Topological Aspects in Genetic Algorithms

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December 27, 1992

Abstract

We investigate topological aspects in Genetic Algorithms (GAs). Two dimensional combinatorial optimization problems, cell placement problems, are concerned. We construct topological recombination and uniform recombination based on exchange operations, and compare their performance. Simulation results show that the contributions of these recombinations are qualitatively different.

1 Introduction

Though GAs are used in wide variety of optimization problems, they contains several factors to be tuned according to each problem. Among those factors, design of coding and operators has strong effects on performance, since it makes GA different from local nor random searches [1, 2].

In this paper we examine topological aspects of GAs. Under this category, one natural question arises: how are three dimensional structures of

proteins are coded effectively on strings of bases in natural genetics? Another problem is more pragmatic: how can we use intrinsic topology of problems in optimization task?

Here we concern two dimensional combinatorial optimization problems, cell placement problems[3]. Natural interest goes on influence of topological design of algorithms. We construct topological recombinations in GA and compare it with GA of zero-dimensional, or uniform, recombinations. It is easily generalized to include topological mutations, which we don't describe here.

2 Cell Placement Problems

Cell placement problems are derived from designing task of, for examples, gate array. They are defined as the following:

> A set C of cells c_i and a set $D \subset C \times C$ of pairs of cells (c_i, c_j) which are to be connected are given. Each cell can be placed on a slot s of the given slot array S (Figure 1) A placement is a map
>
> $$g : S \longrightarrow C \cup \{\phi\},$$
>
> where $g(s)$ is a cell placed on a slot s or null. A placement g induces an injection map
>
> $$p_g : C \longrightarrow S,$$
>
> where $p_g(c)$ is a slot on which a cell c is placed under a placement g. A trivial identity
>
> $$g(p_g(c)) = c$$
>
> holds for $\forall c \in C$ The problem is to find out the placement g of cells which minimize the total length $L(g)$ of connections
>
> $$L(g) = \sum_{(c_i,c_j)\in D} l((c_i, c_j), g),$$
>
> where $l((c_i, c_j), g)$ is a suitable distance between slots of the i-th and the j-th cells under a placement g.

To construct a GA for cell placement problems, we need to introduce a population of genes on which configurations are coded. In the following we regard a map g as a gene in which an alphabet $g(s)$ is stored on the locus s.

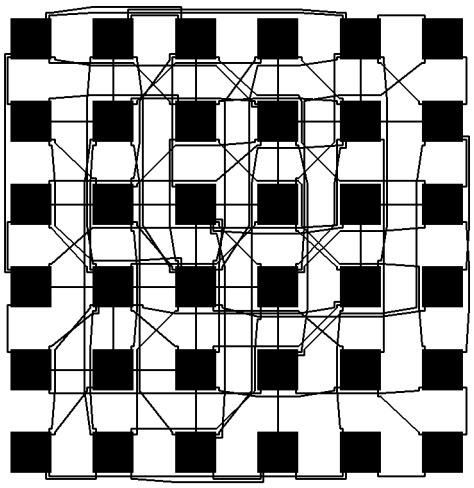

Figure 1: An example of placement of 36 cells. Black squares indicates cells on slots and lines connects pre-defined cells

3 Topological Recombination

We construct GAs of a mutation, a recombination and a selection on a population of genes. Uniformly random mutation and recombination don't depend on the representation.

In R^2a family of rectangles forms one of the simplest neighbors [4]. Topological recombination which keeps positions of cells in a rectangle is of our most interest. But we must care another critical problem, "lethal gene". Simple crossovers usually don't guarantee that the resultant gene satisfies conditions of the problem. In cell placement problems, one-to-one property of the induced map p_g is equivalent the validity of the gene g. Depending on problems several heuristics in representation are investigated to guarantee that simple crossovers work [5].

Here we employ another method based on exchange operators [6]. This method is useful for a class of problems in which a gene keeps validity under change of order. The class contains cell placement problems, Traveling Salesperson Problems, and so on. This method guarantees the validity for

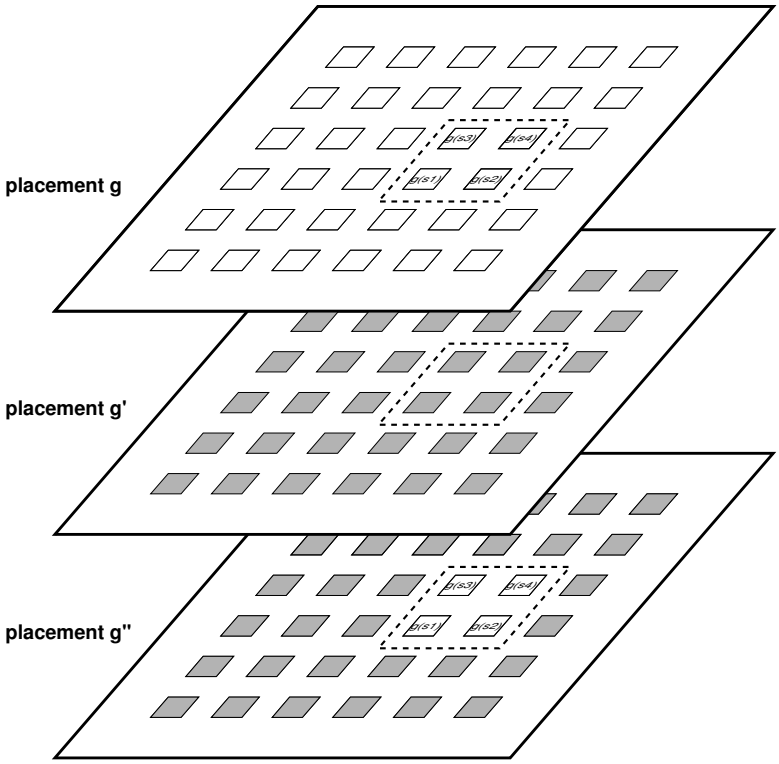

Figure 2: Topological recombination generating a new placement g'' from placements g and g'. Placement of cells in a rectangle U (denoted by broken line) in placement g are inherited to g''

the class and offer a way to construct topological recombinations.

An exchange operator E of slots s_1, s_2 acting on a gene g is defined by

$$\begin{aligned} E(s_1, s_2)g(s_1) &= g(s_2) \\ E(s_1, s_2)g(s_2) &= g(s_1) \\ E(s_1, s_2)g(s) &= g(s)(s \neq s_1, s_2). \end{aligned}$$

Topological recombination keeping a rectangle U which generate a gene g'' from two genes g, g' is constructed by the product

$$g'' = \prod^{s \in U} E(s, p_{g'}(g'(s)))g'$$

of the proper order(Figure 2). Let's think about the simplest case

$$g'' = E(s, p_{g'}(g(s)))g'.$$

In that case from the following equation

$$\begin{aligned} g''(s) &= E(s, p_{g'}(g(s)))g'(s) \\ &= g'(p_{g'}(g(s))) \\ &= g(s), \end{aligned}$$

one can see that the gene g inherits an alphabet on the locus s from the gene g'' and inherits from the gene g' on other loci except the locus $p_{g'}(g''(s))$ which is used for guaranteeing validity. An uniform recombination is defined in the similar form

$$g'' = \prod^{random\ s} E(s, p_{g'}(g(s)))g'.$$

A mutation generating a new gene g' from a gene g is defined

$$g' = E(s, t)g$$

where two slots s, t are randomly chosen.

We use simple selection rule; throw away worser genes among original and generated one, to keep difference between two recombinations clear apart from randomness.

4 Simulation Results

We compare two GAs: One using a topological recombination and the other using a uniform recombination. Problems of randomly chosen connections with probability 0.1 for 36 cells on 6×6 slot array are optimized by both GAs. A set P of randomly generated 300 genes, called population, is used for both. The average lengths over a population

$$\tilde{L}_\mu(t) = \frac{\sum_{g \in P} L(g)}{\#(P)}$$

against generation t, are plotted in Figure 3, where $\mu = topological$ means with using topological recombination scheme and $\mu = uniform$ means with

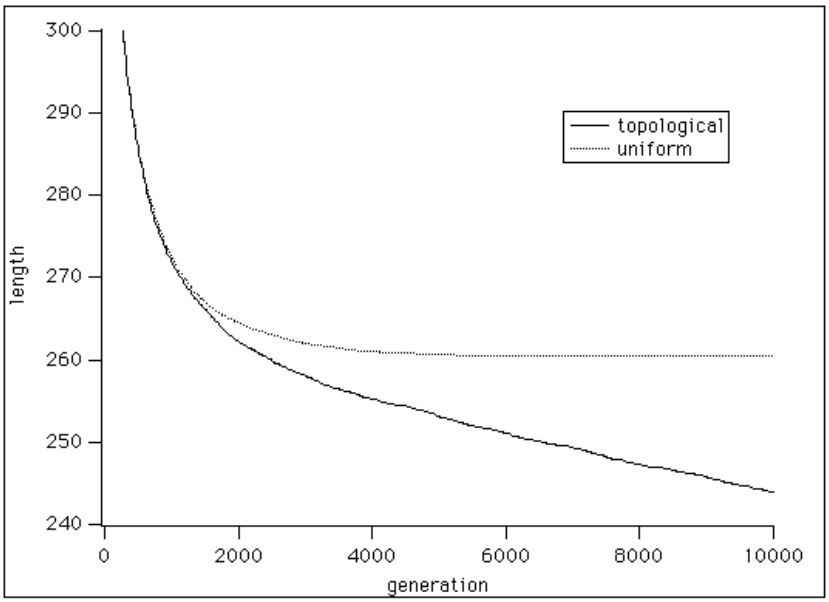

Figure 3: Average lengths

using uniform recombination scheme. and generation is a period in which the number of mutations is the same as the number of genes in a population. The ratio of a recombination to a mutation was set to 1/100 and simulation were continued until $T = 10000$ $generation$. Both averages show similar evolution only in the initial stage when randomly generated genes are quickly improved. In GA of uniform recombination, average length show no change over a considerable long period. On the other hand, in GA of topological recombination average length keeps being improved.

Standard deviations of the total length in population

$$\sigma_\mu = \sqrt{\frac{\sum_{g \in P} L_\mu^2(g)}{\#(P)} - \tilde{L}_\mu^2},$$
$$\mu = topological, uniform$$

are plotted for both in Figure 4. From this figure one may say initial stage ends at about 2000 generations. In GA of topological recombination diversity of population is sustained till about 7000 generation. On the other hand, the

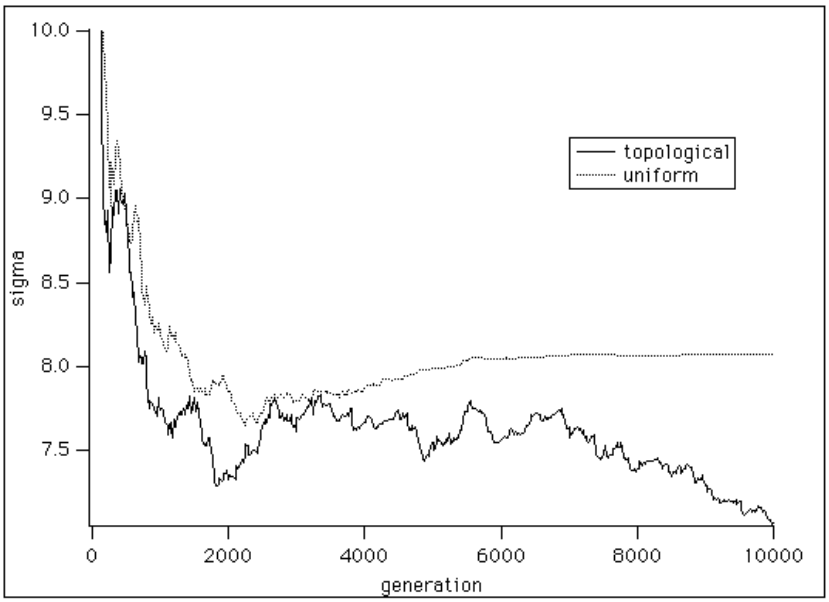

Figure 4: Standard deviation of total length

standard deviation in GA of uniform recombination increases which indicate that propagation of information among genes are weaker than improvement.

Relative differences of average total length of both GAs

$$\frac{\tilde{L}_{uniform}(t) - \tilde{L}_{topological}(t)}{\tilde{L}_{topological}(T)}$$

are plotted for four different connections in Figure 5. They shows same tendency.

5 Conclusion

We investigated topological aspects of representation in cell placement problems. Topological recombination is constructed based on exchange operators. Simulation show qualitative difference between topological and uniform recombination.

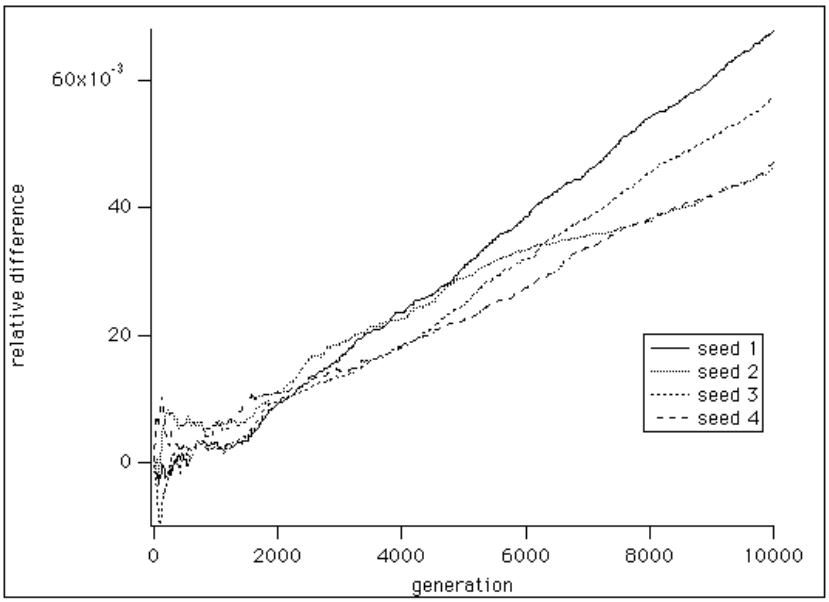

Figure 5: relative differences of average total length.

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