Lab 7: Optimization using Genetic Algorithms

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1 Objectives

The main objective for this lab is to create a numerical optimization example using Genetic Algorithms and then to develop your own custom version of the optimizer for more general purpose applications.

- 1. Learn how Genetic Algorithms (GA) optimization works using an example
- 2. Create a simple Genetic Algorithms (GA) function to optimize a number
- 3. Create a Genetic Algorithm (GA) to optimize a function

At the end of this laboratory session you should have the basic framework for Genetic Algorithm (GA) optimization and you could explore how to potentially apply this to optimization of neural network parameters.

2 Getting Started

2.1 Introduction

In this example we will take the case of trying to optimize a set of numbers (with size N) such that the sum of the numbers adds up to a target value. For example, we might have N=5 (5 numbers) and optimize them such that the sum of these 5 numbers adds up to 173.

2.2 Example Code

I have provided a basic example (Source: https://lethain.com/genetic-algorithms-cool-name-damn-simple/) which accomplishes this in Python. The source code for this is provided on Moodle.

```
1 from random import randint, random
2 from operator import add
3 import matplotlib.pyplot as plt
4
5 def individual(length, min, max):
```

```
'Create_a_member_of_the_population.'
 7
        return [ randint(min, max) for x in xrange(length) ]
8
9
   def population (count, length, min, max):
10
11
   Create_a_number_of_individuals_(i.e._a_population).
12
   ___count: _the _number_of _individuals _in _the _population
13
   ___length:_the_number_of_values_per_individual
14
   ____min:_the_minimum_possible_value_in_an_individual's_list_of_values
15
   ___max: _the _maximum_possible _value _in _an _individual's _list _of _values
16
17
   18
        return [ individual(length, min, max) for x in xrange(count) ]
19
20
21
   def fitness (individual, target):
22
23
   ____Determine_the_fitness_of_an_individual._Higher_is_better.
24
25
   ___individual: _the _individual _to _evaluate
   ____target:_the_target_number_individuals_are_aiming_for
   ....""
27
28
       sum = reduce(add, individual, 0)
29
        return abs(target-sum)
30
   def grade(pop, target):
31
32
        'Find_average_fitness_for_a_population.'
33
        summed = reduce(add, (fitness(x, target) for x in pop))
34
        return summed / (len(pop) * 1.0)
35
   def evolve(pop, target, retain=0.2, random_select=0.05, mutate=0.01):
36
37
        graded = [ (fitness(x, target), x) for x in pop ]
38
        graded = [x[1] \text{ for } x \text{ in } sorted(graded)]
39
        retain_length = int(len(graded)*retain)
        parents = graded[:retain_length]
40
41
        # randomly add other individuals to
42
        # promote genetic diversity
        for individual in graded[retain_length:]:
43
44
            if random_select > random():
45
                parents.append(individual)
46
        # mutate some individuals
47
        for individual in parents:
48
            if mutate > random():
49
                pos\_to\_mutate = randint(0, len(individual)-1)
50
                # this mutation is not ideal, because it
51
                # restricts the range of possible values,
52
                # but the function is unaware of the min/max
53
                # values used to create the individuals,
54
                individual [pos_to_mutate] = randint (
                    min(individual), max(individual))
55
```

```
56
        # crossover parents to create children
57
        parents_length = len(parents)
58
        desired_length = len(pop) - parents_length
59
        children = []
        while len(children) < desired_length:
60
61
            male = randint(0, parents\_length-1)
62
            female = randint(0, parents\_length-1)
63
            if male != female:
                male = parents [male]
64
65
                female = parents [female]
                half = len(male) / 2
66
                child = male[:half] + female[half:]
67
68
                children.append(child)
69
        parents.extend(children)
70
        return parents
71
72
73 # Example usage
74
   target = 550
   p_count = 100
   i_length = 6
   i_min = 0
77
78
   i_max = 100
79
   generations = 100
   p = population(p_count, i_length, i_min, i_max)
80
   fitness_history = [grade(p, target),]
82
   for i in xrange (generations):
83
        p = evolve(p, target)
84
        fitness_history.append(grade(p, target))
85
86
   for datum in fitness_history:
87
       print datum
88
89
   plt.plot(fitness_history)
90
   plt.show()
```

The plot at the end of the simulation will plot the fitness history (i.e. how close the best population matches the target value). The default values for the code provided are as follows:

```
    target = 550
    p_count = 100
    i_length = 6
    i_min = 0
    i_max = 100
```

6. generations=100

We can look at the sections of code and observe the functions mapping onto the key stages of the GA.

2.3 Stage 1: Create an Initial Population

```
1 def individual(length, min, max):
2    'Create_a_member_of_the_population.'
3     return [ randint(min, max) for x in xrange(length) ]
```

In this function a member of the population individual is created, limited between the min and max values. This function is then called p_count times to create the population:

```
def population(count, length, min, max):
    """

cull Create Launumber Lof Lindividuals Linuthe Lopopulation).

cullength: Linumber Lof Lindividuals Linuthe Lopopulation

cullength: Linumber Lof Lindividual Linumber Linumber Lof Lindividual

cullength: Linumber Lof Lindividual Linum Lindividual Sulist Lof Linumber Li
```

2.4 Stage 2: Iterate over the Generations

In the main loop, the evolve function is called a number of times (the "generations")

```
1 for i in xrange(generations):
2     p = evolve(p, target)
3     fitness_history.append(grade(p, target))
```

the evolve function is where the key stages of the GA occur

2.5 Stage 3: Ranking the Population

The Population is first graded:

```
graded = [ (fitness(x, target), x) for x in pop]
graded = [ x[1] for x in sorted(graded)]
retain_length = int(len(graded)*retain)
parents = graded[:retain_length]
and this requires calling the fitness function:
```

```
def fitness(individual, target):
    """

Determine_the_fitness_of_an_individual._Higher_is_better.

Judy individual:_the_individual_to_evaluate
```

In this case the fitness is the absolute value of the difference between the target and the current value of the summation. This would need to be modified for the specific application.

2.6 Stage 4: Random Parent Selection and Mutation

Before the crossover can take place we need to randomly select parents - remember you could aply some other techniques here such as elitism if you wish or a combination of techniques including roulette wheel selection.

```
# randomly add other individuals to
1
2
       # promote genetic diversity
3
        for individual in graded [retain_length:]:
4
            if random_select > random():
                parents.append(individual)
5
       # mutate some individuals
6
7
       for individual in parents:
            if mutate > random():
8
9
                pos\_to\_mutate = randint(0, len(individual)-1)
                # this mutation is not ideal, because it
10
                # restricts the range of possible values,
11
                # but the function is unaware of the min/max
12
13
                # values used to create the individuals,
14
                individual [pos_to_mutate] = randint (
15
                    min(individual), max(individual))
```

A random mutation is applied to the genetic material at this point, but we could equally well apply it to the offspring

2.7 Stage 5: Crossover/Breeding

The crossover is then completed and the resulting population is returned ready for the next iteration:

```
1
       # crossover parents to create children
2
        parents_length = len(parents)
3
        desired_length = len(pop) - parents_length
4
        children = []
5
        while len(children) < desired_length:
            male = randint(0, parents_length - 1)
7
            female = randint(0, parents_length - 1)
            if male != female:
9
                male = parents [male]
10
                female = parents [female]
11
                half = len(male) / 2
                child = male[:half] + female[half:]
12
```

```
13 children.append(child)
14 parents.extend(children)
15 return parents
```

Note, that we have lots of options with the algorithm, we can allow the population to expand, we can limit to a certain size, we can implement elitism, we can implement mutation in a different stage (i.e. post cross-over) etc.

3 Lab Exercise

- 1. Modify the code (or create your own from scratch) to create a simple optimization where the function of the optimizer is to simply find a number specified in the shortest number of iterations
- 2. How do the number of generations, mutation and crossover parameters affect how quickly a solution is found?
- 3. How could you stop the algorithm when a suitabe solution had been found to avoid excessive computation time?
- 4. Create an optimization to optimize a set of parameters for a curve of order n e.g.

$$y = p_n x^n + p_{n-1} x^{n-1} + \dots p_0 (1)$$

Exercises:

- 1. Modify the code (or create your own from scratch) to create a simple optimization where the function of the optimizer is to simply find a number specified in the shortest number of iterations.
- 2. How do the population size, mutation and crossover parameters (such as mutation probability and crossover probability) affect how quickly a solution is found?
- 3. How could you stop the algorithm when a suitable solution had been found to avoid excessive computation time?
- 4. Create an optimization using GA to optimize a set of parameters for a curve of a 5th-order polynomial as given below:

$$y = 25x^5 + 18x^4 + 31x^3 - 14x^2 + 7x - 19$$

5. Show your understanding on the Holland's Schema Theorem. Explain the Holland's Schema Theorem based on Question 4 using GA with binary encoding.

Submission Requirements:

- 1. You need submit a report in PDF file.
- 2. An appendix of coding should be given (no page limit).

40% - quality of writing 60% - performance of the results

More Explanations on Coursework B

Actually, the exercises have open solutions. As different students have different programming capabilities, I don't want to constrain the solutions in a strict format.

1. For Exercises 1-4, binary encoding is optional. For Exercise 5, you should use binary encoding to explain Holland Schema Theorem with quantitative analysis.

2. Exercise 4:

You can do it based on two ideas:

- i) The 5 coefficients and 1 constant term are set as targets, and you use GA to find them. It is similar to Exercise 1.
- ii) You give a range for x, for example, -100 to 100, and randomly select some points of the polynomial provided, for example, 100 points as targets. You use GA to find these targets and generate a new line that should match the polynomial provided. It is similar to exercise 4 in Lab of Simulated Annealing.

You may do Exercise 4 using either one of the above two ideas. You may use both ideas to do a comparison study if you can.

You may also use other ideas of GA to accomplish Exercise 4. The solutions are open!

3. Report:

There is no page limit for the main report.

The code should be given in Appendix.

In main report, you may show the results and figures, explain the results, and analyse your design.

For example, regarding Exercise 4, at the beginning, what is the initial curve generated by GA? After 100, 200, 500, generations, what are the curves generated by GA? In final, how about the curve matching the target polynomial in a figure?

Test and explain the key parameter settings.

For example, if the mutation probability is changed, 1%, 5%, 10%, how about the effect on the final performance?

How about the effect of different crossover probabilities?

How about the results if you use different fitness functions?

How about the results if you use different selection methods, Roulette wheel, ranking, and elitism?

How about the results if you use different termination criteria?

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