

May 13, 2021

1 Proyecto final

2 Técnicas de inteligencia artificial

3 Contreras Aguilar Fernando - 201735460

Importaciones

```
[1]: # Imports
import matplotlib.pyplot as plt
import networkx as nx
import pandas as pd
import random
```

Grafo inicial

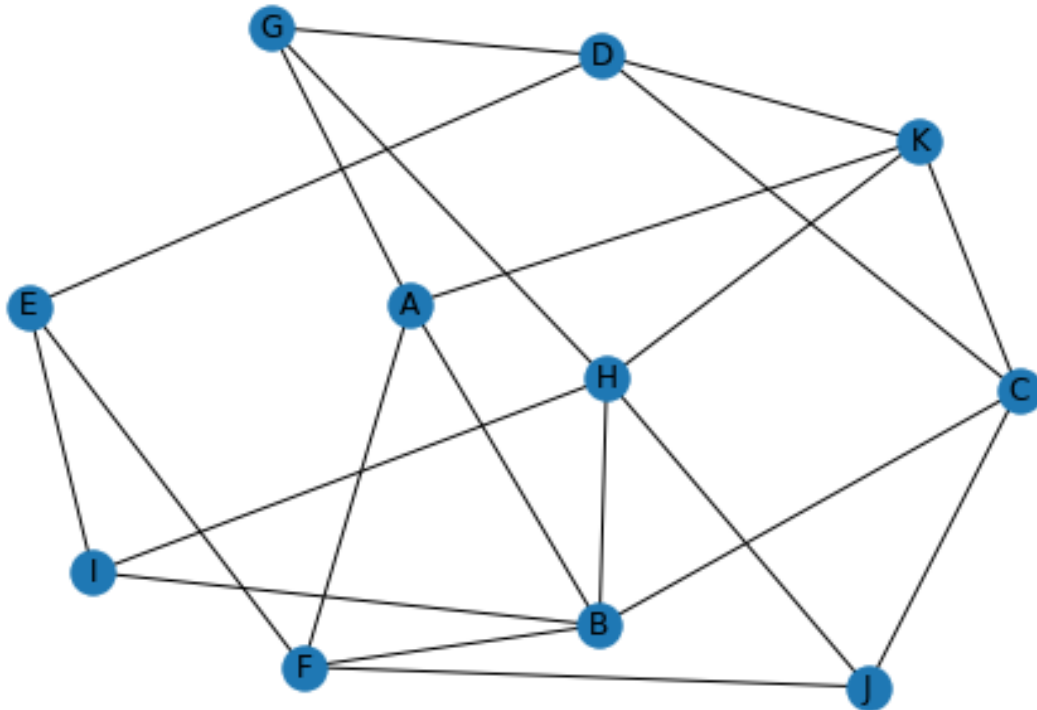
```
[2]: G = nx.Graph()

# relationships
relationships = pd.DataFrame({'from': ['A', 'B', 'C', 'D', 'E', 'F', 'A', 'D', 'G', 'H', 'H', 'B', 'C', 'E', 'F', 'B', 'K', 'C', 'H', 'D', 'B'],
                              'to': ['B', 'C', 'D', 'E', 'F', 'A', 'G', 'G', 'H', 'I', 'J', 'I', 'J', 'I', 'J', 'H', 'A', 'K', 'K', 'K', 'F']})
tuples = list(relationships.to_records(index=False))
print(tuples)

# Graph object
G = nx.from_pandas_edgelist(relationships, 'from', 'to', create_using=nx.Graph())

#plot
pos = nx.kamada_kawai_layout(G)
nx.draw(G, pos, with_labels=True)
plt.show()
```

```
[('A', 'B'), ('B', 'C'), ('C', 'D'), ('D', 'E'), ('E', 'F'), ('F', 'A'), ('A', 'G'), ('D', 'G'), ('G', 'H'), ('H', 'I'), ('H', 'J'), ('B', 'I'), ('C', 'J'), ('E', 'I'), ('F', 'J'), ('B', 'H'), ('K', 'A'), ('C', 'K'), ('H', 'K'), ('D', 'K'), ('B', 'F')]
```



Métodos

```
[38]: class Chromosome(object):
    '''
    Class representing a Chromosome in population
    '''
    def __init__(self, genes):
        self.genes = genes
        self.fitness = self.fit()

    '''
    Calculates fitness of a chromosome
    '''
    def fit(self):
        # Convert a gene in a dictionary, e.g. 'A':"red"
        # i.e. value "red" is accessed by the key 'A'
        dic = dict(self.genes)
        # tuples contains the connections accross the graph
        count = len(tuples)
        for tup in tuples:
            # take a connection, search it's colors with the key
            # if the color matches, the fitness decreases
            if dic[tup[0]] == dic[tup[1]]:
```

```

        count+=-1
    fitness = count*100/len(tuples)
    return fitness

'''
Crossover two chromosomes
'''
def crossover(parent1, parent2):
    s = random.randint(0, len(parent1.genes)-1)
    # Take from 0 to s genes from parent 1
    p1_genes = parent1.genes[:s]
    # Take from s to len from parent 2
    p2_genes = parent2.genes[s:]
    # Add genes from 2 to 1
    p1_genes.extend(p2_genes)
    # Child 1 = Genes1 + Genes2
    child1 = p1_genes
    p1_genes = parent1.genes[s:]
    p2_genes = parent2.genes[:s]
    p2_genes.extend(p1_genes)
    child2 = p2_genes

    return child1, child2

'''
Mutate a chromosome
'''
def mutate(chromosome, colors):
    p = random.random()

    # Since mutation occurs rarely
    if p > 0.90:
        mp = random.random()
        # mutate one gen
        if mp <= 0.40:
            pos = random.randint(0, len(chromosome.genes)-1)
            # Take a random gene and assigns it a random a color
            node = chromosome.genes[pos][0]
            chromosome.genes[pos] = (node, random.choice(colors))
        # mutate third of the genes
        if (mp > 0.40 and mp < 0.60):
            pos = random.sample(range(0, len(chromosome.genes)), int(len(chromosome.
→genes)/3))
            for i in pos:
                node = chromosome.genes[i][0]
                chromosome.genes[i] = (node, random.choice(colors))
        # mutate half of the genes

```

```

    if mp > 0.60 and mp < 0.75:
        pos = random.sample(range(0,len(chromosome.genes)),int(len(chromosome.
→genes)/2))
        for i in pos:
            node = chromosome.genes[i][0]
            chromosome.genes[i] = (node,random.choice(colors))
        # mutate 3/4 of the genes
    if mp > 0.75 and mp < 0.90:
        pos = random.sample(range(0,len(chromosome.genes)),int(len(chromosome.
→genes)*75/100))
        for i in pos:
            node = chromosome.genes[i][0]
            chromosome.genes[i] = (node,random.choice(colors))
        # mutate all of the genes
    if mp >= 0.90:
        for i in range(len(chromosome.genes)):
            node = chromosome.genes[i][0]
            chromosome.genes[i] = (node,random.choice(colors))

```

Población inicial

```

[45]: colors = ['red', 'blue', 'green']
nodes = ['A', 'B', 'C', 'D', 'E', 'F', 'G', 'H', 'I', 'J', 'K']
RV, SV, CV = [], [], []

# Generate a random population size between 20 and 80
pop_size = random.randint(100, 200)

RV = colors
print(RV)

SV = nodes
print(SV)

# Connections r,s between nodes and colors
for _ in range(pop_size):
    chromosome = []
    for x in range(len(SV)):
        chromosome.append((SV[x], random.choice(RV)))
    CV.append(Chromosome(chromosome))

generation = 1
finish = False

```

```

['red', 'blue', 'green']
['A', 'B', 'C', 'D', 'E', 'F', 'G', 'H', 'I', 'J', 'K']

```

```

[46]: while not finish:

    # Sort CV in increasing order of fitness score
    # Puts the fittest chromosome first
    CV = sorted(CV, key = lambda c: c.fitness, reverse=True)

    # If the fittest chromosome has a fitness value of 100, then break
    if CV[0].fitness == 100:
        finish = True
        break

    new_generation = []
    # Elitism on the 10% of the fittest chromosomes
    new_generation.extend(CV[:int((10*len(CV)/100))])

    # Get all chromosomes whose fitness value > 60%
    fittest = []
    for chromosome in CV:
        if chromosome.fitness <= 60:
            break
        fittest.append(chromosome)

    # Crossover two chromosomes and append to the new generation
    for _ in range(50):
        parent1, parent2 = random.choice(fittest), random.choice(fittest)
        child1, child2 = crossover(parent1, parent2)
        new_generation.append(Chromosome(child1))
        new_generation.append(Chromosome(child2))

    CV = new_generation
    mutate(CV[0], colors)

    # Print the best chromosome of the generation
    print("Generation: ", generation, " Genes", CV[0].genes, " Fitness:", CV[0].
    ↪fitness)

    generation += 1

    # End of the algorithm, CV[0] is the fittest chromosome because it's sorted by
    ↪fitness
    print("Generation: ", generation, " Genes", CV[0].genes, " Fitness:", CV[0].
    ↪fitness)

```

```

Generation:  1  Genes [('A', 'red'), ('B', 'blue'), ('C', 'red'), ('D',
'green'), ('E', 'red'), ('F', 'green'), ('G', 'red'), ('H', 'green'), ('I',
'blue'), ('J', 'blue'), ('K', 'blue')]  Fitness: 90.47619047619048
Generation:  2  Genes [('A', 'red'), ('B', 'blue'), ('C', 'red'), ('D',
'green'), ('E', 'red'), ('F', 'green'), ('G', 'red'), ('H', 'green'), ('I',

```



```

'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 19 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'blue'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 20 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'blue'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 21 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'blue'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 22 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'blue'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 23 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'blue'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 24 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'blue'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 25 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'blue'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 26 Genes [('A', 'blue'), ('B', 'green'), ('C', 'red'), ('D',
'green'), ('E', 'green'), ('F', 'red'), ('G', 'blue'), ('H', 'blue'), ('I',
'red'), ('J', 'blue'), ('K', 'green')] Fitness: 95.23809523809524
Generation: 27 Genes [('A', 'red'), ('B', 'blue'), ('C', 'red'), ('D',
'green'), ('E', 'red'), ('F', 'green'), ('G', 'blue'), ('H', 'red'), ('I',
'green'), ('J', 'blue'), ('K', 'blue')] Fitness: 100.0

```

```

[37]: G = nx.Graph()

colors_map = []
for node in CV[0].genes:
    colors_map.append(node[1])

print(colors_map)

# Graph object
G = nx.from_pandas_edgelist(relationships, 'from', 'to', create_using=nx.
    ↳Graph())

#plot
pos = nx.kamada_kawai_layout(G)
nx.draw(G, pos, with_labels=True, node_color=colors_map)
plt.show()

```

```

['red', 'green', 'blue', 'red', 'green', 'blue', 'blue', 'red', 'blue', 'green',
'green']

```

