# Visualization of the Fitness Landscape, a Steady-State Genetic Search, and Schema Traces

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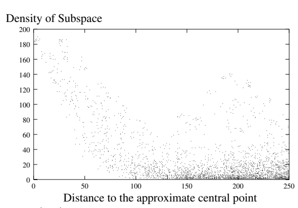
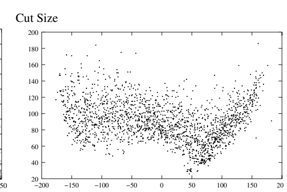
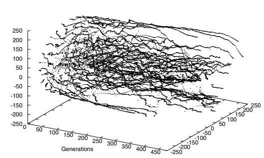
An NP-hard problem such as graph partitioning has a finite solution set and each solution has a cost. Although finite, the problem space is intractably large even for a small but nontrivial problem. A number of studies about the ruggedness and the properties of problem search spaces were done. Visualization is one of the most basic tools for studies of search spaces. A notable method for fitness landscapes is the plotting of fitness-distance correlation [1]. For genetic algorithm (GA) visualization, the most popular method is the fitness flow over time as in many GA papers. In this paper, we propose new visualization techniques primarily using Sammon's mapping. We analyze the problem space for graph partitioning more elaborately. We visualize the solutions associated with the genetic search. We also trace schemata.



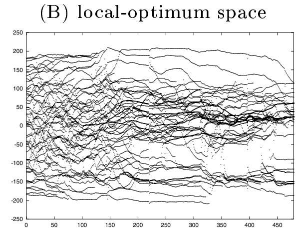

(A) local-optimum space



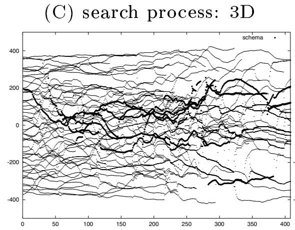

(B) local-optimum space



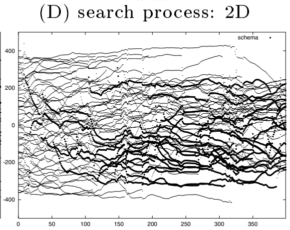

(C) search process: 3D




(D) search process: 2D




(E) no reordering




(F) reordering

We agree with the conjecture of Boese *et al.* [1] about the global convexity of local-optimum space but it is difficult to obtain further deduction. Figure (A) shows that the density of local optima near the center of the problem space is remarkably high. Interesting enough, one can also observe fairly high-density areas far from the center. It suggests the existence of "medium valleys."

Sammon's mapping [3] is a mapping technique for transforming a dataset from a high-dimensional input space onto a low-dimensional output space. The basic idea is to arrange all the data points on output space in such a way that minimizes the distortion of the relationship among data points. Sammon's mapping is a good visualization tool for the multi-dimensional dataset. The local-optimum space is a good candidate for Sammon's mapping. Figure (B) shows Sammon's mapping of the local-optimum space. The result visualizes the existence of valleys in more than one place.

Recently, Dybowski *et al.* [2] proposed a GA visualization method using Sammon's mapping. We extend their works. We make experiments with different distance measures, visualize the population space in 3-dimensional space, and provide a new technique for a steady-state GA to visualize the whole genetic search process. More detailed description is omitted by space limit. In the final experiments, we visualize the whole genetic search process of a steady-state GA. which generates only one offspring per iteration. It does not make fast change in population space. Hence, if previous positions are used for the initial positions of next generation Sammon's mapping, the positions change steadily over the generations. This makes it possible to visualize solutions over the genetic search process. Figure (C) and (D) show the visualization of the genetic search process.

It is important to preserve valuable schemata. The reordering heuristic transforms the shapes of valuable schemata to those advantageous for survival. We provide experiments for visualization of high-quality schema traces. Through the visualization combined with the techniques mentioned above, we observe the creation and extinction of schemata (see Figure (E) and (F)). Without reordering, despite of its early appearance, the schema did not spread all over the population as fast as the reordered version. On the other hand, the reordered version showed fairly stable preservation of the schema.

Our approach goes beyond those of Boese *et al.* [1] and Dybowski *et al.* [2]. Our approach will be also useful for other optimization problems.

## References

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[3] J. W. Sammon, Jr. A non-linear mapping for data structure analysis. *IEEE Transactions on Computers*, 18:401–409, 1969.

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