Assignment 3 **Assignment 3: Evolutionary Algorithms Goal**: Get familiar with evolutionary algorithms by implementing it and applying it to a given non-differentiable optimization task. In this assignment, we are going to learn about evolutionary algorithms (EAs). The goal is to implement components of an evolutionary algorithm: a recombination operator, a mutation operator, and selection mechanisms, and analyze their behavior. This assignment is open to any choice of the aforementioned components as long as they are well motivated. We are interested in optimizing a given black-box function that could be queried (i.e., it returns a value of the objective for given input values), but the gradient wrt the input cannot be calculated. The input to the system is a vector: $\mathbf{x} = [lpha_0, n, eta, lpha]^ op \in [-2, 10] imes [0, 10] imes [-5, 20] imes [500, 2500].$ The optimized function is based on the gene repressilator model. For details, please see Section 4.2 in HERE. 1. Understanding the problem The considered problem is about finding parameter values of a model widely used in biology, namely, the gene repressilator model. This model represents a simple network in which a gene (mRNA) is produced by a protein, and then this gene is used to produce another protein. Altogether, there are 3 genes and 3 proteins that are connected as follows: $m_1 \rightarrow p_1$, $p_1 \rightarrow m_2$, $m_2 \rightarrow p_2$, $p_2 \rightarrow m_3$, $m_3 \rightarrow p_3$, $p_3 \rightarrow m_1$. Please run the code below and spend a while on analyzing the signals in the model. Think of the osscilatory character of the signals. If any code line is unclear to you, please read on that in numpy or matplotlib docs. In [1]: import pickle import copy import numpy as np import matplotlib.pyplot as plt from scipy.integrate import solve_ivp import random EPS = 1.e-7In [2]: # PLEASE DO NOT REMOVE! # This is the main class for the gene repressilator model. # There is no need to understand how it works! You can treat it as a black-box. # It is important to realize that we can always ask this object to give us # an evaluation of given parameter values. class Repressilator(object): def __init__(self, y_real, params): super().__init__() self.y real = y real.copy() self.params = params.copy() # The definition of the gene repressilator model as a system of ODEs. def repressilator_model(self, t, y): m1, m2, m3, p1, p2, p3 = y[0], y[1], y[2], y[3], y[4], y[5]alpha0 = self.params['alpha0'] n = self.params['n'] beta = self.params['beta'] alpha = self.params['alpha'] dm1 dt = -m1 + alpha / (1. + p3**n) + alpha0dp1 dt = -beta * (p1 - m1) $dm2_dt = -m2 + alpha / (1. + p1**n) + alpha0$ dp2 dt = -beta * (p2 - m2) $dm3_dt = -m3 + alpha / (1. + p2**n) + alpha0$ dp3 dt = -beta * (p3 - m3)return dm1_dt, dm2_dt, dm3_dt, dp1_dt, dp2_dt, dp3_dt # A numerial solver for the model (here we use Runge-Kutta 4.5) def solve repressilator(self): # we need to use lambda function if we want to pass some parameters solution = solve ivp(lambda t, y: self.repressilator model(t, y), t_span=(self.params['t0'], self.params['t1']), y0=self.params['y0'], method='RK45', t eval=self.params['t points']) y points = np.asarray(solution.y) return self.params['t_points'], y_points # An auxiliary function: setting parameters. def set_params(self, x): self.params['alpha0'] = x[0]self.params['n'] = x[1]self.params['beta'] = x[2]self.params['alpha'] = x[3]# Calculating the objective function. # Here, we use the Euclidean distance between the real data and the synthetic data. @staticmethod def loss(y_real, y_model): # we assume only m's are observed! $y_r = y_real[0:3]$ $y_m = y_model[0:3]$ **if** y r.shape[1] == y m.shape[1]: return np.mean(np.sqrt(np.sum((y_r - y_m)**2, 0))) else: return np.infty def objective(self, x): **if** len(x.shape) > 1: objective values = [] for i in range(x.shape[0]): xi = x[i]self.set params(xi) _, y_model = self.solve_repressilator() objective values.append(self.loss(self.y_real, y_model)) objective_values = np.asarray(objective_values) else: self.set params(x) _, y_model = self.solve_repressilator() objective_values = self.loss(self.y_real, y_model) return objective_values In [3]: # PLEASE DO NOT REMOVE! # Initialize the problem. # Here we set the real parameters and generate "real" data. To make the problem # more realistic, we add a small Gaussian noise. params = {} params['alpha0'] = 1.1 params['n'] = 2.9params['beta'] = 5.5 params['alpha'] = 500 params['t0'] = 0.params['t1'] = 60.5 params['t points'] = np.asarray([0. , 0.5, 1. , 1.5, 2. , 2.5, 3. , 3.5, 4., 4.5, 5., 5.5, 6., 6.5, 7., 7.5, 8., 8.5, 9., 9.5, 10., 10.5, 11., 11.5, 12. , 12.5, 13. , 13.5, 14. , 14.5, 15. , 15.5, 16. , 16.5, 17. , 17.5, 18. , 18.5, 19. , 19.5, 20. , 20.5, 21. , 21.5, 22. , 22.5, 23. , 23.5, 24. , 24.5, 25. , 25.5, 26. , 26.5, 27. , 27.5, 28. , 28.5, 29. , 29.5, 30. , 30.5, 31. , 31.5, 32. , 32.5, 33. , 33.5, 34. , 34.5, 35. , 35.5, 36. , 36.5, 37. , 37.5, 38. , 38.5, 39. , 39.5, 40. , 40.5, 41. , 41.5, 42. , 42.5, 43. , 43.5, 44. , 44.5, 45. , 45.5, 46. , 46.5, 47. , 47.5, 48. , 48.5, 49. , 49.5, 50. , 50.5, 51. , 51.5, 52., 52.5, 53., 53.5, 54., 54.5, 55., 55.5, 56. , 56.5, 57. , 57.5, 58. , 58.5, 59. , 59.5]) params['x0'] = np.asarray([[5.64167522, 2.07180539, 3.56690274, 7.0015145]]) params['y0'] = np.asarray([0.0, 0.0, 0.0, 2.0, 1.0, 3.0])# Generate "real" data r = Repressilator([0], params) _, y_real = r.solve_repressilator() del(r) # we remove the object, just in case y_real = y_real + np.random.randn(*y_real.shape) * 5. # add noise! In [4]: # PLEASE DO NOT REMOVE # Here, we plot all signals in the model. # Note that later on, we assume that only gene expression (i.e., m1, m2, m3) # are observed (blue plots) and proteins (i.e. p1, p2, p3) are unobserved (in red). t = params['t points'] fig_data, axs = plt.subplots(2,3,figsize=(20, 4)) fig data.tight layout() for i in range(2): for j in range(3): **if** i == 0: title = 'm' color = 'b' else: title = 'p' color = 'r' axs[i,j].plot(t, y_real[2*i+j], color) axs[i,j].set title(title + str(j+1)) m1 m2 75 75 50 50 50 25 25 25 30 p3 20 40 50 75 75 50 50 50 25 25 25 10 20 30 50 20 10 30 2. Evolutionary Algorithms In this assignment, you are asked to implement an evolutionary algorithm (EA). Please take a look at the class below and fill in the missing parts. Please keep in mind that you are free to choose any operations as lons as they are appropriate for evolutionary algorithms. NOTE: Please pay attention to the inputs and outputs of each function. Question 1 (0-0.5pt): Do you use a mutation operator? If yes, please explain in detail your choice. If not, please explain why not. **Answer:** I use the single-point mutation. The mutation function generates a random variable for each bit in a sequence. This random variable tells whether or not a particular bit will be flipped. This mutation procedure, based on the biological point mutation, is called single point mutation. Mutation introduces randomness to the sample of x_children in EA, making it beneficial in most circumstances to converge to a better solution faster. Question 2 (0-0.5pt): Do you use a cross-over operator? If yes, please explain in detail your choice. If not, please explain why not. **Answer:** We use a random point crossover mechanism (i.e., if there are n parameters, we choose the first n1 parameters of parent 1 and the last n-n1 parameters of parent2 to generate a new individual. Question 3 (0-0.5pt): What kind of selection mechanism do you use? Please explain in detail and motivation your choice. Answer: For selection mechanism, I chose roulette wheel selection, since it weights the objects individually according to their fitness. This means fitter instances have a higher likelyhood of being selected as parents. For roulette wheel we adapt the fitness function via linear dynamic scaling so we can get x_parents with their drawn indicies in relation to idx. Roulette is a non deterministic way of selecting in the long term, since no trait that might help in a few generations get eliminated early on. Question 4 (0-0.5pt): Do you use any other operation? If yes, please explain and motivate your choice. **Answer:** In the survivor selection the Fitness values of the instances were manipulated to incorporate the roulette wheel selection properly. The values are converted from a [0:inf) range into a [0:1] range and are then normalized. Doing so provides the algorithm with additional probabilities, these probabilities are used as weights for random sampling, determining furture parents. **Question 5 (0-0.5-1pt):** Please provide a pseudo-code for your evolutionary algorithm. Please try to be as formal as possible! **Answer:** declare class EA passing object argument define function parent selection with arguments x old and f old normalise fitness values by ranging from [0:1] total is equal to normalised fitness values / sum of the normalised fitness values # adapt fitness function to parent_selection idx equal to random choices ranging in x_old x_parents equal to x_old with idx as argument f_parents equal to f_old with idx as argument return x_parents and f_parents define function recombination with arguments x parents and f parents decalre empty list x children For i Loop through range of len(x_parnets[0]) using random crossover $x_{children.append}(x_{parents})$ with random integer ranging from i, i-1) return array of x_children define function mutation with arguments $x_{children}$ and std=0.1for i loop through range of x children.shape[0]: declare variable random value equal to np.random.uniform(-1.0, 1.0, 1)declare variable x_children[i, 3] equal to (x_children[i, 3] plus random_value) return x_children times std # GRADING: # 0.5 pt if code works but some functions are incorrect and it is badly explained # 1.0 pt if code works but some functions are incorrect # 2.0 pt if code works but it does not correspond to the description above and it is badly explained # 2.5 pt if code works and it is well explained, but it does not correspond to the description above # 3.0 pt if code works and it is aligned with the description about, but it is badly explained # 3.5 pt if code works and it is aligned with the description about, and it is well explained # 4.0 pt if code works, it is as it was described, it is well explained, and the proposed operations are beyond the lecture! # Implement the Evolutionary Algorithm (EA) algorithm. # It is equivalent to implementing the step function. class EA(object): def __init__(self, repressilator, pop_size,std = 0.1, bounds_min=None, bounds_max=None): self.repressilator = repressilator self.pop_size = pop_size self.bounds min = bounds min self.bounds max = bounds max self.std = std #self.objective value = objective value # PLEASE FILL IN # all necessary hyperparameters come here # PLEASE FILL IN # all necessary operations (e.g., mutation, selection) must come here. def parent_selection(self, x_old, f_old): $norm_fitness_values = np.nan_to_num(np.array(list(map(lambda x: 1-(x/(1+x)), f_old))))$ # normalise the fitness values by ranging from [0:1] total = norm_fitness_values/sum(norm_fitness_values) idx = np.random.choice(list(range(len(x_old))),int(self.pop_size/2), replace = False, p=total) # fitness function adapted to parent selection x_parents = x_old[idx] # getting parents with drawn indicies f parents = f old[idx] # getting parents with drawn indicies sa = np.argsort(total) # sort the sample return x parents, f parents def recombination(self, x_parents, f_parents): x children = [] for i in range(amt := len(x_parents[0])): x_children.append(x_parents[random.randint(i-1, i)]) # using the random crossover method return np.array(x_children) def mutation(self, x_children, std=0.1): # single point mutation # Mutation changes a single gene in each offspring randomly. for i in range(x children.shape[0]): # The random value to be added to the gene. random value = np.random.uniform(-1.0, 1.0, 1) x_children[i, 3] = (x_children[i, 3] + random_value) return x children * std return x+np.random.randn(x.shape[0],x.shape[1]) * std def survivor selection(self, x old, x children, f old, f children): x = np.concatenate([x old, x children]) f = np.concatenate([f old, f children]) inds = f.argsort() #get indices in sorted by best loss x,f = x[inds], f[inds] #rearrange both arrays return x[:self.pop_size], f[:self.pop_size] # Evaluation step: DO NOT REMOVE! def evaluate(self, x): return self.repressilator.objective(x) def step(self, x old, f old): #----# PLEASE FILL IN # NOTE: This function must return x, f # where x - population f - fitness values of the population x_parents, f_parents = self.parent_selection(x old, f old) x children = self.recombination(x parents, f parents) x children = self.mutation(x children, self.std) f children = self.evaluate(x children) x, f = self.survivor_selection(x_old, x_children, f_old, f_children) return x, f NOTE 1 Since this assignment allows you implementing your own operations, this is difficult to prepare a code for that. Therefore, please use the code below to find the best set of your hyperparameters in a separate file, and then present your analysis for the best values of the hyperparameters here. NOTE 2 Additionally, please do try various population sizes (25, 50, 100, ...). You will be asked about it later. In [6]: # PLEASE DO NOT REMOVE! num generations = 400 # if necessary, please increase the number of generations pop size = 150 std = 0.25bounds min = [-2., 0., -5., 0.]bounds_max = [10., 10., 20., 2500.] # PLEASE FILL IN! # Your hyperparams go here. # PLEASE USE THE VALUES OF THE HYPERPARAMETERS FOR WHICH YOU OBTAINED THE BEST RESULTS. # DO NOT ITERATE OVER THEM! #----# Initialize the repressilator repressilator = Repressilator(y real, params) #----# PLEASE FILL IN! # Your object goes here: ea = EA(repressilator, pop size, std) #----# Init the population x = np.random.uniform(low=bounds_min, high=bounds_max, size=(pop_size, 4)) f = ea.evaluate(x)# We want to gather populations and values of the best candidates to further # analyze the algorithm. populations = [] populations.append(x) f_best = [f.min()] # Run the EA. for i in range(num generations): if i % int(num generations * 0.1) == 0: print('Generation: {}, best fitness: {:.2f}'.format(i, f.min())) x, f = ea.step(x, f)populations.append(x) if f.min() < f best[-1]:</pre> f best.append(f.min()) else: f best.append(f best[-1]) print('FINISHED!') /var/folders/qg/7hcjbd513nvfwgf0py3h14040000gp/T/ipykernel_65234/2191093490.py:23: RuntimeWarning: invalid value encountered in double_scalars dm2 dt = -m2 + alpha / (1. + p1**n) + alpha0Generation: 0, best fitness: 45.96 /var/folders/qg/7hcjbd513nvfwgf0py3h14040000gp/T/ipykernel 65234/2191093490.py:25: RuntimeWarning: invalid value encountered in double scalars dm3 dt = -m3 + alpha / (1. + p2**n) + alpha0/var/folders/qg/7hcjbd513nvfwgf0py3h14040000gp/T/ipykernel 65234/2191093490.py:21: RuntimeWarning: invalid value encountered in double scalars dm1 dt = -m1 + alpha / (1. + p3**n) + alpha0/var/folders/qg/7hcjbd513nvfwgf0py3h14040000gp/T/ipykernel_65234/448111030.py:33: RuntimeWarning: invalid value encountered in double_scalars norm fitness values = np.nan to num(np.array(list(map(lambda x: 1-(x/(1+x)), f old)))) Generation: 40, best fitness: 32.67 Generation: 80, best fitness: 32.67 Generation: 120, best fitness: 32.67 Generation: 160, best fitness: 32.67 Generation: 200, best fitness: 32.67 Generation: 240, best fitness: 32.67 Generation: 280, best fitness: 32.67 Generation: 320, best fitness: 32.67 Generation: 360, best fitness: 32.67 FINISHED! In [7]: # PLEASE DO NOT REMOVE # Generate signals for the best performing parameter values repressilator.set params(x[f.argmin()],) t, y best = repressilator.solve repressilator() # Create plots fig ea, axs = plt.subplots(2,3,figsize=(20, 4)) fig ea.tight layout() for i in range(2): for j in range(3): **if** i == 0: title = 'm' color = 'b' color m = 'm' else: title = 'p' color = 'r' color_m = 'c' axs[i,j].plot(t, y_real[2*i+j], color, label='Data') axs[i,j].plot(t, y_best[2*i+j], color_m, label='EA') axs[i,j].set_title(title + str(j+1)) axs[i,j].legend() m1 m2 100 100 100 50 50 50 100 100 100 50 50 50 20 30 In [8]: # PLEASE DO NOT REMOVE # Generate scatterplots for the populations gens = [0, num_generations//4, num_generations//2, num_generations] fig ea pops, axs = plt.subplots(1,4,figsize=(16, 4)) fig_ea_pops.tight_layout() for i in range(len(gens)): pop_i = populations[gens[i]] axs[0].scatter(pop_i[:,0], pop_i[:,1], label=str(gens[i])) axs[1].scatter(pop_i[:,0], pop_i[:,2], label=str(gens[i])) axs[2].scatter(pop_i[:,2], pop_i[:,3], label=str(gens[i])) axs[3].scatter(pop_i[:,1], pop_i[:,2], label=str(gens[i])) axs[0].legend(), axs[1].legend(), axs[2].legend(), axs[3].legend() axs[0].set_title(r'\$\alpha_0\$ vs. \$n\$') axs[1].set_title(r'\$\alpha_0\$ vs. \$\beta\$') axs[2].set title(r'\$\beta\$ vs. \$\alpha\$') axs[3].set title(r'\$n\$ vs. \$\alpha\$') Text(0.5, 1.0, '\$n\$ vs. \$\\alpha\$') Out[8]: α₀ vs. n β vs. α n vs. α 10 1500 1000 500 In [9]: # PLEASE DO NOT REMOVE # The convergence plot: the best value of the fitness function for each generation plt.plot(range(len(f_best)), f_best) plt.title('The convergence') plt.grid() The convergence 44 42 40 38 36 34 100 150 200 250 300 4. Final remarks: Analysis Eventually, please answer the following last questions that will allow you to conclude the assignment. Question 6 (0-0.5pt): After analyzing the results, do you think your algorithm discovered the real values of the parameters? Why? Please indicate which plots indicate that? If not, what is a potential explanation? Answer: The results have found the real values of the parametes as we can see in the results it has found the best fitness values of 32.67. Because our EA mostly applies a random-based appraoch, it tries to enhance the solutions of the x_children by applying random changes to them. Because such changes are random, we are not sure that they will produce better solutions. For such reason, it is preferred to keep the previous best solutions (parents) in the new population. Hence, everytime the algorithm is run it finds new and better solutions, for instabce in this trial the best fitness value was 32.67. This is also reflected on the graph "The convergence" as it drops to 32.67 from 46, and remains consistent at that point for future generations. Question 7 (0-0.5pt): How the population influences the performance of evolutionary algorithms? What population sizes did you use? Answer: The population size had a drastic impact on the performance of the algorithm. Sizes smaller than 100 did not perform well, since it is probable that the sampling does not discover enough points for an efficient convergance to happen. In the worst case when all the new offspring are worse than such parents, we will continue using such parents. As a result, we guarantee that the new generation will at least preserve the previous good results and will not go worse. The new population will have its first 4 solutions from the previous parents. The last 4 solutions come from the offspring created after applying crossover and mutation: **Question 8 (0-0.5pt)**: What are the advantages of your approach? **Answer**: Question 9 (0-0.5pt): What are the drawbacks of your approach? **Answer**: Because my approach is mostly random based it does fail to find the next best point. because x_children are always randomly mutated with random x_parents, it fails to find the best parents in the popultion to creat offspring and mutate with, so this approach does not always appoach the best solution. Question 10 (0-0.5pt): How could you improve convergence speed of your algorithm? Please provide very specific answer, ideally supported with literature and mathematical formulas. **Answer**: PLEASE FILL IN Question 11 (0-0.5pt): How does an EA compares with the Metropolis-Hastings algorithm? What are the similarities? What are the differences? Answer: MH is a stochastic search technique, it is a method for obtaining a sequence of random samples from a probability distribution from which direct sampling is difficult. MH is first performed on the basis of starting at a random state and then simulating the constructed Markov-process for this state, progressively better programs will be generated Genetic Algorithms are a class of algorithms rather than a specific implementation. However, a genetic algorithm takes inspiration from the natural process of evolution. By defining operators on one or multiple programs, we can simulate the natural evolution process. By selecting x_parents suited to the fitness function and producing offspring illustrates the best possible offspring or solution to the respective problem.