AI CA 1 Report

Reyhaneh Esmailizadeh

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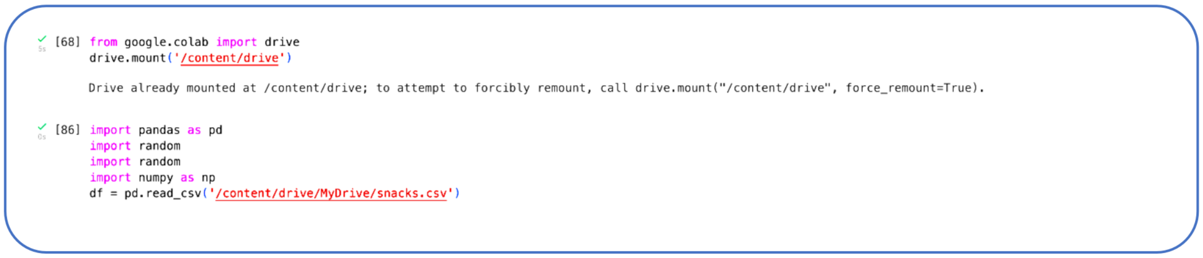
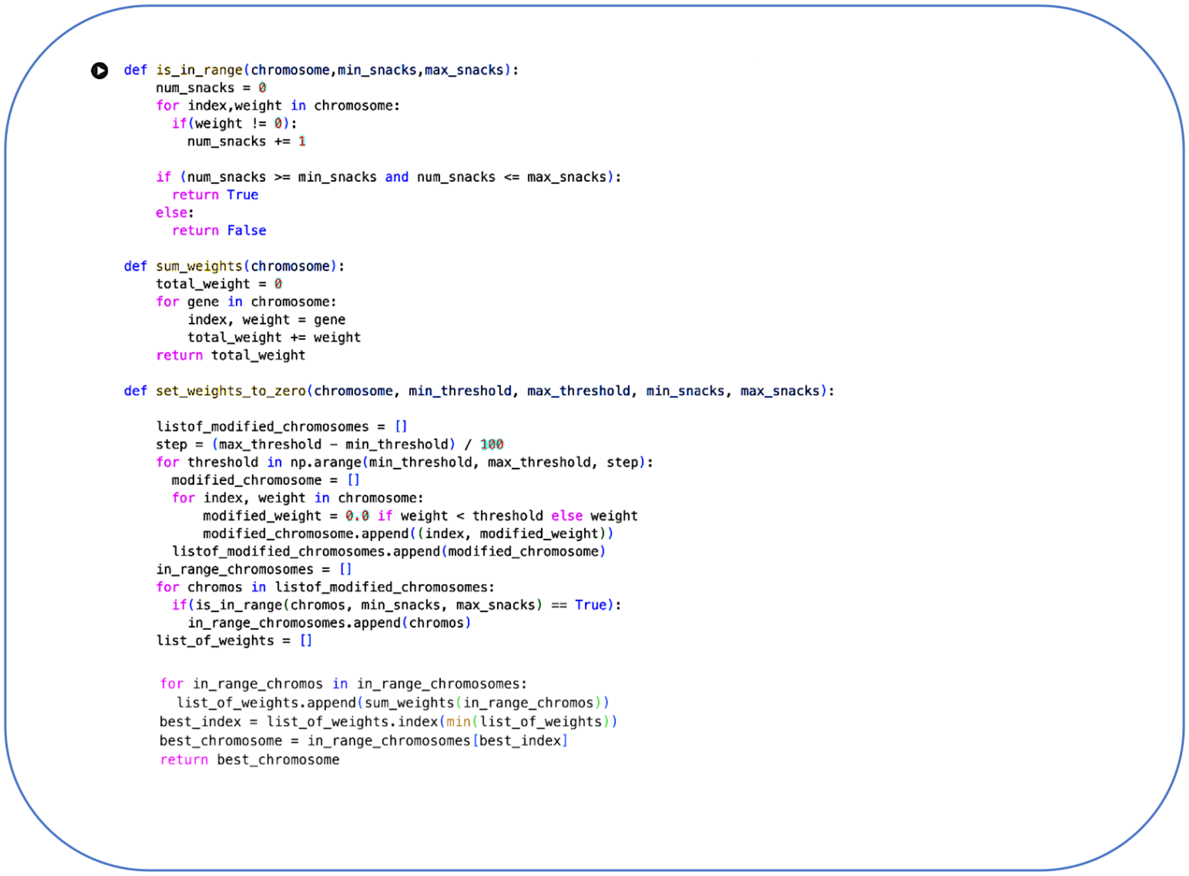


```
[68] from google.colab import drive
     drive.mount('/content/drive')

     Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).

[86] import pandas as pd
     import random
     import random
     import numpy as np
     df = pd.read_csv('/content/drive/MyDrive/snacks.csv')
```

First we mount to google drive and upload snack.csv from there.



```
def is_in_range(chromosome,min_snacks,max_snacks):
    num_snacks = 0
    for index,weight in chromosome:
      if(weight != 0):
        num_snacks += 1

    if (num_snacks >= min_snacks and num_snacks <= max_snacks):
      return True
    else:
      return False

def sum_weights(chromosome):
    total_weight = 0
    for gene in chromosome:
        index, weight = gene
        total_weight += weight
    return total_weight

def set_weights_to_zero(chromosome, min_threshold, max_threshold, min_snacks, max_snacks):

    listof_modified_chromosomes = []
    step = (max_threshold - min_threshold) / 100
    for threshold in np.arange(min_threshold, max_threshold, step):
      modified_chromosome = []
      for index, weight in chromosome:
          modified_weight = 0.0 if weight < threshold else weight
          modified_chromosome.append((index, modified_weight))
      listof_modified_chromosomes.append(modified_chromosome)
    in_range_chromosomes = []
    for chromos in listof_modified_chromosomes:
      if(is_in_range(chromos, min_snacks, max_snacks) == True):
        in_range_chromosomes.append(chromos)
    list_of_weights = []

    for in_range_chromos in in_range_chromosomes:
      list_of_weights.append(sum_weights(in_range_chromos))
    best_index = list_of_weights.index(min(list_of_weights))
    best_chromosome = in_range_chromosomes[best_index]
    return best_chromosome
```

In this section, several required functions are defined, and we will explain each one in order:

The `is_in_range` function checks whether the entered chromosome contains the desired number of snacks as inputs. In other words, if the number of snacks in the entered chromosome is within the specified range, this function returns `true`.

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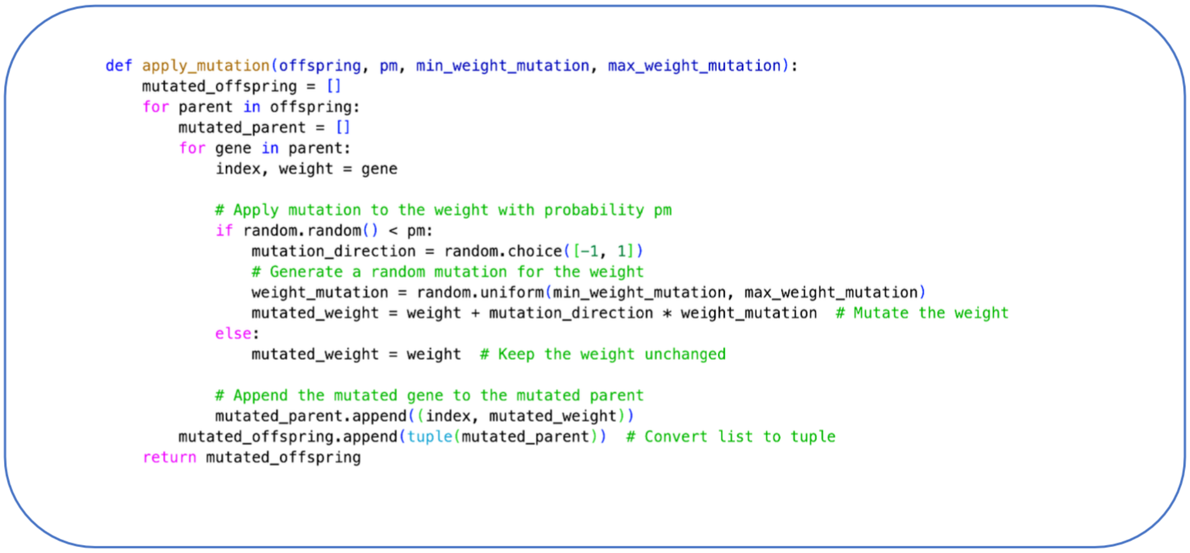
The `sum_weights` function sums up the weights of each gene in the entered chromosome. In fact, it calculates the total weight of all snacks in the given chromosome.

The `set_weights_to_zero` function changes the weights of the entered chromosome that are below a certain threshold to zero. Finally, based on the different thresholds given to the function, it returns a chromosome. Among these chromosomes, it considers those whose number of snacks is within the input range and returns the chromosome with the minimum total weight.



```python
def apply_mutation(offspring, pm, min_weight_mutation, max_weight_mutation):
    mutated_offspring = []
    for parent in offspring:
        mutated_parent = []
        for gene in parent:
            index, weight = gene

            # Apply mutation to the weight with probability pm
            if random.random() < pm:
                mutation_direction = random.choice([-1, 1])
                # Generate a random mutation for the weight
                weight_mutation = random.uniform(min_weight_mutation, max_weight_mutation)
                mutated_weight = weight + mutation_direction * weight_mutation  # Mutate the weight
            else:
                mutated_weight = weight  # Keep the weight unchanged

            # Append the mutated gene to the mutated parent
            mutated_parent.append((index, mutated_weight))
        mutated_offspring.append(tuple(mutated_parent))  # Convert list to tuple
    return mutated_offspring
```

The `apply_mutation` function receives the offspring population and applies a mutation to each one. This mutation may involve adding or subtracting a random number to/from any of the chromosomes. This random number must fall within the range provided to the function. Additionally, the probability that each gene in a chromosome undergoes mutation is determined by `pm` or the mutation probability.

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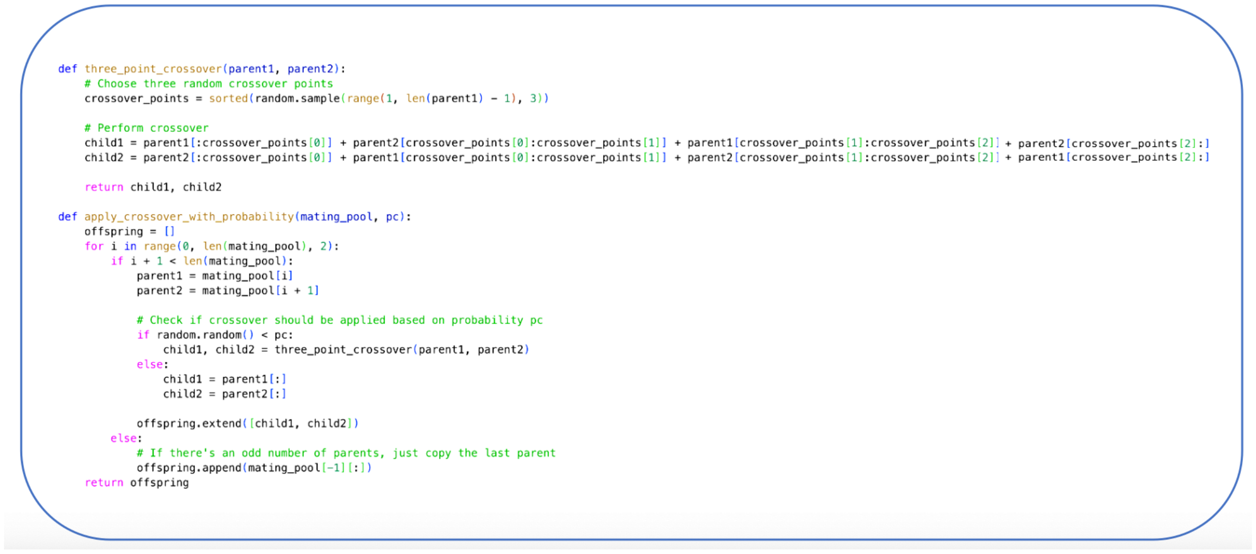
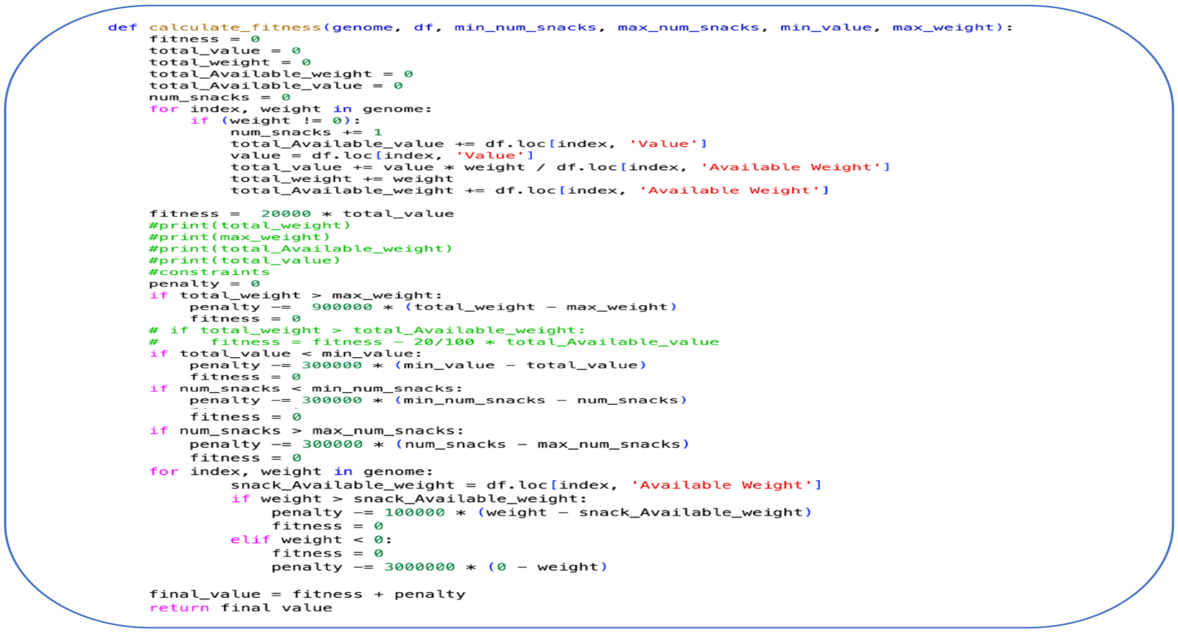


```python
def three_point_crossover(parent1, parent2):
    # Choose three random crossover points
    crossover_points = sorted(random.sample(range(1, len(parent1) - 1), 3))

    # Perform crossover
    child1 = parent1[:crossover_points[0]] + parent2[crossover_points[0]:crossover_points[1]] + parent1[crossover_points[1]:crossover_points[2]] + parent2[crossover_points[2]:]
    child2 = parent2[:crossover_points[0]] + parent1[crossover_points[0]:crossover_points[1]] + parent2[crossover_points[1]:crossover_points[2]] + parent1[crossover_points[2]:]

    return child1, child2

def apply_crossover_with_probability(mating_pool, pc):
    offspring = []
    for i in range(0, len(mating_pool), 2):
        if i + 1 < len(mating_pool):
            parent1 = mating_pool[i]
            parent2 = mating_pool[i + 1]

            # Check if crossover should be applied based on probability pc
            if random.random() < pc:
                child1, child2 = three_point_crossover(parent1, parent2)
            else:
                child1 = parent1[:]
                child2 = parent2[:]

            offspring.extend([child1, child2])
        else:
            # If there's an odd number of parents, just copy the last parent
            offspring.append(mating_pool[-1][:])
    return offspring
```

The `three_point_crossover` function is responsible for receiving two chromosomes of the same length and then performing the crossover operation by specifying three random points between the genes of these chromosomes. Ultimately, it returns two offspring chromosomes that will later enter the mutation stage.

The second function, `apply_crossover_with_probability`, receives the selected population of parents and then, with a probability of `pm`, gives every two consecutive chromosomes to the `three_point_crossover` function.



```python
def calculate_fitness(genome, df, min_num_snacks, max_num_snacks, min_value, max_weight):
    fitness = 0
    total_value = 0
    total_weight = 0
    total_Available_weight = 0
    total_Available_value = 0
    num_snacks = 0
    for index, weight in genome:
        if (weight != 0):
            num_snacks += 1
            total_Available_value += df.loc[index, 'Value']
            value = df.loc[index, 'Value']
            total_value += value * weight / df.loc[index, 'Available Weight']
            total_weight += weight
            total_Available_weight += df.loc[index, 'Available Weight']

    fitness =  20000 * total_value
    #print(total_weight)
    #print(max_weight)
    #print(total_Available_weight)
    #print(total_value)
    #constraints
    penalty = 0
    if total_weight > max_weight:
        penalty -=  900000 * (total_weight - max_weight)
        fitness = 0
    # if total_weight > total_Available_weight:
    #     fitness = fitness - 20/100 * total_Available_value
    if total_value < min_value:
        penalty -= 300000 * (min_value - total_value)
        fitness = 0
    if num_snacks < min_num_snacks:
        penalty -= 300000 * (min_num_snacks - num_snacks)
        fitness = 0
    if num_snacks > max_num_snacks:
        penalty -= 300000 * (num_snacks - max_num_snacks)
        fitness = 0
    for index, weight in genome:
            snack_Available_weight = df.loc[index, 'Available Weight']
            if weight > snack_Available_weight:
                penalty -= 100000 * (weight - snack_Available_weight)
                fitness = 0
            elif weight < 0:
                fitness = 0
                penalty -= 3000000 * (0 - weight)

    final_value = fitness + penalty
    return final value
```

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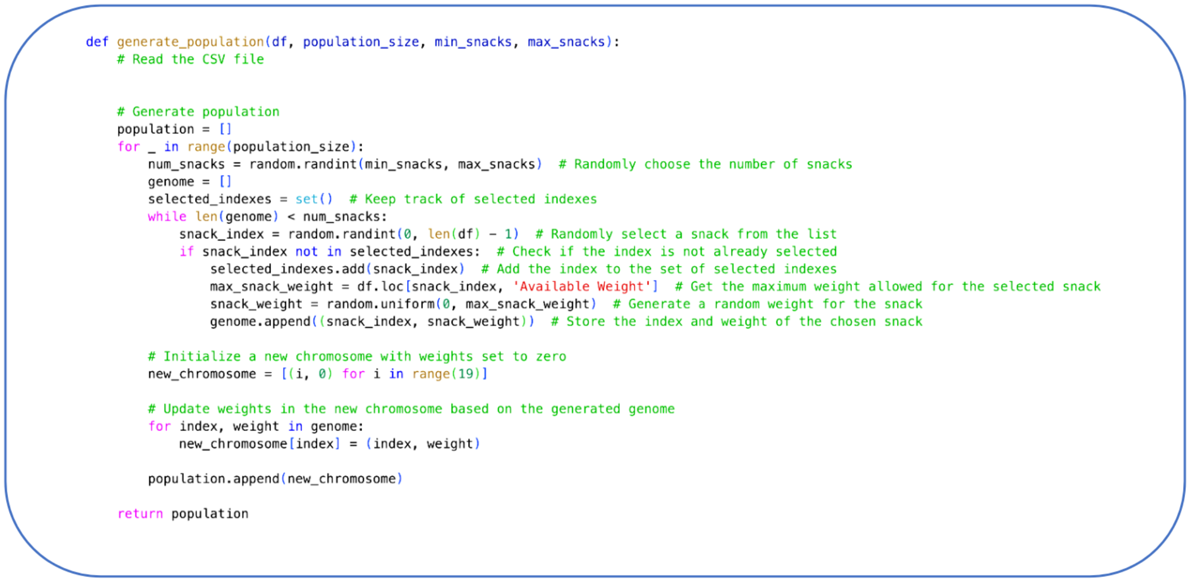
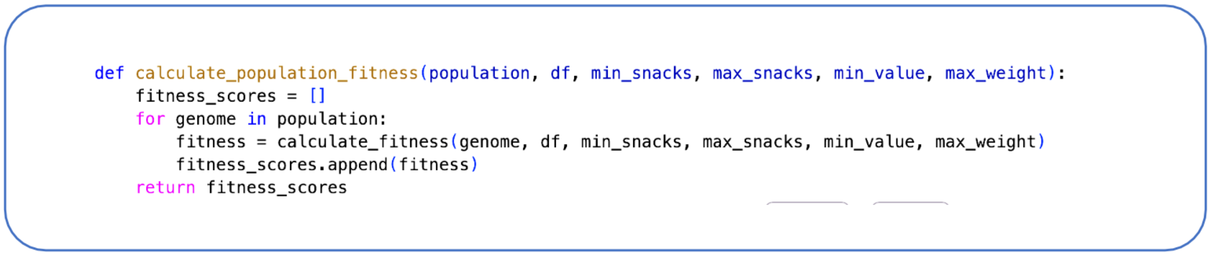
The `calculate_fitness` function, which is a critical part of the code, receives a chromosome and calculates its fitness value. If any of the conditions are violated, a penalty is applied. If a chromosome satisfies all the conditions, its value is determined as a multiple of the sum of its genes' values. The reason for the large penalty coefficients is to ensure that the algorithm converges to the correct solution more quickly and that solutions violating any conditions are eliminated from the population.



```python
def generate_population(df, population_size, min_snacks, max_snacks):
    # Read the CSV file


    # Generate population
    population = []
    for _ in range(population_size):
        num_snacks = random.randint(min_snacks, max_snacks)  # Randomly choose the number of snacks
        genome = []
        selected_indexes = set()  # Keep track of selected indexes
        while len(genome) < num_snacks:
            snack_index = random.randint(0, len(df) - 1)  # Randomly select a snack from the list
            if snack_index not in selected_indexes:  # Check if the index is not already selected
                selected_indexes.add(snack_index)  # Add the index to the set of selected indexes
                max_snack_weight = df.loc[snack_index, 'Available Weight']  # Get the maximum weight allowed for the selected snack
                snack_weight = random.uniform(0, max_snack_weight)  # Generate a random weight for the snack
                genome.append((snack_index, snack_weight))  # Store the index and weight of the chosen snack

        # Initialize a new chromosome with weights set to zero
        new_chromosome = [(i, 0) for i in range(19)]

        # Update weights in the new chromosome based on the generated genome
        for index, weight in genome:
            new_chromosome[index] = (index, weight)

        population.append(new_chromosome)

    return population
```

The `generate_population` function generates a random population of chromosomes. It is worth noting that the condition that the number of snacks falls within the input range is considered when generating the initial population. Additionally, in the initial population, the random weight assigned to each gene is less than the available weight of that gene or snack.



```python
def calculate_population_fitness(population, df, min_snacks, max_snacks, min_value, max_weight):
    fitness_scores = []
    for genome in population:
        fitness = calculate_fitness(genome, df, min_snacks, max_snacks, min_value, max_weight)
        fitness_scores.append(fitness)
    return fitness_scores
```

The `calculate_population_fitness` function is responsible for evaluating all the chromosomes in the generated population so that we can select the best ones among them. The evaluation phase of the chromosomes in the population is carried out in this function.

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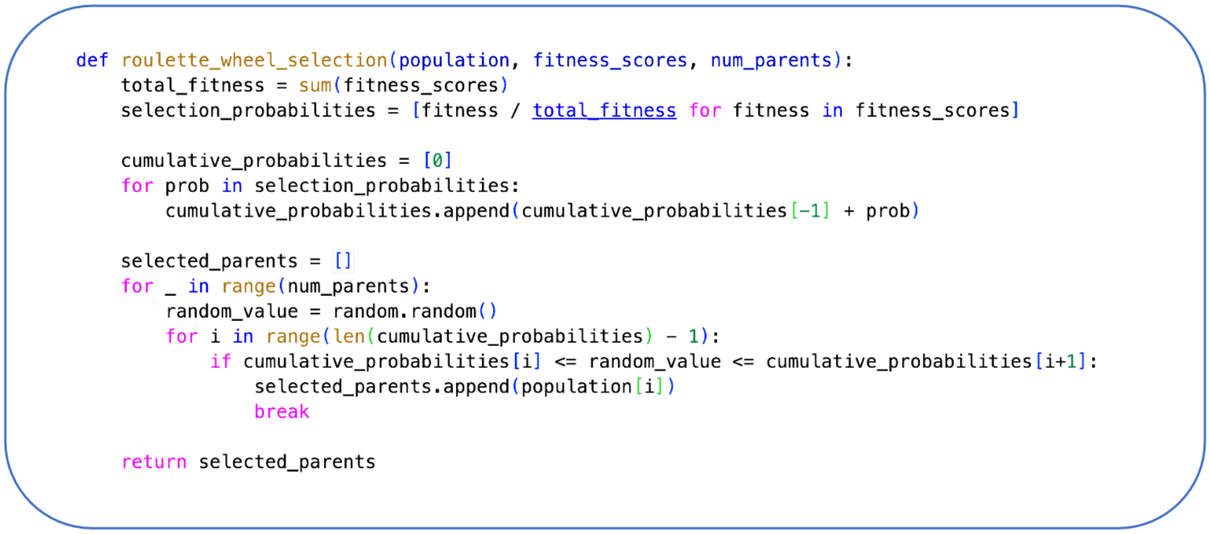


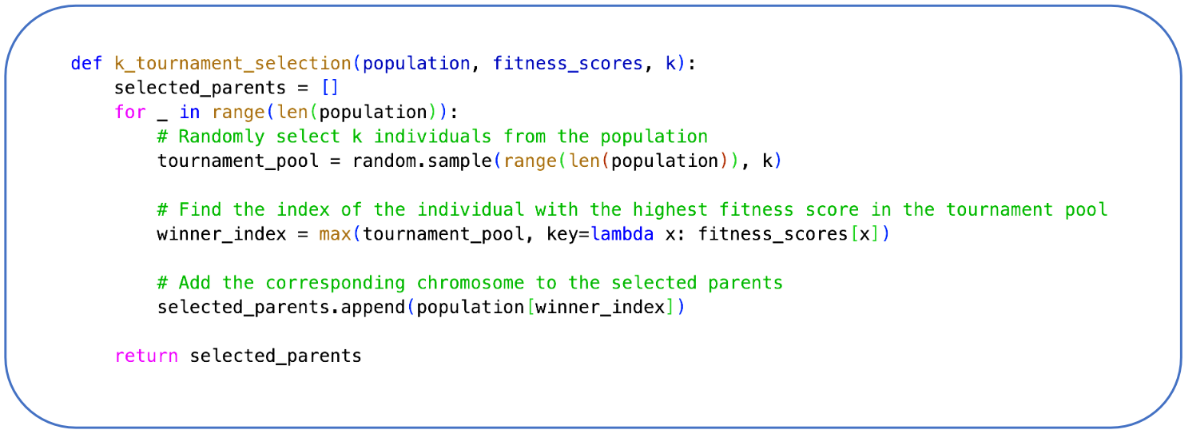
```python
def roulette_wheel_selection(population, fitness_scores, num_parents):
    total_fitness = sum(fitness_scores)
    selection_probabilities = [fitness / total_fitness for fitness in fitness_scores]

    cumulative_probabilities = [0]
    for prob in selection_probabilities:
        cumulative_probabilities.append(cumulative_probabilities[-1] + prob)

    selected_parents = []
    for _ in range(num_parents):
        random_value = random.random()
        for i in range(len(cumulative_probabilities) - 1):
            if cumulative_probabilities[i] <= random_value <= cumulative_probabilities[i+1]:
                selected_parents.append(population[i])
                break

    return selected_parents
```

The `roulette_wheel_selection` function is a method for selecting parents from a population. In this method, chromosomes with higher fitness values have a higher probability of being selected as parents. However, in this code, this method is not used due to the negative fitness values.



```python
def k_tournament_selection(population, fitness_scores, k):
    selected_parents = []
    for _ in range(len(population)):
        # Randomly select k individuals from the population
        tournament_pool = random.sample(range(len(population)), k)

        # Find the index of the individual with the highest fitness score in the tournament pool
        winner_index = max(tournament_pool, key=lambda x: fitness_scores[x])

        # Add the corresponding chromosome to the selected parents
        selected_parents.append(population[winner_index])

    return selected_parents
```

The `k_tournament_selection` function is another method for selecting parents from a population. In this method, for each selection round and for a specified number kkk, we randomly select kkk chromosomes, and then choose the one with the highest fitness.

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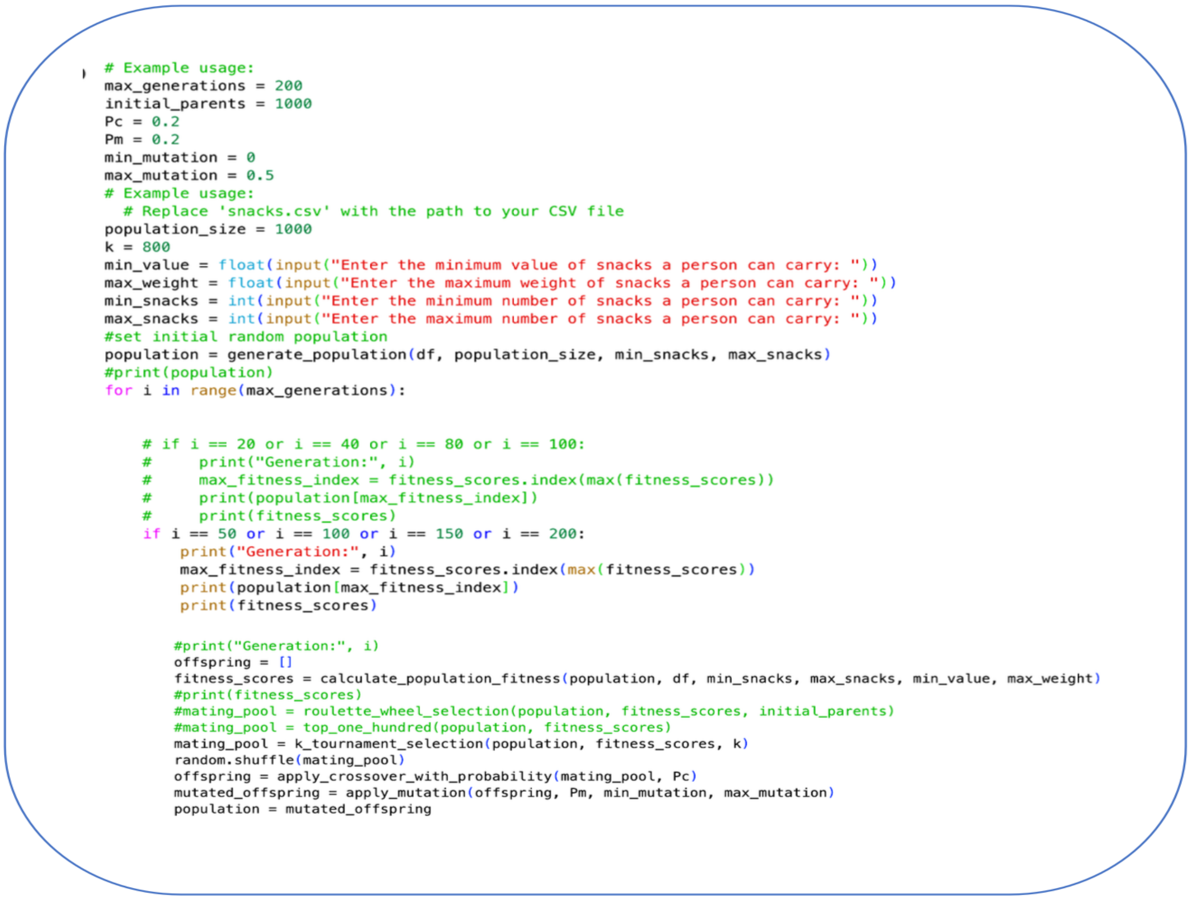
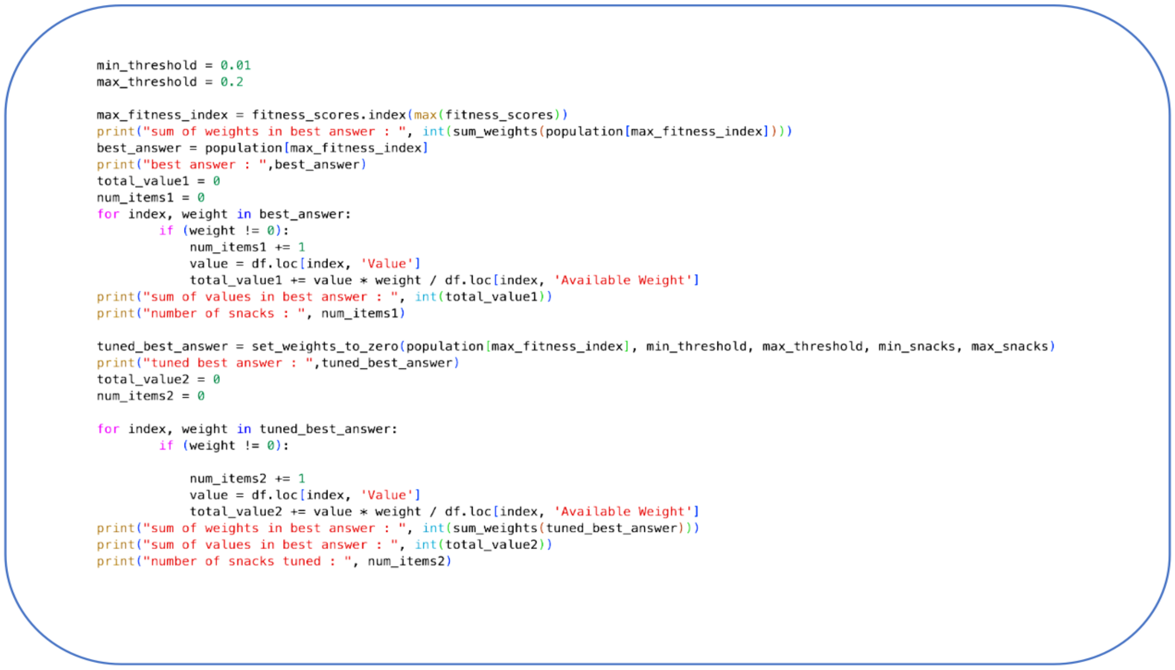


```
# Example usage:
max_generations = 200
initial_parents = 1000
Pc = 0.2
Pm = 0.2
min_mutation = 0
max_mutation = 0.5
# Example usage:
  # Replace 'snacks.csv' with the path to your CSV file
population_size = 1000
k = 800
min_value = float(input("Enter the minimum value of snacks a person can carry: "))
max_weight = float(input("Enter the maximum weight of snacks a person can carry: "))
min_snacks = int(input("Enter the minimum number of snacks a person can carry: "))
max_snacks = int(input("Enter the maximum number of snacks a person can carry: "))
#set initial random population
population = generate_population(df, population_size, min_snacks, max_snacks)
#print(population)
for i in range(max_generations):


    # if i == 20 or i == 40 or i == 80 or i == 100:
    #     print("Generation:", i)
    #     max_fitness_index = fitness_scores.index(max(fitness_scores))
    #     print(population[max_fitness_index])
    #     print(fitness_scores)
    if i == 50 or i == 100 or i == 150 or i == 200:
        print("Generation:", i)
        max_fitness_index = fitness_scores.index(max(fitness_scores))
        print(population[max_fitness_index])
        print(fitness_scores)

        #print("Generation:", i)
        offspring = []
        fitness_scores = calculate_population_fitness(population, df, min_snacks, max_snacks, min_value, max_weight)
        #print(fitness_scores)
        #mating_pool = roulette_wheel_selection(population, fitness_scores, initial_parents)
        #mating_pool = top_one_hundred(population, fitness_scores)
        mating_pool = k_tournament_selection(population, fitness_scores, k)
        random.shuffle(mating_pool)
        offspring = apply_crossover_with_probability(mating_pool, Pc)
        mutated_offspring = apply_mutation(offspring, Pm, min_mutation, max_mutation)
        population = mutated_offspring
```



```
min_threshold = 0.01
max_threshold = 0.2

max_fitness_index = fitness_scores.index(max(fitness_scores))
print("sum of weights in best answer : ", int(sum_weights(population[max_fitness_index])))
best_answer = population[max_fitness_index]
print("best answer : ",best_answer)
total_value1 = 0
num_items1 = 0
for index, weight in best_answer:
        if (weight != 0):
            num_items1 += 1
            value = df.loc[index, 'Value']
            total_value1 += value * weight / df.loc[index, 'Available Weight']
print("sum of values in best answer : ", int(total_value1))
print("number of snacks : ", num_items1)

tuned_best_answer = set_weights_to_zero(population[max_fitness_index], min_threshold, max_threshold, min_snacks, max_snacks)
print("tuned best answer : ",tuned_best_answer)
total_value2 = 0
num_items2 = 0

for index, weight in tuned_best_answer:
        if (weight != 0):

            num_items2 += 1
            value = df.loc[index, 'Value']
            total_value2 += value * weight / df.loc[index, 'Available Weight']
print("sum of weights in best answer : ", int(sum_weights(tuned_best_answer)))
print("sum of values in best answer : ", int(total_value2))
print("number of snacks tuned : ", num_items2)
```

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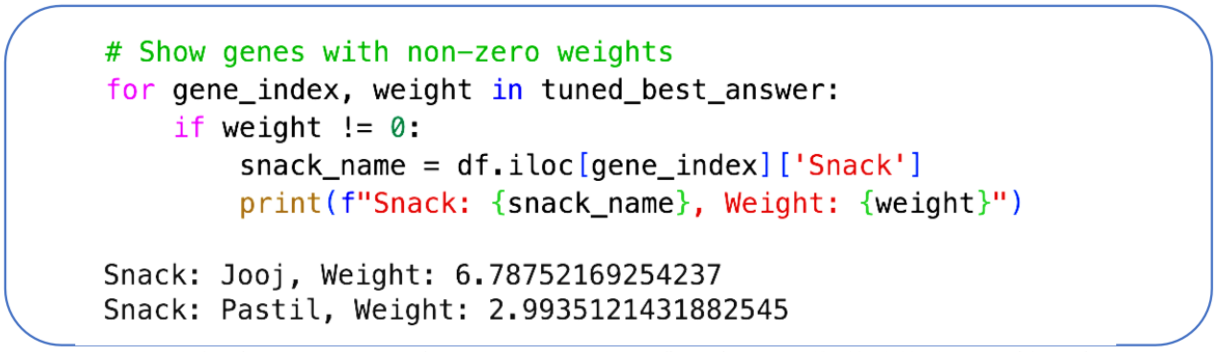
In this section, we are ultimately looking to use this algorithm for the knapsack problem. Here's how it works: first, we need to set the parameters and initialize the initial random population. Then, for a specified number of generations, we perform the following steps iteratively: `k_tournament_selection`, `calculate_population_fitness`, shuffling the parent population, `apply_crossover_with_probability`, and mutation. Finally, after iterating through the specified number of generations, we return the best solution, which has the highest fitness.

RESULTS

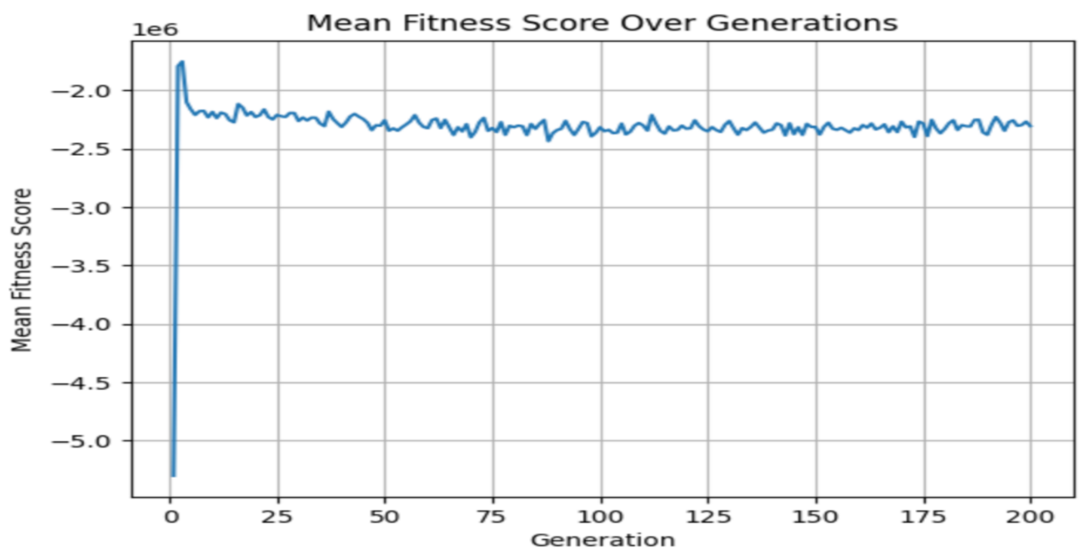


```python
# Show genes with non-zero weights
for gene_index, weight in tuned_best_answer:
    if weight != 0:
        snack_name = df.iloc[gene_index]['Snack']
        print(f"Snack: {snack_name}, Weight: {weight}")
```

```
Snack: Jooj, Weight: 6.78752169254237
Snack: Pastil, Weight: 2.9935121431882545
```

These are results with these inputs:

- **Maximum Weight**: 12
- **Minimum Value**: 10
- **Minimum Number of Items**: 2
- **Maximum Number of Items**: 4



As observed, the fitness increases over time. The reason for high oscillations is the use of k-tournament selection. To smooth out this function, we could have used top-k selection instead.