1. Consider genomes are the order of nodes in the graph. Now a genome is valid if path exists between given order, and if not we should return the highest fitness value. Fitness value for each valid genome is the cost of the path.

Crossover between two chromosomes, uses the first 4 items of first chromosome and take others from the second chromosome. I did the crossover for the best 50 chromosomes.

We have mutation with probability of 0.001. When mutation occurs, we swap two random nodes in a chromosome and consider it as the new chromosome and add it to the population for next selection phase.

Selection method is "Proportional Selection", which is selects chromosomes from distribution  $\varphi$ :

$$\varphi_{\scriptscriptstyle S}(x_i) = \frac{\gamma(x_i)}{\sum_{l=1}^{n_{\scriptscriptstyle S}} \gamma(x_l)}$$

Where  $\gamma$  is the scaled fitness of x, and because we want to minimize the fitness function I used  $\gamma$  as:

$$\gamma = \frac{1}{1 + f(x_i) - f_{min}}$$

Where  $f_{min}$  is the minimum observed fitness up to time step t.

2. Consider genome as the answer to the equation. To compute the fitness value, calculate the equation by setting genome as x, then the square of the calculated value can be used as the fitness value. Crossover between two chromosomes is the mean of genomes of them.

We have mutation with probability 0.05, and adds or subtracts a random number between -1 and 1 to the genome.

Selection method is "Proportional Selection".