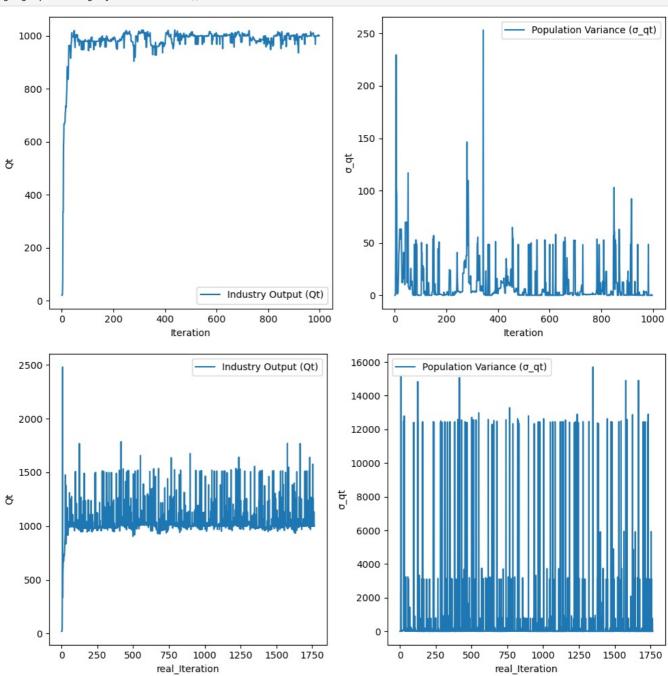
```
In [130...
          import random
          import matplotlib.pyplot as plt
          def binary_to_decimal(binary_str):
              Converts a binary string to a decimal integer.
              decimal num = int(binary str, 2)
              return decimal num
          class GeneticAlgorithm:
              def __init__(self, population_size, alpha, cost, chromosome length):
                   self.population size = population size
                  self.alpha = alpha
                  self.cost = cost
                  self.chromosome_length = chromosome_length
                  self.population = []
                  # Lists to store industry output (Qt) and population variance (\sigma qt) values for each iteration
                  self.industry output values = []
                  self.population variance values = []
                  # Lists to store industry output (Qt) and population variance (\sigma_{-}qt) values for each real iteration
                  self.real_industry_output_values = []
                  self.real population variance values = []
              def initialize_population(self):
                  Initializes the population.
                  self.population = [''.join(random.choice('0') for _ in range(self.chromosome_length-1))+"1" for _ in ra
              def Q(self):
                  Calculates the sum of the decimal values of the chromosomes in a population.
                  return sum(binary_to_decimal(chromosome) for chromosome in self.population)
              def varianceOfg(self, Q):
                  Calculates the variance of q, the decimal values of the chromosomes in a population.
                  return sum((binary_to_decimal(chromosome) - 1.0 * Q / self.population_size) ** 2 for chromosome in self
              def crossover_binary_strings(self, parent1, parent2, p_cross):
                  Performs crossover between two parents.
                  if random.random() < p_cross:</pre>
                       crossover_point = random.randint(1, self.chromosome_length - 1)
                      child1 = parent1[:crossover_point] + parent2[crossover_point:]
child2 = parent2[:crossover_point] + parent1[crossover_point:]
                       return child1, child2
                  else:
                       return parent1, parent2
              def mutate binary string(self, binary str, p mut):
                  Mutates a binary string.
                  mutated_str = ""
                  for bit in binary str:
                       if random.random() < p_mut:</pre>
                           # Flip the bit if mutation probability is met
mutated_str += '1' if bit == '0' else '0'
                       else:
                           mutated str += bit
                  return mutated str
              def total PiOfi(self, pt):
                  Calculates the sum of (pt - c) * valueOfChromosome for all chromosomes.
                  total result = sum(self.PiOfi(chromosome, pt) for chromosome in self.population)
                  return total_result
              def PiOfi(self, chromosome, pt):
                      chromosome: A binary string representing a chromosome.
                      pt: Market demand level.
                  value of chromosome = binary to decimal(chromosome)
                  result = (pt - self.cost) * value_of_chromosome
                  return result
```

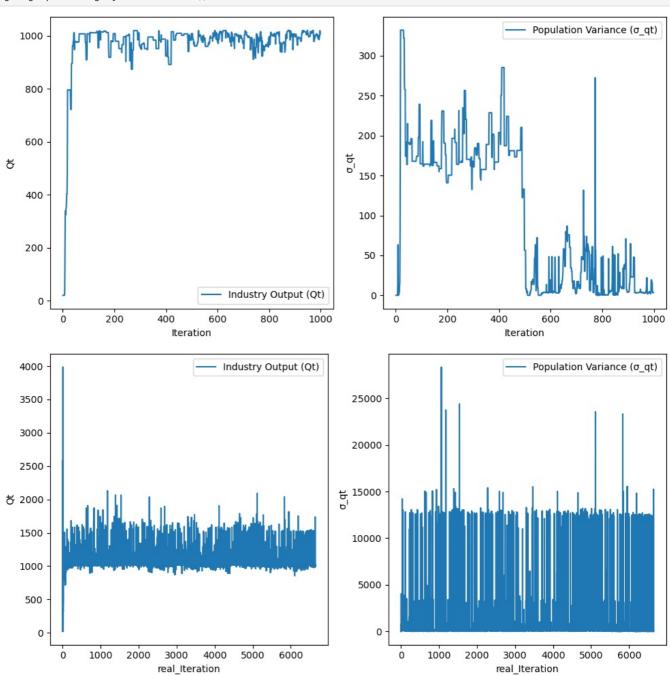
```
def evolve(self, T, crossover_factor = 0.5, mutation_factor = 0.003):
    Performs the evolution of the genetic algorithm.
    self.first = self.population
    self.second = self.population
    self.initialize_population()
    while t < T:
        """print(f"Market Output: {MarketOutput}")"""
        MarketOutput = self.Q()
        pt = max(0,self.alpha-MarketOutput)
        self.real_industry_output_values.append(MarketOutput)
        self.real population variance values.append(self.variance0fq(MarketOutput))
        if pt == 0:
            self.population = self.second
            self.first = self.second
            t -= 1
            MarketOutput = self.Q()
            pt = max(0,self.alpha-MarketOutput)
            self.real_industry_output_values.append(MarketOutput)
            self.real_population_variance_values.append(self.varianceOfq(MarketOutput))
            if 2 < len(self.real industry output values):</pre>
                self.industry_output_values.append(self.real_industry_output_values[-2])
                self.population variance values.append(self.real population variance values[-2])
        self.second = self.first
        self.first = self.population
         ""for i, chromosome in enumerate(self.population, start=1):
            result = self.PiOfi(chromosome, pt)
            print(f"P{i}({chromosome}): {result}")"""
        total_output_value = self.total_PiOfi(pt)
        """print(f"Toplam PiOfi: {total_output_value}")"""
        new generation = self.Recombination(pt)
        """print("Yeni Oluşan Popülasyon:")
        for chromosome in new generation:
            print(chromosome)""
        new generation crossover mutate = self.crossover and mutate(new generation, crossover factor, mutat
        """print("Yeni Oluşan Popülasyon (Çaprazlama ve Mutasyon):")
        for chromosome in new generation crossover mutate:
            print(chromosome)"
        self.population=new_generation_crossover_mutate
    self.industry output values.append(self.real industry output values[-1])
    self.population variance values.append(self.real population variance values[-1])
    print("Final Population:")
    for chromosome in self.population:
    print(chromosome, " ",binary_to
                             ",binary_to_decimal(chromosome) )
    return self.population
def relative_fitness(self, chromosome, pt):
    Parameters:
        chromosome: A binary string representing a chromosome.
        pt: Market demand level.
    individual_PiOfi = self.PiOfi(chromosome, pt)
    total PiOfi value = self.total PiOfi(pt)
    if total PiOfi value != 0:
        relative_fitness_value = individual_PiOfi / total PiOfi value
    else:
        # Eğer total PiOfi sıfırsa, göreceli fitness de sıfırdır
        relative_fitness_value = 1.0 / population_size
    return relative_fitness_value
def Recombine(self, CDFrelative_fitness_values):
    point = random.random()
    for i in range(0, len(CDFrelative fitness values)):
        if CDFrelative_fitness_values[i] > point:
```

```
return self.population[i]
        #print(CDFrelative_fitness_values)
        #print(point)
        #print(CDFrelative fitness values[0]<point)</pre>
def Recombination(self, pt):
        Parameters:
        pt: Market demand level.
        relative fitness values = [self.relative fitness(chromosome, pt) for chromosome in self.population]
       for i in range(1, len(relative fitness values)):
               relative_fitness_values[i]+=relative_fitness_values[i-1]
       # Göreceli fitness değerlerine göre sırala ve en yüksek ikiyi seç
        selectedCopies = [self.Recombine(relative_fitness_values) for i in range(0, len(self.population))]
        return selectedCopies
def crossover_and_mutate(self, new_generation, crossover_factor, mutation_factor):
               crossover_factor: Crossover probability factor.
               mutation_factor: Gene mutation probability factor.
       new_population = []
        for i in range(0, len(new_generation), 2):
               parent1, parent2 = new generation[i], new generation[i + 1]
               child1, child2 = self.crossover_binary_strings(parent1, parent2, crossover_factor)
               new population.extend([child1, child2])
        # Mutation
        for i in range(len(new_population)):
               new population[i] = self.mutate binary string(new population[i], mutation factor)
        return new population
def graphOfChangeByIteration(self):
        # Plot the graphs
        plt.figure(figsize=(10, 5))
        # Industry Output (Qt)
       plt.subplot(1, 2, 1)
plt.plot(range(1, len(self.industry_output_values) + 1), self.industry_output_values, label='Industry_output_values, label='Indus
       plt.xlabel('Iteration')
       plt.ylabel('Qt')
       plt.legend()
       # Population Variance (σ qt)
       plt.subplot(1, 2, 2)
        plt.plot(range(1, len(self.population variance values) + 1), self.population variance values, label='Po'
       plt.xlabel('Iteration')
       plt.ylabel('o_qt')
       plt.legend()
       plt.tight_layout()
       plt.show()
def graphOfChangeByRealIteration(self):
       # Plot the graphs
plt.figure(figsize=(10, 5))
        # Industry Output (Qt)
       plt.subplot(1, 2, 1)
        plt.plot(range(1, len(self.real_industry_output_values) + 1), self.real_industry_output_values, label='
       plt.xlabel('real_Iteration')
       plt.ylabel('Qt')
        plt.legend()
        # Population Variance (σ qt)
       plt.subplot(1, 2, 2)
       plt.plot(range(1, len(self.real_population_variance_values) + 1), self.real_population_variance_values,
plt.xlabel('real_Iteration')
        plt.ylabel('o_qt')
        plt.legend()
        plt.tight_layout()
        plt.show()
```

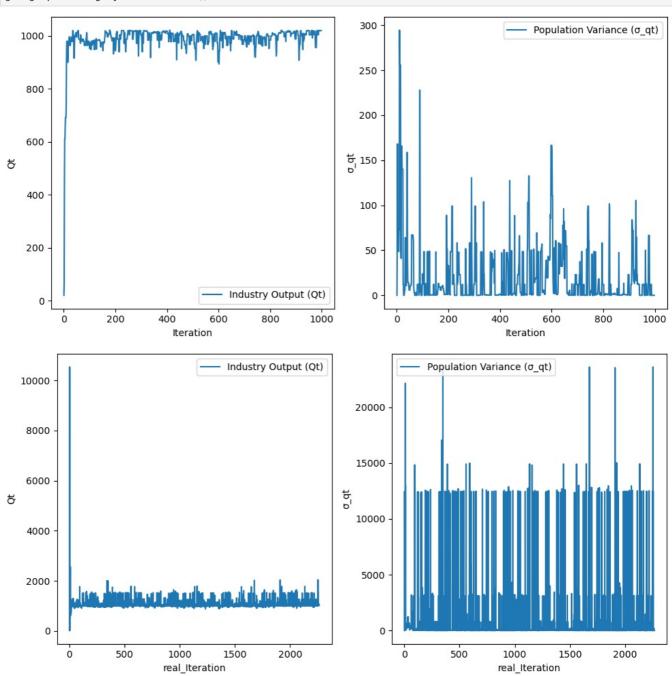
```
In [141... # Example Usage:
    ga = GeneticAlgorithm(population_size=20, alpha=1023, cost=0, chromosome_length=10)
    ga.initialize_population()
    final_population = ga.evolve(T=1000, crossover_factor = 0.5 + 6*0.001, mutation_factor = 0.003 + 6*0.00001)
```



In [135...
ga2 = GeneticAlgorithm(population_size=20, alpha=1023, cost=0, chromosome_length=10)
ga2.initialize_population()
final_population = ga2.evolve(T=1000, crossover_factor = 0.5 + 0.1 + 6*0.001, mutation_factor = 0.003 + 6*0.000



In [137... ga3 = GeneticAlgorithm(population_size=20, alpha=1023, cost=0, chromosome_length=10)
 ga3.initialize_population()
 final population = ga3.evolve(T=1000, crossover factor = 0.5 + 6*0.001, mutation factor = 0.003 + 0.001 + 6*0.0



$$Q_{1}$$

q, e[0, x] V.

a)
$$P(\Sigma_{iq}^{q_i}) = \alpha - \sum_{i \in N} q_i$$
 $\pi_i(q_i, \sum_{i \in N} q_i) = P(\sum_{j \in N} q_j) q_i - cq_i$
 $\pi_i(q_i, \sum_{i \in N} q_j) = \alpha q_i - q_i^2 - q_i \sum_{j \in N} q_j - cq_i$
 $\frac{d n_i(c)}{d q_i} = \alpha - c - 2q_i - \sum_{j \in N} q_j$
 $q_i - q_i - q_i$
 $q_i = RR_i(Q)$

It is synethic, Thus $q_i = q_j$ $\forall i, \forall j \in N$ on Nash equilibrium $\alpha - c - nq_i = \alpha_i$
 $(n+1)q_i = \alpha - c$
 $q_i = \frac{\alpha - c}{2q_i}$

b) My code consists of recombination, crossover and mutation. I added also backup-load. it means that if Industry output exceeds & (demand), all companies go bonkrupt. Therefore, code loads the backup two iterations ago. Thus, iteration of evolve and real iteration of evolve may be different I showed graph of these.

ii) it is almost converged to (ournot (Nash) equilibrium. Since it is experimental. There exists some oscillation on Cournot equilibrium. Thus, it is possible that these are not some like Cournot equilibrium. However, it is converged

iii) it is still conveged. In normal treations, speed has increased. But real speed is almost some.

iv) it is still converged. However algorithm has stopped while all comparies not bankrupt. speed has increased but again real speed is almost some