Nature Inspired Optimization Method

Hydrozoan Algorithm for Solving Continuous Problems

PROJECT REPORT

Under the Guidance of

Dr. Kapil Ahuja

Submitted by :-

Sunand Agarwal (160001057) Vishal Maurya (160001061)

Introduction

Nature Inspired Algorithms have been solving difficult survival problems and many plants and animals have evolved with surprising efficiency in optimizing their evolutionary purposes.

Some examples of nature inspired algorithms are :-

- 1. Genetic Algorithm :- This algorithm is based on Darwinian evolution model.
- 2. ABC Algorithm :- This algorithm was based on behaviour of honey bees.
- 3. FPA ALgorithm :- This algorithm was based on development processes of flowering plant.

The optimization method discussed in this project is based on hydrozoan life cycle (HA), specifically, its process of regeneration and transplantation.

Nature inspired optimization methods are search algorithms for finding the best solution to various problems.

The proposed algorithm is used as a means for finding global optimum.

Hydrozoan Life Cycle

Hydrozoa are a group of cnidarians that are known for their complexity and diversity in life cycles. The algorithm was inspired by three main stages of hydrozoan colonies in our effort to make effective search optimization processes:

- 1. Motile Planula (Larvae)
- 2. Polyps
- 3. Pelagic Medusa

The Planula stage is about crossing over to produce next generation of chromosomes and random mutation of chromosomes in new generation.

The Polyps stage is about the overall growth values of all chromosomes. All chromosomes are ranked for selection and inclusion in the next generation.

The medusa stage is about gradual mutations and then selection by Roulette-Wheel Method to obtain the parent chromosomes for next generations.

The proposed algorithm mimics the process of hydrozoan reproduction in order to develop solutions into best solution.

Algorithm

Regeneration and Transplantation process consisted of Cloning , Splitting and Mutation processes.

- Cloning transfers the good fitness of better parents to offsprings.
- Splitting promotes generation of more offspring with better fitness.
- Mutation results in rich diversity of offspring.

In order to help produce a new and better offspring, each hydrozoan uses its personal best offspring achieved in previous iterations and global best offspring of the whole population to produce the next generation.

Mathematical Formulation

Step 1:- Specify an initial population of N hydrozoans and randomly generate the initial positions of every hydrozoan with following equation-

$$h_i(0) = [h_1^i, h_2^i, \dots, h_d^i, \dots, h_D^i]$$
 (1)

$$h_{d}^{i}(0) \in [low, high]$$
 (2)

where i = 1 to N , with a D dimensional continuous search space. $h_{\ d}^{i} \ denotes \ the \ genes \ of \ the \ hydrozoan$ lower and upper are the bounds of the D dimensional search space.

<u>Step 2</u>:- Input the initial position of each hydrozoan into the objective function and evaluate it to obtain its fitness value for that position.

<u>Step 3</u>:- Growth value of each hydrozoan ($G_i(t)$) is derived from the activator value (Ac_i^β) and the inhibitor value (In_i^α) according to the equations-

$$G_i \propto Ac_i^{\beta}$$
 (3)

$$G_{i} \propto 1 / In_{i}^{\alpha}$$
 (4)

$$G_{i} = Ac_{i}^{\beta} / In_{i}^{\alpha}$$
 (5)

where G_i (t) is the growth rate of hydrozoan (i) at time (t)

 $Ac_i^{\ \beta}$ is the activator value of hydrozoan (i) at time (t) $In_i^{\ \alpha}$ is the inhibitor value of hydrozoan (i) at time (t) α is the significance factor of inhibitor β is the significance indicator of activator

Step 4: Input the growth rate of every hydrozoan G_i(t)

$$G_{i}(t) = [G_{1}^{i}, G_{2}^{i}, \dots, G_{d}^{i}, \dots, G_{D}^{i}]$$
 (6)

where i = 1 to N

<u>Step 5</u>:- Find the median value of growth values $G_i(t)$.

To find the median, we first need to sort the G_i 's and then take the middle element. For even numbers of G_i 's, there will be two middle elements so we will take the average of both the values.

Step 6: We will calculate the swarm value for each hydrozoan.

$$Swarm_{j} = G_{j} - median(G_{j})$$
 (7)

Then hydrozoan are split into swarms according to the Split_i values which is equals to -

Split_i =

$$0$$
, if $Swarm_i < 0$ (8)

- 1, if $Swarm_i > 0$ and $Swarm_i = min$
- 3, if $Swarm_i > 0$ and $Swarm_i = max$
- 2, otherwise

Step 7: Choose and clone the hydrozoan based on their split value i.e the number of copies generated will be equal to the Split; value.

Step 8 :- Mutate the clonal hydrozoan. Mutation is defined as a small random adjustment of gene. A gene h i is selected and mutated by a low probability of mutation as follows:

$$RP = (max - min)*\phi + min$$
 (9)

$$h_{d}^{i} = h_{d}^{i} + (h_{d}^{i} \times RP)$$
 (10)

where RP is a constant derived from 'max' and 'min' which are the lower and upper bounds of mutation rate specified as percentages by the user. ϕ is a random number within the range [0,1].

Step 9: Select new hydrozoans that has already been mutated by using Roulette-Wheel selection method.

P_j is the probability that an individual hydrozoan i is selected, which is computed as follows:

$$P_{j} = f_{hi} / \sum_{q=1 \text{ to N}} f_{hq}$$
 (11)

where f_{hi} = fitness value or function value of hydrozoan (i) at (t).

<u>Step 10</u>:- Crossover the genes of the selected parents with an N - point crossover operator in order to obtain a variety of better offspring for the next generation. Random crossover points are selected and the tails of the two parents are swapped between these points to get new offsprings.

Step 11: Then, a mutation operator operates on the offspring. The index of a gene to be mutated is found by randomization then replace the gene with a random value in the range between the upper and lower bounds. These processes are expressed by following equations:

$$h_{i}(0) = [h_{1}^{i}, h_{2}^{i}, \dots, h_{d}^{i}, \dots, h_{D}^{i}],$$

$$A_{1} = h_{d}, h_{d} \in [low, high]$$

$$A_{1} = h_{d}^{i}, h_{d}^{i} \in [low, high]$$

This operation is applied to all offsprings.

<u>Step 12</u>:- Evaluate the fitness values of every offspring. Combine and sort all hydrozoans according to their fitness value, select a specified number of the best hydrozoans, and update the best hydrozoan with the highest fitness value 'I' the best for that iteration.

$$I_{best} = \operatorname{argmin}_{i} (f(h_{i}(t))t)$$
 (13)

<u>Step 13</u>:- Check the stopping criterion. If the maximum number of iterations is reached, the algorithm will then be terminated.

Result

We calculated the fitness value of different function from our algorithm and compared it with the optimum function value achieved by the newton method.

Due to the randomization in the algorithm we calculated the average fitness value of the function over some iterations and then compared that with the value calculated using newton method.

We experimented with the **Rosenbrock function** in 2-D, given by:

$$f(x1,x2) = 100(x2-x1^2)^2 + (1-x1)^2$$

The fitness values we get for some random inputs, from Rosenbrock function using this algorithm are:

Iteration Number	Fitness Value (f(x1,x2))
1	2.5681649
2	2.2373194
3	1.4409521

Taking number of iterations = 3 and initial point = [-2,1],

The value that we achieved from the Newton method = 180.432

The average of the fitness value = (2.5681649+2.2373194+1.4409521)/3 = 2.0821455

Conclusion

The hydrozoan algorithm is a meta-heuristic optimisation method which is population based. The algorithm converges much more accurately to the global optimum as compared to Newton Algorithm.

Github link to the project which contains both the algorithm codes in scilab and a sample problem solved on paper to show how continuous problems can be solved using this algorithm -

Optimisation Project

References

Research Paper Link