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Genetic algorithm Monte Carlo

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# Abstract

The aim of this project is to solve the travelling salesman problem (TSP) which consists in finding the shortest cycle among all the cities. The problem is a *NP-hard* problem and therefore there exist no feasible algorithm to solve if for any possible set of cities in input. The appromximately optimal solution was computed by the simulated annealing, while the possible cycles are produced by a genetic algorithm.

# 1 Introduction

The travelling salesman problem consists in finding the shortest route a travelling salesman has to take to visit all the city he must reach only once and to return to the starting point. The route described is called in graph theory *hamiltonian cycle* (i.e a cycle that pass through each vertex of a graph just once), indeed the oldest and more technical formulation of the problem was proposed by Hamilton.

An algorithm that provides a solution to TSP can be exploited in a wide variety of applications: indeed it can be used in logistics to optimize the path of vehicles and therefore to reduce costs. It is possible to model the problem usign an undirected, weighted and fully connected graph [1] $G = (N, E)$, where $N$ is the set of the cities to visit and $E = N \times N$ is the weight of the path. In this particular instance of the probelm the weights correspond to the euclidean between each couple of cities. THe mailtonian cycle can be defined as a sequence $(n_0, .., n_{k-1})$ of length k such that $n_i \neq n_j \; \forall i, j \in \{1, ..., |N|\}$ and such that $(i, j) \in E \; \forall i, j \in \{1, ..., |N|\}$ The most naive solution is to compute all the possible paths but they are factorial in the number of cities $n$ in input. The number of possible cycles is $(n-1)!$ and grows faster that $2^n$ (i.e $2^n = o(n!)$). Therefore even if it was possible to find them in constant time the algorithm will have an expnential time complexity and would not be solved in finite time for large $n$. More techically, TSP is an NP-hard problem. A NP-hard problem is a problem at least as hard as the hardest NP-complete problem. NP-complete problem is a problem that can be solved in polynomial time by a non-deterministic algorithm. For such a class of problem there exists no polynomial algorithm that can solve the problems and may not exist, still noone was able to prove that such algorithms does not exists. Bearing in mind the complexity problem to face, the most reasonable solution is to solve the problem approximately. The technique I to generate the possible hamiltonian cycles is a genetic algorithm, while the choice of the fittest hamiltonian cycle is done by the simulated annealing algorithm

# 2 Simulated annealing

# 3 Metropolis algorithm

# 4 Genetic Algotirthm

Genetic algorithms are a widespread class of algotirhms that mimic nature. Indeed there are three fundamental operations they perform, each operation is inspired by the theory of evolution by Darwin. Among a specie evolution selects the fittest individuals and therefore the algorithm will

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[1] For an hamiltinian cycle to exist the graph must be at least connected
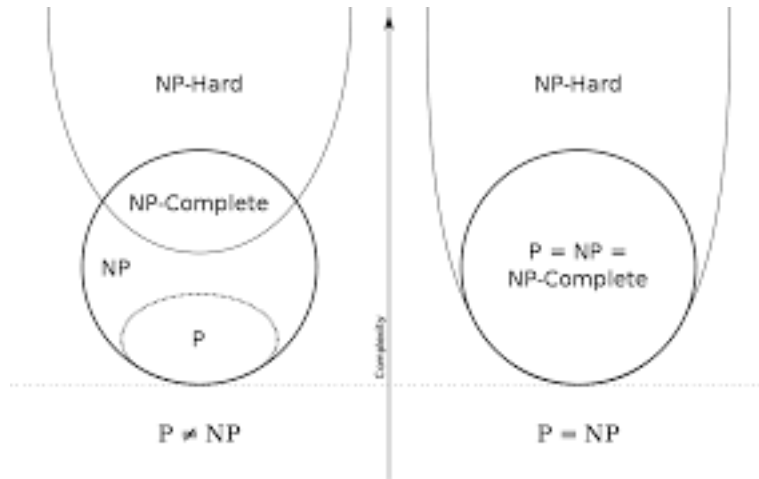
chose the fittest (i.e shortest) hamiltonian cycles. The breeding of the fittest individuals produces new individuals that inherits traits from the parents, therefore in the crossbreeding phase we mix some subsection of the fittest hamiltonian cycles. As random mutations can occur in nature but they are not so likely to accur, the algorithms swaps two nodes (cities) with a fixed and low probability. My own implementation of the algorithms performs the selection operation as follows: where **population** is an array of hamiltonian cycles

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1: **function** SELECTION(**population**,n_paths)
2:     $n\_parents \leftarrow$ unif[2,n_paths/2]
3:     order the population by fitness
4:     **fittest_subpopulation** $\leftarrow$ extract $n\_parents$ in order from the sorted population
5:     return **fittest_subpopulation**
6: **end function**

---

2) Crossbreeding –¿ obtain new hamiltonian cycles exchanging the gines of the parents 3) Mutation –¿ exchange genes randomly

# 5   dataset

# 6   results

```
 1: function CROSSBREEDING(fittest_subpopulation)
 2:     for i in 1, ..., n_paths do
 3:         choose parent1 uniformely among the fittest_subpopulation
 4:         Choose parent2 uniformely among the fittest_subpopulation
 5:         if parent1 different from parent2 then
 6:             choose position1 randomly among uni([0,length of cycles-1)
 7:             choose position2 randomly among uni([0,length of cycles-1)
 8:             divide parent1 in three sections:
 9:             [parent10:position1]
10:             parent1[position1:position2]
11:             parent1[posotion2:]
12:             divide parent2 in three sections:
13:             parent2[0:position1]
14:             parent2[position1:position2]
15:             parent2[posotion2:]
16:             breed child1 justapposing in the order:
17:             parent1[0:position1]
18:             all the cities not in parent1[0:position1] and not in parent2[posotion2:]
19:             parent2[posotion2:]
20:             breed child2 justapposing in the order:
21:             parent2[0:position1]
22:             all the cities not in parent2[0:position1] and not in parent1[posotion2:]
23:             parent1[posotion2:]
24:         else
25:             child1 ← parent1
26:             child2 ← parent1
27:         end if
28:     end for
29:     new_population is a vector of the children
30: end function
```

1: **function** MUTATE(**new_population**, p)
2:     test ← unif[0,1]
3:     **if** t **then**est < p
4:         choose position1 randomly among uni([0,length of cycles-1)
5:         choose position2 randomly among uni([0,length of cycles-1)
6:         swap the cities in position1 and position2
7:     **end if**
8:     order the population by fitness
9:     **fittest_subpopulation** ← extract $n\_parents$ in order from the sorted population
10:     return **fittest_subpopulation**
11: **end function**