

A dark blue vertical bar runs down the left side of the page. A blue arrow points to the right from this bar, containing the date.

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AI LAB ASSIGNMENT 1B

Several thin, curved lines in dark blue and light grey originate from the bottom left corner and sweep upwards and to the right.

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1. הוסיפו למנוע תמיכה בשיטות הבחירה שונות: parent selection

a. RWS + Scaling

b. SUS + Scaling

c. RANKING וטורניר דטרמיניסטי עם פרמטר K

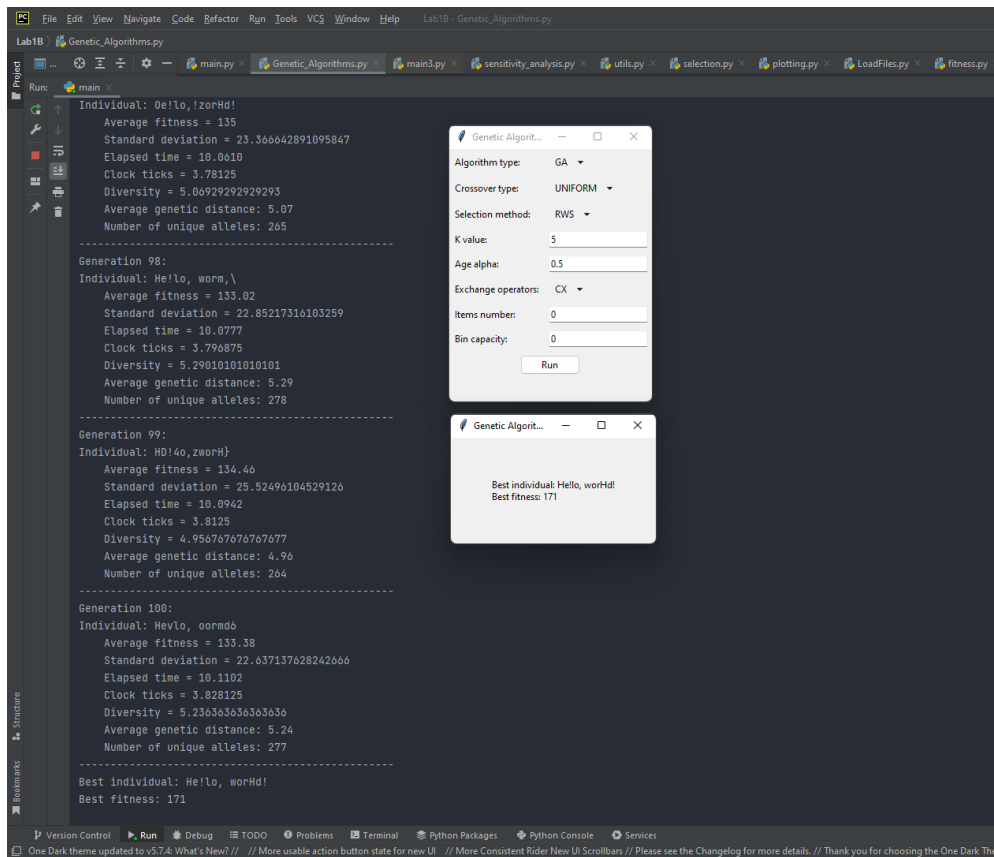
```
def winsorize(data, percentile):
    lower_bound = np.percentile(data, percentile)
    upper_bound = np.percentile(data, 100 - percentile)
    data = np.where(data < lower_bound, lower_bound, data)
    data = np.where(data > upper_bound, upper_bound, data)
    mean = np.mean(data)
    std = np.std(data)
    data = (data - mean) / std
    return data
```

```
# Modify the scale_fitness function to use the winsorize function
def scale_fitness(fitnesses, generation, max_generations):
    # Calculate the percentile based on the current generation
    start_percentile = 10
    end_percentile = 5
    percentile = start_percentile - (generation / max_generations) * (start_percentile - end_percentile)

    # Apply the winsorize function with the dynamic percentile
    scaled_fitnesses = winsorize(np.array(fitnesses), percentile)
    return scaled_fitnesses
```

In the provided code, the **scale_fitness** function calculates the dynamic percentile based on the current generation number and the maximum number of generations. As the generation number increases, the percentile decreases from the start percentile (e.g., 10) to the end percentile (e.g., 5). This way, the scaling process adapts to the state of the population, allowing the genetic algorithm to balance exploration and exploitation as it evolves.

```
# Roulette Wheel Selection (RWS) with scaling
def roulette_wheel_selection(population, fitnesses, scaled_fitnesses):
    total_fitness = sum(scaled_fitnesses)
    r = random.uniform(0, total_fitness)
    partial_sum = 0
    for i, individual in enumerate(population):
        partial_sum += scaled_fitnesses[i]
        if partial_sum >= r:
            return individual
```



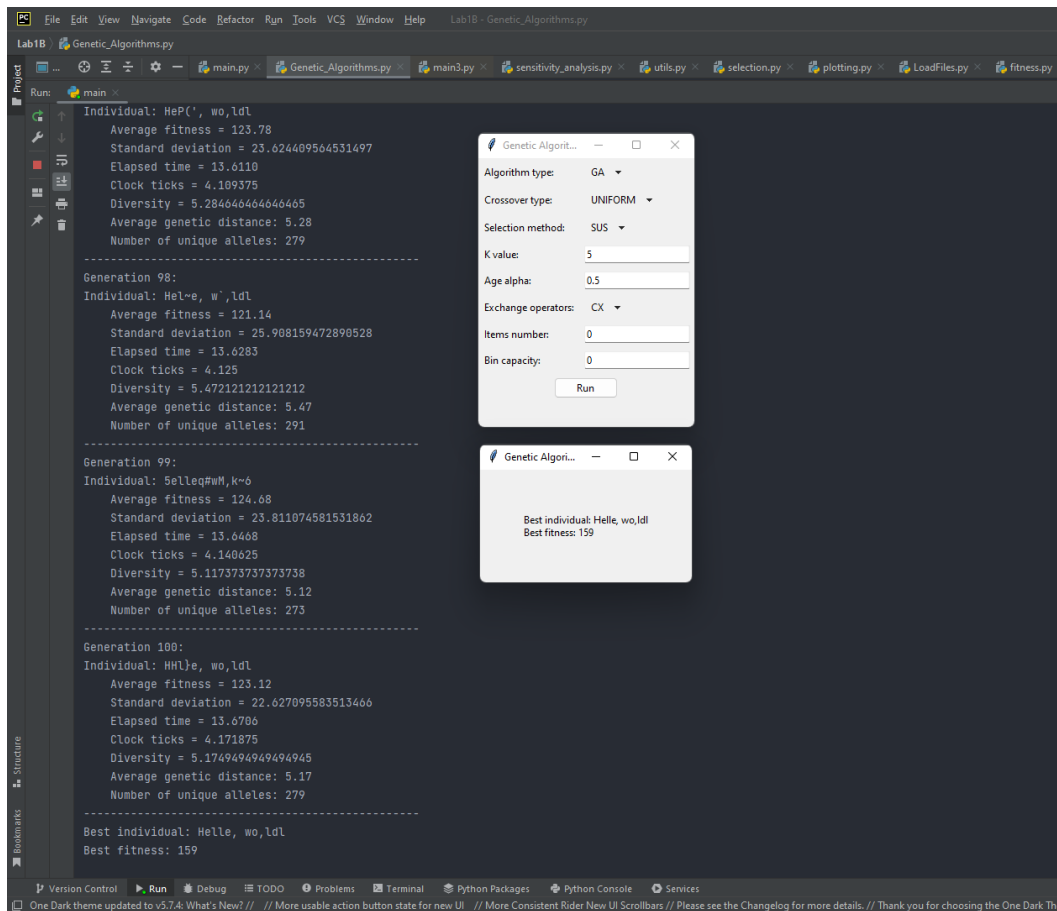
```

# Stochastic Universal Sampling (SUS) with scaling
def stochastic_universal_sampling(population, fitnesses, scaled_fitnesses, num_parents=2):
    selected_parents = []
    total_fitness = sum(scaled_fitnesses)
    pointer_distance = total_fitness / num_parents
    start_pointer = random.uniform(0, pointer_distance)

    for _ in range(num_parents):
        pointer = start_pointer
        partial_sum = 0
        for i, individual in enumerate(population):
            partial_sum += scaled_fitnesses[i]
            if partial_sum >= pointer:
                selected_parents.append(individual)
                break
        start_pointer += pointer_distance

    parent1 = selected_parents.pop(random.randrange(len(selected_parents)))
    parent2 = selected_parents.pop(random.randrange(len(selected_parents)))
    return parent1, parent2

```



```

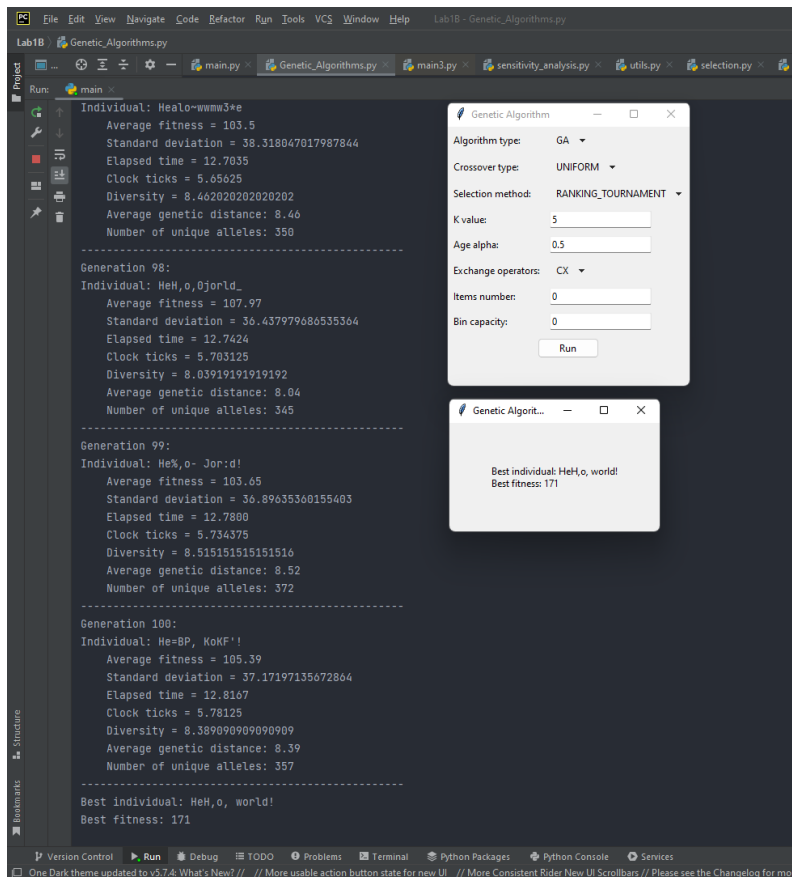
# Ranking and deterministic tournament selection with parameter K
def ranking_and_tournament_selection(population, fitnesses, K):
    selected_parents = []
    num_parents = len(population)

    # Ranking
    ranked_indices = sorted(range(num_parents), key=lambda i: fitnesses[i], reverse=True)
    ranked_population = [population[i] for i in ranked_indices]

    for _ in range(num_parents):
        # Deterministic tournament
        tournament_indices = random.sample(range(num_parents), K)
        best_index = max(tournament_indices, key=lambda i: fitnesses[i])
        selected_parents.append(ranked_population[best_index])

    parent1 = selected_parents.pop(random.randrange(len(selected_parents)))
    parent2 = selected_parents.pop(random.randrange(len(selected_parents)))
    return parent1, parent2
# returnn selected_parents

```



In the GA function we changed the parent selection to be one of the selection methods we implemented:

```
# Generate new individuals by applying crossover and mutation operators
offspring = []
while len(offspring) < pop_size - elite_size:
    # genetic_algorithm function snippet
    if selection_method == "RWS":
        parent1 = roulette_wheel_selection(population, fitnesses, scaled_fitnesses)
        parent2 = roulette_wheel_selection(population, fitnesses, scaled_fitnesses)
    elif selection_method == "SUS":
        parent1, parent2 = stochastic_universal_sampling(population, fitnesses, scaled_fitnesses, 2)
    elif selection_method == "RANKING_TOURNAMENT" and K is not None:
        parent1, parent2 = ranking_and_tournament_selection(population, fitnesses, K)

    child1, child2 = crossover(parent1, parent2, crossover_type)
    for child in [child1, child2]:
        for i in range(num_genes):
            if random.randint(0, 100) < GA_MUTATION:
                child[i] = chr(random.randint(32, 126))
    offspring.append(child1)
    offspring.append(child2)

population = elites + offspring
```

2. הוסיפו שיטת שרידות נוספת Aging

Adding the aging component to the fitness function in a genetic algorithm helps maintain diversity within the population and encourages exploration of new solutions, potentially leading to better overall results.

```
# Modify the fitness function to include age
def fitness_with_age(individual, age, fitness_func, alpha, max_age):
    # calculate the fitness score for the candidate solution
    original_score = fitness_func(individual)
    # normalize the age component
    normalized_age = age / max_age # divide age by the maximum age in the population
    # calculate the age component of the fitness score
    age_score = 1 - normalized_age # reverse the age score so that younger candidates get higher scores
    # combine the two scores with a weighted sum
    total_score = (1 - alpha) * original_score + alpha * age_score

    return total_score
```

We also updated the GA function to use genetic_algorithm_with_age

3. הוסיפו תמיכה למופע חדש של בעיה – בעית N המלכות על לוח שחמט לצורך כך

a. ממשו ייצוג מתאים לגן באורך N

b. ממשו 2 אופרטורי שיחלוף לתמורות PMX, CX

c. ממשו 2 מוטציות חלופיות לתמורות: היפוך ועירבול

d. בחרו פונקציית פיטנס יעילה ככל הניתן – נמקו בחירתכם

a. Representation of the N-Queens problem:

We will represent each individual as a list of integers, where the index represents the column number, and the value represents the row number of each queen. This ensures that no two queens share the same column, simplifying the problem.

b. Exchange operators:

The current code implements the single-point, two-point, and uniform crossover operators, which are not suitable for permutation-based problems like the N-Queens problem. Instead, we will implement the PMX (Partially Mapped Crossover) and CX (Cycle Crossover) operators.

```
# N-Queens
def pmx(parent1, parent2):
    size = len(parent1)
    p1, p2 = [0] * size, [0] * size

    # Choose crossover points
    cx1 = random.randint(0, size)
    cx2 = random.randint(0, size - 1)
    if cx2 >= cx1:
        cx2 += 1
    else: # Swap the two crossover points
        cx1, cx2 = cx2, cx1

    # Apply crossover between cx1 and cx2
    for i in range(cx1, cx2):
        p1[i] = parent2[i]
        p2[i] = parent1[i]

    # Map the remaining elements
    for i in range(size):
        if i < cx1 or i >= cx2:
            p1[i] = parent1[i]
            p2[i] = parent2[i]

            while p1[i] in p1[cx1:cx2]:
                p1[i] = parent1[parent2.index(p1[i])]

            while p2[i] in p2[cx1:cx2]:
                p2[i] = parent2[parent1.index(p2[i])]

    return p1, p2
```

```
def cx(parent1, parent2):
    size = len(parent1)
    p1, p2 = [-1] * size, [-1] * size
    indices = [0]

    # Find the first cycle
    while indices[-1] != 0 or len(indices) == 1:
        indices.append(parent1.index(parent2[indices[-1]]))

    # Assign the values in the first cycle
    for i in indices[:-1]:
        p1[i] = parent1[i]
        p2[i] = parent2[i]

    # Fill in the remaining values
    for i in range(size):
        if p1[i] == -1:
            p1[i] = parent2[i]
            p2[i] = parent1[i]

    return p1, p2
```

c. Alternative mutations for permutations:

We will implement two mutation operators specifically designed for permutation problems: inversion mutation and shuffling mutation.

```
# N-Queens
def inversion_mutation(individual):
    size = len(individual)
    m1, m2 = random.sample(range(size), 2)
    if m1 > m2:
        m1, m2 = m2, m1
    individual[m1:m2] = reversed(individual[m1:m2])
    return individual

def shuffling_mutation(individual):
    size = len(individual)
    m1, m2 = random.sample(range(size), 2)
    if m1 > m2:
        m1, m2 = m2, m1
    individual[m1:m2] = random.sample(individual[m1:m2], m2 - m1)
    return individual
```

The screenshot shows the PyCharm IDE with a project named 'Lab18'. The main window displays the output of a Genetic Algorithm for the N-Queens problem. The output shows the progress of the algorithm, including clock ticks, diversity, average genetic distance, and the number of unique alleles. A 'Genetic Algorithm' configuration window is open on the right, showing settings for GA_NQueens, UNIFORM crossover, RANKING_TOURNAMENT selection, and 10 queens. A 'Genetic Algorithm Results' window at the bottom shows the best individual found: [6, 0, 3, 8, 4, 7, 9, 2, 5, 1] with a best fitness of 0.

Genetic Algorithm Configuration:

- Algorithm type: GA_NQueens
- Crossover type: UNIFORM
- Selection method: RANKING_TOURNAMENT
- K value: 5
- Age alpha: 0.5
- Exchange operators: CX
- Number of Queens: 10
- Items number: 0
- Bin capacity: 0

Genetic Algorithm Results:

- Best individual: [6, 0, 3, 8, 4, 7, 9, 2, 5, 1]
- Best fitness: 0

d. Fitness function:

We will use a fitness function that counts the number of non-attacking queen pairs, aiming to maximize this value. Alternatively, you can count the number of attacking queen pairs and minimize that value.

```
def n_queens_fitness(individual):
    size = len(individual)
    conflicts = 0

    for i in range(size):
        for j in range(i+1, size):
            if individual[i] == individual[j]:
                conflicts += 1
            elif abs(individual[i] - individual[j]) == abs(i - j):
                conflicts += 1

    return conflicts
```

This is a good fitness function for the N-Queens genetic algorithm because it effectively measures the quality of a potential solution, which is an important aspect of any genetic algorithm.

The function calculates the number of conflicts in a given solution, where a conflict occurs if two queens are attacking each other, either horizontally, vertically, or diagonally. By counting the number of conflicts, the function provides a measure of how "fit" a potential solution is.

The goal of the N-Queens genetic algorithm is to find a solution with the minimum number of conflicts, or ideally, a solution with zero conflicts. Therefore, the fitness function is designed to return higher values for solutions that have more conflicts and lower values for solutions that have fewer conflicts.

This fitness function is also appropriate because it is simple and computationally efficient, making it possible to evaluate a large number of potential solutions in a reasonable amount of time.

4. הוסיפו תמיכה למופע חדש של בעיה בעית ה-BIN PACKING: יש

לארוז עצמים בנפחים שונים במספר מיכלים בנפח V במינימום

מיכלים https://en.wikipedia.org/wiki/Bin_packing_problem

a. גם לבעיה זו מצאו יצוג ופונקצית פיטנס יעילים – נמקו
בחירתכם

b. הריצו את האלגוריתם שלכם על חמשת הבעיות הראשונות
בקובץ binpack1.txt – הסבר על פורמט באתר

```
def bin_packing_fitness(individual, item_sizes, bin_capacity):
    num_bins = max(individual) + 1
    bin_space = [bin_capacity] * num_bins

    for i, bin_index in enumerate(individual):
        bin_space[bin_index] -= item_sizes[i]

    unused_space = sum(space for space in bin_space if space >= 0)
    return unused_space
```

```
elif algorithm == "GA_BinPacking_vs_FirstFit":
    ...

    file_path = "binpack1.txt"
    compare_binpack_algorithms(file_path, pop_size=100, max_generations=100, crossover_type=crossover,
                               selection_method=selection, k=k)
```

```
def compare_binpack_algorithms(file_path, pop_size=100, max_generations=100, crossover_type="single_point",
                               selection_method="RWS", k=None):
    import Genetic_Algorithms # import the module here instead
    ga_runtimes = []
    first_fit_runtimes = []
    ga_solutions = []
    first_fit_solutions = []

    # Run the genetic algorithm and First Fit algorithm on each problem instance in the input file
    for bin_capacity, item_sizes in read_binpack_input_file(file_path):
        # Run the genetic algorithm
        start_time = time.time()
        best_individual, best_fitness = Genetic_Algorithms.genetic_algorithm_BinPacking(pop_size=pop_size, num_genes=len(item_sizes),
                                                                                          fitness_func=bin_packing_fitness,
                                                                                          max_generations=max_generations,
                                                                                          crossover_type=crossover_type,
                                                                                          selection_method=selection_method, K=k,
                                                                                          item_sizes=item_sizes,
                                                                                          bin_capacity=bin_capacity)

        ga_runtime = time.time() - start_time
        ga_solution = best_fitness

        # Run the First Fit algorithm
        start_time = time.time()
        first_fit_solution = first_fit(item_sizes, bin_capacity)
        first_fit_runtime = time.time() - start_time

        # Add the results to the lists
        ga_runtimes.append(ga_runtime)
        first_fit_runtimes.append(first_fit_runtime)
        ga_solutions.append(ga_solution)
        first_fit_solutions.append(first_fit_solution)
```

5. הוסיפו שיטות למדידת לחץ הבחירה Selection Pressure

Exploitation Factor

Fitness Variance .a

Top-Average Selection Probability Ratio .b

~~Relative Fitness~~ .c

דווחו מדדים אלה בכל דור של אבולוציה

```
def fitness_variance(population, fitness_func, item_sizes, bin_capacity, problem):
    if problem == "n_queens":
        fitnesses = [fitness_func(individual) for individual in population]
    elif problem == "bin_packing":
        fitnesses = [fitness_func(individual, item_sizes, bin_capacity) for individual in population]
    else:
        raise ValueError(f"Unsupported problem type: {problem}")
    variance = statistics.variance(fitnesses)
    return variance

def top_avg_selection_probability_ratio(population, selection_method, K):
    if selection_method == "RANKING_TOURNAMENT":
        top_individual_probability = 1 / K
        avg_individual_probability = 1 / len(population)
        ratio = top_individual_probability / avg_individual_probability
        return ratio
    else:
        return None
```

```
-----
Generation 100:
Best Individual: [4, 2, 0, 6, 1, 7, 5, 3]
    Best fitness = 0
    Average fitness = 0.98
    Standard deviation = 1.42828568570857
    Elapsed time = 1.9924
    Clock ticks = 1.9688
    Diversity = 1.8226
    Fitness variance = 2.0400
    Top-Average Selection Probability Ratio = 20.0
-----

** N queens **
Best individual: [4, 2, 0, 6, 1, 7, 5, 3]
Best fitness: 0
```

6. הוסיפו שיטות למדידת הגוון הגנטי Genetic Diversification (חלק זה

מותאם בעיה) - Exploration Factor

a. המרחקים בין גנים

b. מספר האללים השונים באוכלוסיה

c. ~~אנטרופיית שנון~~

דווחו מדדים אלה בכל דור של אבולוציה

```
def average_genetic_distance(population):
    distances = []
    for i in range(len(population)):
        for j in range(i+1, len(population)):
            distance = sum(a != b for a, b in zip(population[i], population[j]))
            distances.append(distance)
    return sum(distances) / len(distances) if distances else 0

def unique_alleles(population):
    unique_alleles_per_gene = [set() for _ in range(len(population[0]))]
    for individual in population:
        for i, gene in enumerate(individual):
            unique_alleles_per_gene[i].add(gene)
    return sum(len(unique_set) for unique_set in unique_alleles_per_gene)
```


7. בדקו באמצעות סימולציות את רגישות פתרון שתי הבעיות (N המלכות ו"bin packing") לפי הקריטריונים של מהירות ההתכנסות, איכות הפתרון וזמני ריצה עפ"י הפרמטרים הבאים:

- a. לגודל האוכלוסיה
- b. להסתברות למוטציות
- c. לאסטרטגיית הבחירה
- d. לאסטרטגיית השרידות (ELITISM, AGING)
- e. לאסטרטגיית השיחלוף והמוטציה

We ran the code for different pop_size, mutation_rates, selction_methods, survival_strategies, exchange_operators and printed the results.

```
File Edit View Navigate Code Refactor Run Tools VCS Window Help Lab1B - main.py
Lab1B main.py
Run: main.py
Project
Number of unique alleles: 40
-----
Generation 33:
Best Individual: [0, 5, 7, 2, 6, 3, 1, 4]
Best fitness = 0
Average fitness = 17.419354838709676
Standard deviation = 9.193382379184088
Elapsed time = 0.0439
Clock ticks = 0.03125
Diversity = 3.789247311827957
Average genetic distance: 3.79
Number of unique alleles: 41
-----
Solution found.
Running NQueens with pop_size=30, mutation_rate=0.1, selection_method=RWS, survival_strategy=AGING, exchange_operator=PMX...
Generation 1:
Best Individual: [1, 3, 5, 7, 2, 4, 6, 0]
Best fitness = 1
Average fitness = 5.451612903225806
Standard deviation = 2.157756700486555
Elapsed time = 0.0000
Clock ticks = 0.0
Diversity = 6.724731182795699
Average genetic distance: 6.72
Number of unique alleles: 60
-----
Generation 2:
Best Individual: [1, 3, 5, 7, 2, 4, 6, 0]
Best fitness = 1
Average fitness = 5.451612903225806
Standard deviation = 2.5276960481489774
Elapsed time = 0.0020
Clock ticks = 0.015625
Diversity = 6.58494623655914
Average genetic distance: 6.58
Number of unique alleles: 60
-----
Generation 3:
Best Individual: [1, 3, 5, 7, 2, 4, 6, 0]
Best fitness = 1
Average fitness = 6
Standard deviation = 2.756809750418044
-----
Genetic Algorithm
Algorithm type: NQueens_analysis
Crossover type: SINGLE
Selection method: RWS
K value: 5
Age alpha: 0.5
Exchange operators: CX
Number of Queens: 8
Items number: 0
Bin capacity: 0
Run
```