

Results of genetic algorithm on finding the minimum of a function

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Abstract

This homework provides the introduction to genetic algorithms. These algorithms model Darwinian genetic inheritance and struggle for survival. Along with two other directions: evolutionary strategies and evolutionary programming, they form the class of evolutionary algorithms. It focuses on the aspect of achieving a 94% success in finding the minimum of a function. Results are as expected in the good range of expectations. The average is better, the minimum is better and an overall improvement in time is considerably bigger and this allows us to push the limits of computing power and reevaluate the negotiation between speed and accuracy.

1 Objective

Determine which approach is better for getting the minimum for the next functions.

- a. Booth
- b. Eusom
- c. Shubert
- d. Rastrigin

1.1 Definitions

Booth Function

$$f(X) = (x_1 + 2x_2 - 7)^2 + (2x_1 + x_2 - 5)^2 \quad (1)$$

Eusom Function

$$f(x, y) = -\cos(x_1)\cos(x_2)\exp(-(x - \pi)^2 - (y - \pi)^2) \quad (2)$$

Shubert Function

$$f(\mathbf{x}) = f(x_1, \dots, x_n) = \prod_{i=1}^n \left(\sum_{j=1}^5 \cos((j+1)x_i + j) \right) \quad (3)$$

Rastrigin Function

$$f(x, y) = 10n + \sum_{i=1}^n (x_i^2 - 10\cos(2\pi x_i)) \quad (4)$$

2 Setup

Evolutionary algorithms use a vocabulary borrowed from genetics:

The evolution is simulated by a succession of generations of a population of candidate solutions;

A candidate solution is called a chromosome and is represented as a gene string; (in our case, implemented as Bitstring)

The gene is the atomic information of a chromosome; (in our case, the bit)

The position a gene occupies is called a locus;

All possible values for a gene form the set of alleles of the gene;

The population evolves by applying genetic operators: mutation (we mutate with a chance of 0.01%) and crossbreeding (we crossbreed two individuals by swapping the gense from index ind1 to ind2, indexes that are randomly generated);

The chromosome to which a genetic operator is applied is called a parent and the resulting chromosome is called a descendant;

Selection is the procedure by which the chromosomes are chosen that will survive in the next generation; better adapted individuals will be given greater chances; Here we use the wheel of fortune.

The degree of adaptation to the environment is measured by the fitness function;

The solution returned by a genetic algorithm is the best individual of the last generation.

The experiment is done within 2, 5 and 30 dimensions.

For each dimension, each function will be ran with a deterministic aproach to find the minimum.

The final results will be composed of the minimum from all of these 30 runs.

3 Sample Calculation

2 Dimensions - Genetic Algorithm				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	0.00001	0.03786	0.09468178	4.00765
Easom	-0.9999837	-0.4404394	0.4160743	-0.3384428
Shubert	0.0001404771	0.129941	0.1605601	0.06866111
Rastrigin	0.0004495805	0.87353	0.8240688	0.5921164

2 Dimensions - Hill Climbing				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	2	20.33818	30.17318	6.500013
Easom	-1	-0.4330835	0.5037164	-2.7e-09
Shubert	0.01151226	40.62198	22.8239	58.68443
Rastrigin	1e-10	3.134486	3.481765	1.994961

2 Dimensions - Simulated Annealing				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	4.07222	586.9657	544.5047	394.3619
Easom	-5e-10	-3.333333e-11	1.268541e-10	0
Shubert	0.3571665	77.25411	30.87428	76.6366
Rastrigin	4.365741	41.54321	22.93483	40.4976

5 Dimensions - Genetic Algorithm				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	0	0.08409	0.1978363	0.01643
Easom	-0.9999837	-0.4404394	0.4160743	-0.3384428
Shubert	-60.99586	-58.58381	38.42919	-60.02898
Rastrigin	0.008684981	2.684578	2.697075	2.006103

5 Dimensions - Hill Climbing				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	2	17.51634	28.78196	2.281252
Easom	-1	-0.5996907	0.4980161	-0.9991743
Shubert	-60.99756	-37.25598	27.28942	-59.97212
Rastrigin	4e-10	10.49341	12.28039	5.589442

5 Dimensions - Simulated Annealing				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	13.7936	726.852	698.0556	465.2658
Easom	0	0	0	0
Shubert	-60.55382	-29.02078	16.39637	6.98384
Rastrigin	9.244849	86.36404	54.92566	66.9411

30 Dimensions - Genetic Algorithm				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	0.0016	0.4937	0.9045064	0.1139
Easom	-0.9991982	-0.4894756	0.3770736	-0.4704943
Shubert	0	359518206	1965699108	2.555e-08
Rastrigin	0.000863329	10.25588	12.42419	4.304968

30 Dimensions - Hill Climbing				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	2	19.72947	30.50142	2.281252
Easom	-1	-0.3331948	0.4792641	-2.7e-09
Shubert	0	2.634213e+20	1.002482e+21	0
Rastrigin	1.5e-09	40.01471	40.76614	24.71551

30 Dimensions - Simulated Annealing				
Function \ Value	F min	F Mean	F StdDev	F Avg
Booth	3.885553	616.2707	706.4712	342.4231
Easom	0	0	0	0
Shubert	163464.2	1.259035e+36	3.919845e+36	6.631709e+25
Rastrigin	21.36679	408.8735	219.8453	389.8166

Bonus: 30 Dimensions 1000 pop- Genetic Algorithm				
Function \ Value	F min	F Mean	F StdDev	F Avg
Rastrigin	5.676e-07	0.2550468	0.4268485	0.110391

4 Conclusion

The genetic algorithm gives us a better overall result. The genetic algorithm is more stable, because it mimics the conservative nature of natural selection. What is best is kept and the bad things are discarded. The interesting part is when we compare Rastrigin results for 30 Dimensions. The results have an improved average, an improved standard deviation and mean, not to say that we found a better minimum value. This opens the possibility to push the boundaries of such algorithms. As a bonus, I tried to run the algorithm with a population size of 1000 population. We see that it is drastically improved by the number of candidates in a generation. But there is a drawback. The time that it took to run is a lot bigger (raised from 3 mins to 6 days to run all 30 runs). This allows us to better take decisions when it comes to deciding which is more important: speed or accuracy.

5 Bibliography

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