

# Symbiotic Tabu Search

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## Categories and Subject Descriptors

I.2. [Artificial Intelligence]: Genetic Algorithms

## General Terms

Algorithms

## Keywords

Optimization, Symbiogenesis, Tabu Search, Genetic Algorithms, Linkage Problem.

## 1. SYMBIOTIC TABU SEARCH ALGORITHM

Recombination in the Genetic Algorithm (GA) is supposed to extract the component characteristics from two parents and reassemble them in different combinations but this task requires recognition of good characteristics of both parents. Symbiotic Combination is formerly introduced as an alternative for sexual recombination operator to overcome the need of explicit design of recombination operators in GA. This paper presents an optimization algorithm based on using this operator in Tabu Search. The algorithm is presented in Figure 1.

1. Initialize population with all single-bit chromosomes. Create an empty Tabu list.
2. Repeat until stopping condition is met:
  - 2.1. Create a number of assemblies by randomly choosing none conflicting chromosomes from the pool. If an assembly can not be completed using existing chromosomes, create some random chromosomes with one specified bit for all missing locations. If any of the assemblies is already in Tabu list, remove it and create another one.
  - 2.2. Compute the fitness of all contexts.
  - 2.3. Choose the best context and add it to the Tabu list. If Tabu list exceeds its pre-specified size, remove the oldest member.
  - 2.4. For all pairs of members of the best context,
    - 2.4.1. Combine the pair and create an offspring. If the offspring has less than  $\text{Current\_Iteration\_Number} \times \text{Cooling\_Speed}$  specified genes, add it to the pool. Otherwise, randomly break it into some chromosomes (with random sizes) and add them to the pool.
  - 2.5. Remove all symbionts of the bottom 25% assemblies from the pool, except those that have taken part in the top 25% assemblies as well.
  - 2.6. If there is more than one copy of any chromosome in the pool, remove it.

Figure 1. Pseudo code of Symbiotic Tabu Search algorithm

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## 2. EXPERIMENTAL RESULTS

We used two problem sets to compare STS with simple Genetic Algorithm and Symbiotic Evolutionary Adaptation Model algorithm [1]. The first one is Hierarchical If and Only If Function (HIFF) [1] and the second benchmark is the concatenation of multiple 8-Queen problems (M8Q)[2]. Figures 2 present the success rates of the three algorithms on the two benchmark problems. Figure 3 presents a sample of performance of the three algorithms on 128 bit HIFF problem.

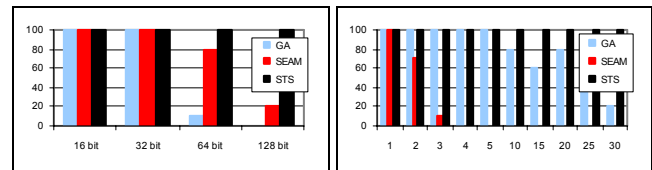


Figure 2. Success Rate Comparison of GA, SEAM, and STS on HIFF problem (left) and M8Q problem (right). Vertical Axis: Percentage of Success, Horizontal Axis: Problem Size.

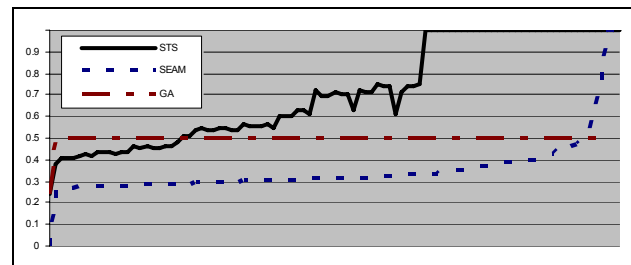


Figure 3. Performance Comparison of GA, SEAM, and STS on 128-Bit HIFF problem. Vertical Axis: Fitness, Horizontal Axis: Time.

## 3. CONCLUSIONS

Symbiotic Tabu Search (STS) algorithm as an evolutionary optimization algorithm that does not require specific chromosome or recombination operator design. The algorithm was tested on a fully deceptive problem and a concatenation of several combinatorial optimization problems and presented higher success rates in compare with sGA and SEAM algorithms and due to its Tabu prohibition mechanism, it can avoid local maxima and search for global optimum points.

## 4. REFERENCES

- [1] Watson, R.A., Pollack, J.B. Symbiotic Combination as an Alternative to Sexual Recombination in Genetic Algorithms, Proceedings of Parallel Problem Solving from Nature (PPSN VI), 2000.
- [2] Eiben, A.E., Raué P.E. and Ruttkay, Z. GA-easy and GA-hard Constraint Satisfaction Problems. Constraint Processing, Ed. Manfred Meyer, Springer-Verlag LNCS 923, 1995, 267-283.