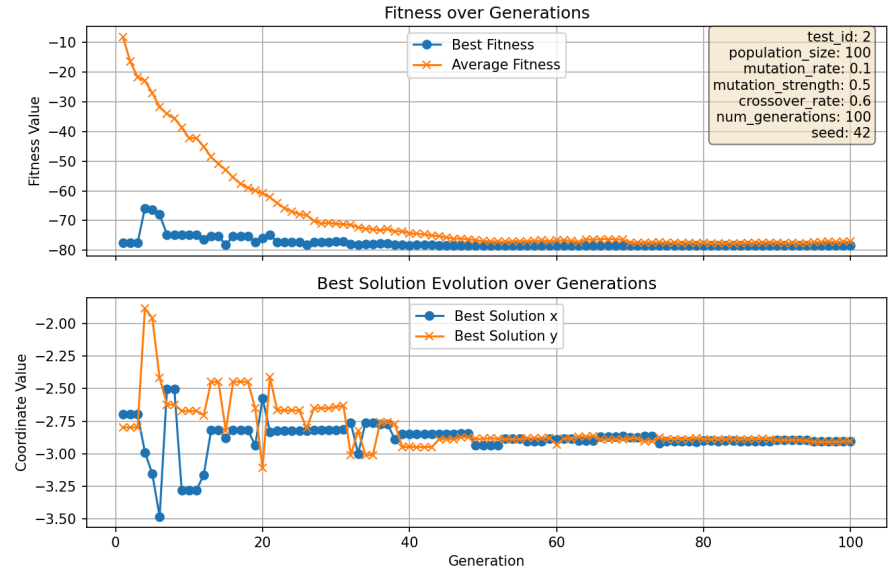
```
#some approximation of global fitness
styblinski_tang_global_minimum = (-78.3323)
# allowed closeness to the global minimum
tolerance = 0.03 * styblinski_tang_global_minimum
```

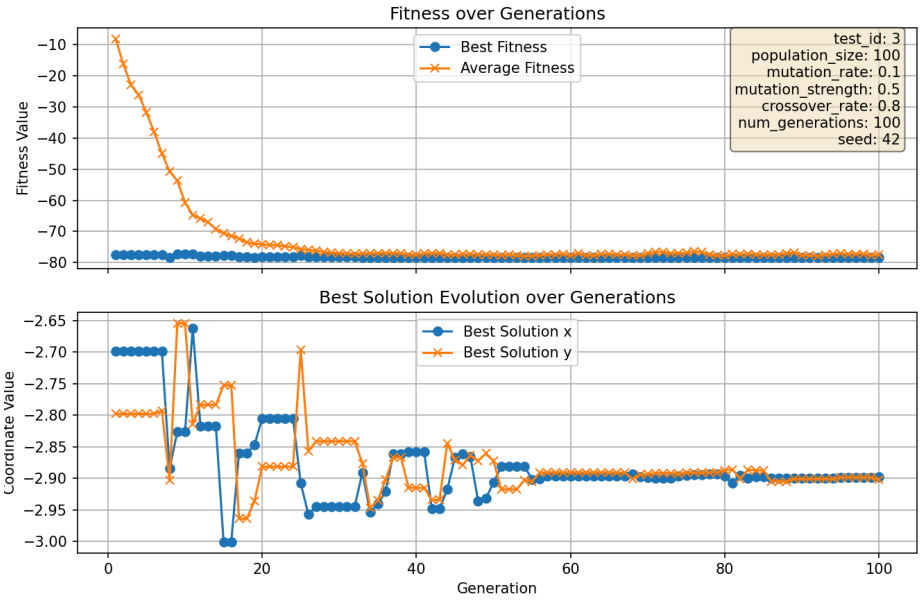
Below there are results of some parameter fine tuning, the last column is after how many generations, the algorithm converged to the global minimum with 3% closeness. Number of generations and population size doesn't matter in this test, they are 1000, and 1000:

ID	MUTATION RATE	MUTATION STRENGTH	CROSSOVER RATE	**CONVERGENCE**
1	0.25	0.3	0.5	46
2	0.08	0.5	0.7	45
3	0.12	0.6	0.7	38
4	0.29	0.4	0.8	36
5	0.5	0.2	0.8	28

Crossover Rate tests:







ID	MUTATION RATE	MUTATION STRENGTH	CROSSOVER RATE	CONVERGENCE
1	0.1	0.5	0.4	62
2	0.1	0.5	0.6	46
3	0.1	0.5	0.8	26

Effect of Crossover Rate

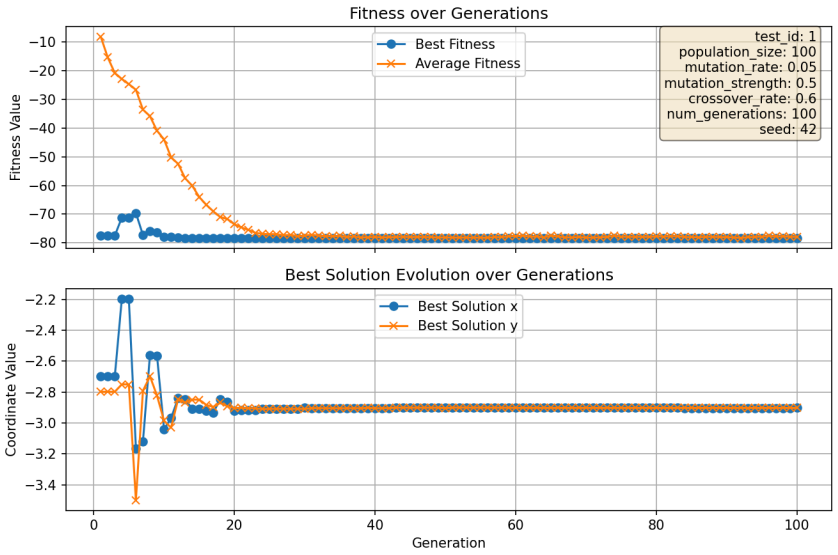
We tested three scenarios:

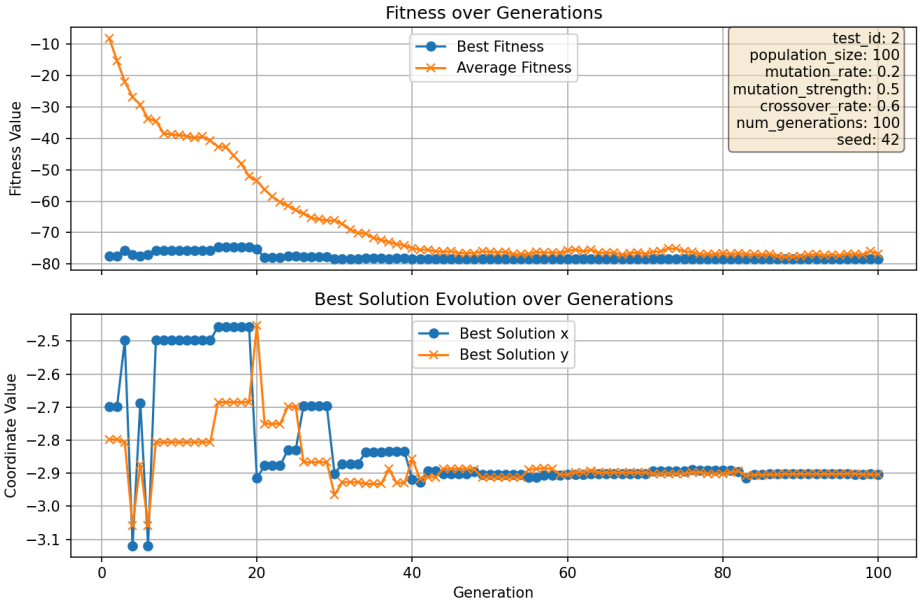
- Low crossover rate (0.4)
- Medium crossover rate (0.6)
- High crossover rate (0.8)

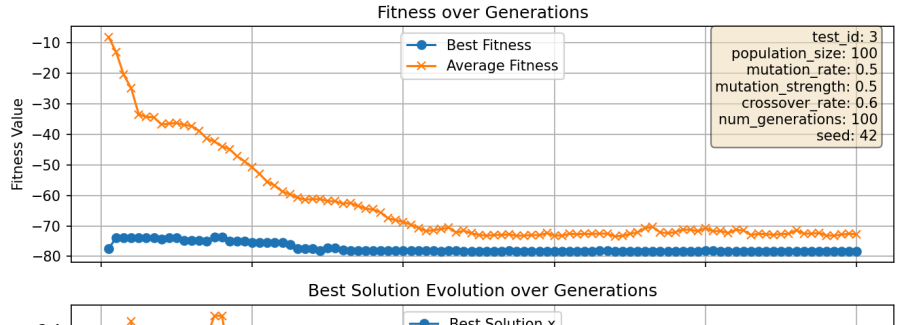
Summary:
Increasing the crossover rate generally improved the convergence speed, as more individuals participated in generating new offspring.

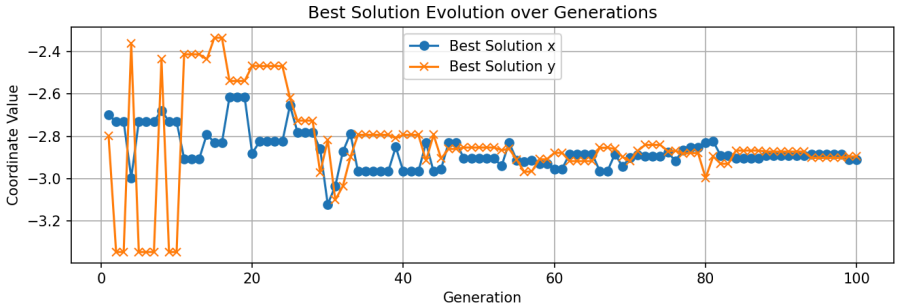
- At low crossover rates, the algorithm preserved too much of the current population, slowing down progress.
- At medium rates, there was a healthy balance between preservation and exploration.
- At high rates, the algorithm explored the search space aggressively, often reaching near-optimal solutions faster

Mutation Rate tests:









ID	MUTATION RATE	MUTATION STRENGTH	CROSSOVER RATE	CONVERGENCE
1	0.05	0.5	0.6	23
2	0.2	0.5	0.6	44
3	0.5	0.5	0.6	-

Effect of Mutation Rate

We tested:

- Low mutation rate (0.05)

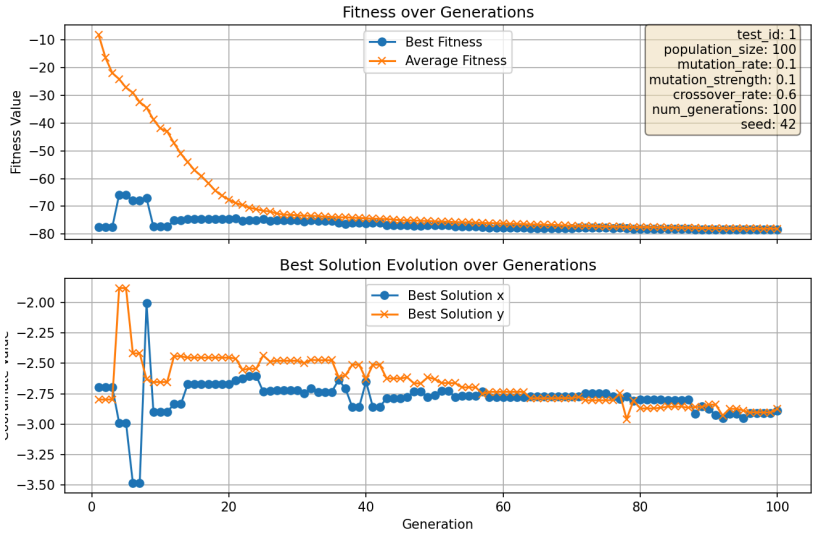
- Medium mutation rate (0.2)
- High mutation rate (0.5)

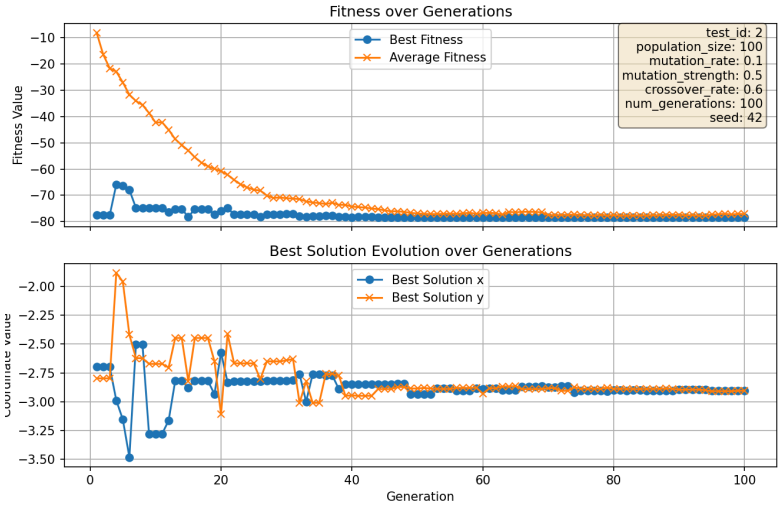
Summary:

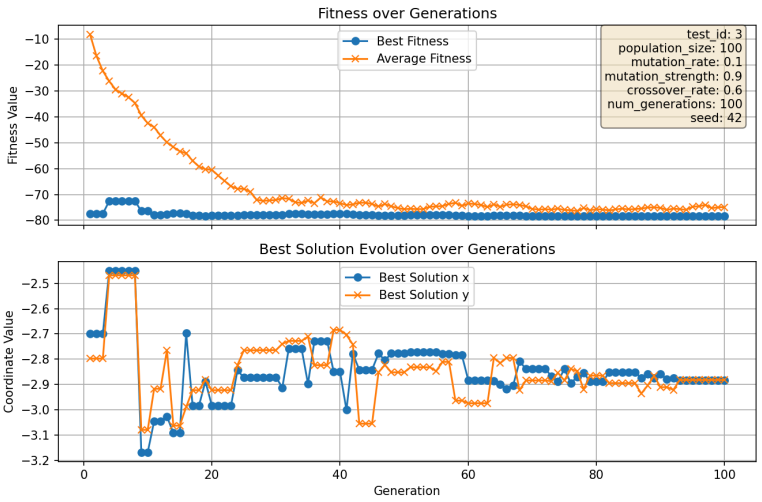
Mutation rate directly influenced the diversity of the population.

- Low mutation rates led to fast convergence, but may be stuck in local minimum
- Medium rates offered a good balance, allowing the algorithm to escape local optima
- High mutation leads to overshooting, and not being able to find the exact minimum, it didn't converge in 100 generations

Mutation Strength tests:







ID	MUTATION RATE	MUTATION STRENGTH	CROSSOVER RATE	CONVERGENCE
1	0.1	0.1	0.6	57
2	0.1	0.5	0.6	46
3	0.1	0.9	0.6	75

Effect of Mutation Strength

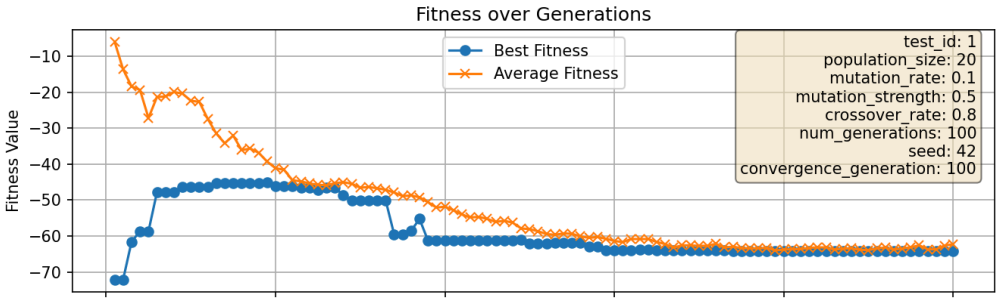
We tested:

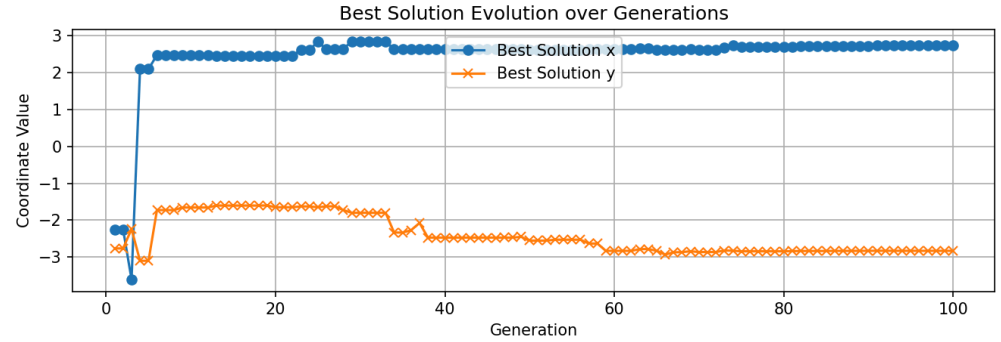
- Low mutation strength (0.1)
- Medium mutation strength (0.5)
- High mutation strength (0.9)

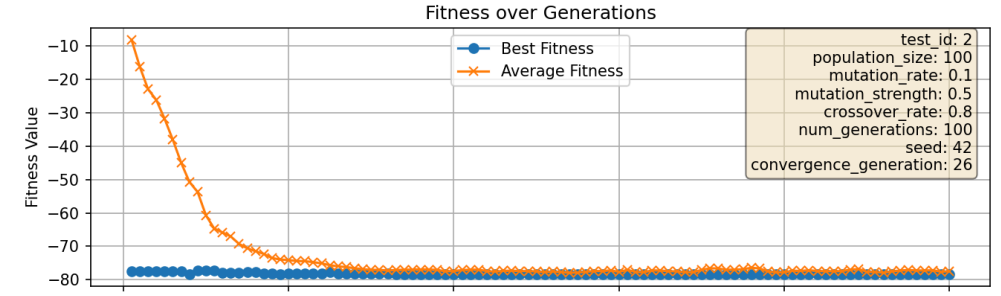
Summary:
Mutation strength controls how big the changes are when a gene is mutated.

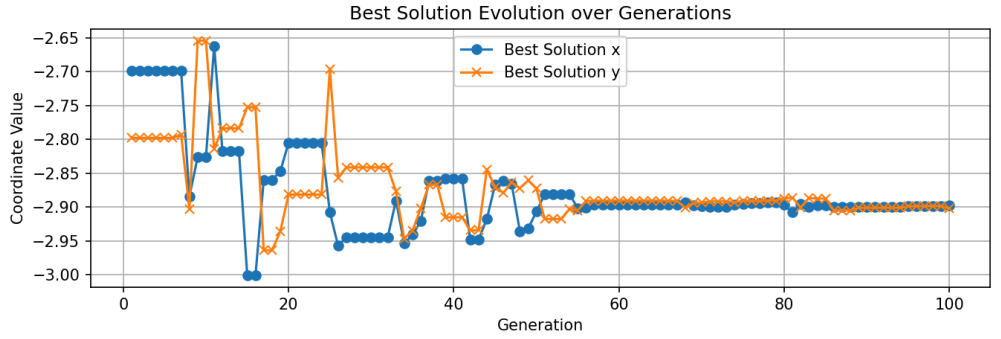
- With low strength, changes are slow and it is ineffective to escape local minimum
- Medium strength helped the algorithm balance local search and broader exploration.
- High strength led to larger jumps which can escape local minima but also overshoot

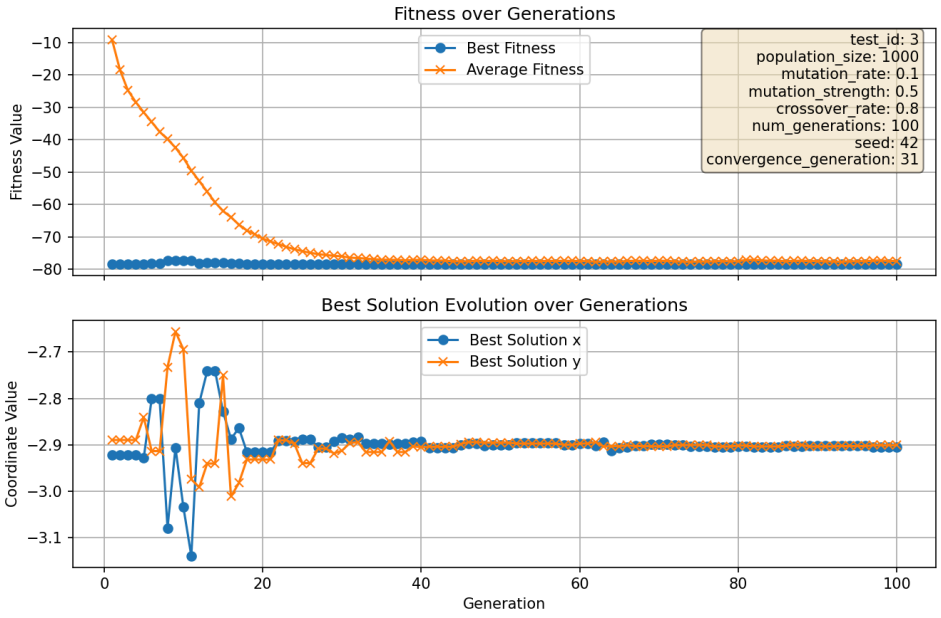
Population size modification

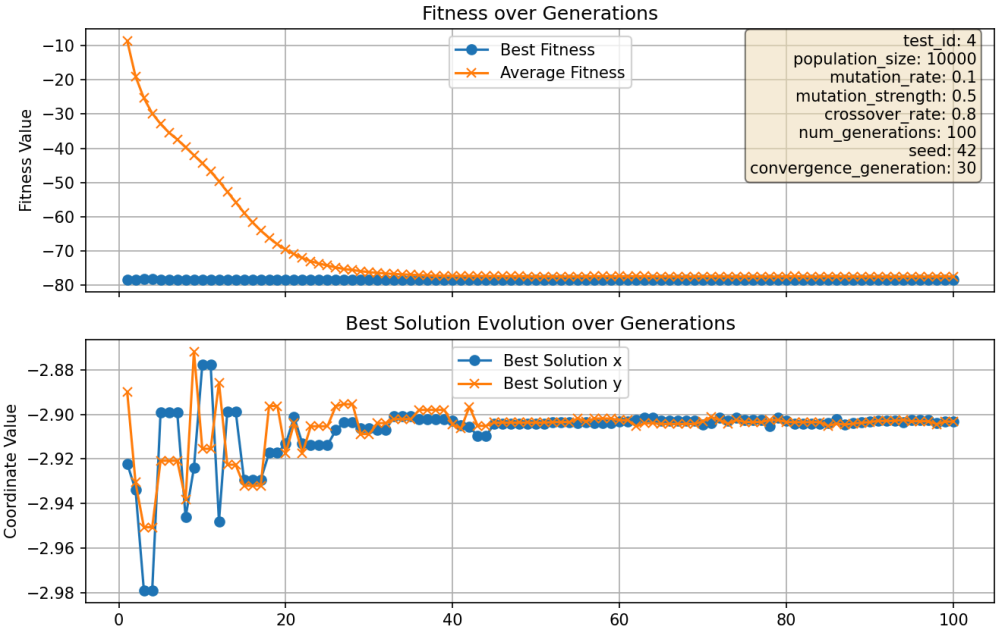

Fitness over Generations
Best Fitness
Average Fitness
test_id: 1
population_size: 20
mutation_rate: 0.1
mutation_strength: 0.5
crossover_rate: 0.8
num_generations: 100
seed: 42
convergence_generation: 100
Fitness Value


Best Solution Evolution over Generations
Best Solution x
Best Solution y
Coordinate Value
Generation


Fitness over Generations
Best Fitness
Average Fitness
test_id: 2
population_size: 100
mutation_rate: 0.1
mutation_strength: 0.5
crossover_rate: 0.8
num_generations: 100
seed: 42
convergence_generation: 26
Fitness Value


Best Solution Evolution over Generations
Best Solution x
Best Solution y
Coordinate Value
Generation





ID	POPULATION SIZE	MUTATION RATE	MUTATION STRENGTH	CROSSOVER RATE	CONVERGENCE
1	20	0.1	0.5	0.8	-
2	100	0.1	0.5	0.8	26
3	1000	0.1	0.5	0.8	31
4	10000	0.1	0.5	0.8	30
5	50000	0.1	0.5	0.8	31

Summary
Population size around 100–1000 gave fastest convergence (26–31 generations). Very large sizes (10000–500000) didn’t improve results. Small size (20) failed to converge. Best balance at 100–1000.

Conclusion

Our experiments confirmed that genetic algorithms can effectively handle the challenges of optimizing non-convex functions with many local minima. However, the algorithm's performance is highly sensitive to parameter tuning, particularly the balance between exploration (via mutation) and exploitation (via selection and crossover).

Observations

- Medium crossover rate gives the best results. It balances keeping good solutions and trying new ones.
- Low crossover rate makes the algorithm slow. High crossover rate can lose good solutions too fast.
- Medium mutation rate helps escape local optima while still improving the solution.
- Low mutation rate can get stuck in bad areas. High mutation rate makes the results too random.
- Medium mutation strength makes helpful changes without jumping too far.
- Low mutation strength changes too little. High mutation strength changes too much and can make the search unstable.