Improved "Aggregated" Model of Evolution with Soft Selection

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Abstract. We present an improved "aggregated model" where a population is replaced by base point representing population and probe point imitating search process. Presented results shows similar dynamic behavior for proposed algorithm in comparison to model of soft selection algorithms specially for small populations.

1 Introduction

Analytical analyses of dynamic of evolutionary algorithms are in most cases difficult due to high amount data necessary to describe an evolving population. Although few results are available for specific assumptions such as infinitive populations [6] or simple fitness functions [1,7,8], other simplifications are still needed. For small populations it is possible to reorganize the traits of individuals to create specific space of states [5]. Alas, larger populations that evolve in high dimensional fitness landscapes require a computation of the fitness function for each individual which leads to even higher computational costs.

Analysis of evolution in the space of population states [2] demonstrates that usually populations explore the search space as clusters of trials with a radius of about one standard deviation of the modification.

Aggregating information describing the traits of population's individuals further reduces a computational effort by replacing a population by two points that compete under certain conditions. The first point represents the population and the second point ensures the exploration capabilities. Preliminary tests of the aggregated model indicated that for hill climbing (Eq. 1) and saddle crossing situations (Eq. 2) the model has certain flaws [8]. For larger populations and large values of mutations the population is trapped in local optimum. This situation is caused when the probe point is generated far from the optimum.

To overcome this problem we have introduced certain modifications to the "aggregated model" (Fig. 1).

2   Model

Here, we consider a model with soft selection [4]. Similarly to [3] the population of m individuals that evolve under proportional selection with normally distributed traits' modifications, referred as original, are replaced by the two points "aggregated" model. A 'base point' represents the gravity center of the population and a 'probe point' is defined as a modification of the base point's trait with the normal distribution N(0,σ). The probe and the base point compete under the proportional selection scheme. In the previous version of the "aggregated model" [3], if the probe point wins the base point is shifted towards the probe point 1/m of the distance and the new test point is generated. If the base point wins it remains in the same positions and a new test point is generated.

$$fitness(x) = e^{-5(|x|^2)} \tag{1}$$

$$fitness(x) = e^{-5(|x|^2)} + 2e^{-5(|x-v|^2)} \text{ , } v = [1,0,..,0] \tag{2}$$

The proposed modification consists in modification of the base point. If the probe point wins, it replaces the base point with regard to its position and fitness. As the result the probe point becomes the base point. According to the soft selection scheme, the probability of the selection (SP) is proportional to the fitness of the probe point and inversely proportional to the sum of the fitness of individuals in the population.

```
F := fitness(μ);
repeat
    x  := μ + N(0,σ);
    ff := fitness(x);
    SP := ff/((m-1)* F + ff);
    if SP > U(0,1) then
      begin
        μ := x;
        F := ff;
      end;
until stop_condition;
```

μ – vector of traits of base point

m – population size

σ – mutation standard deviation

N – random variable with normal distribution

U – random variable with uniform distribution

x – vector of traits of test point

Figure 1. Implementation of aggregated model.

3   Results

The "aggregated" and original model were compared in hill climbing (Eq. 1) and saddle crossing scenarios (Eq. 2). In the first scenario the average number of trials necessary to shift within a set

distance from the optimum was estimated. The second scenario evaluated the population ability to cross saddles. For this purpose the average number of trials (from 400 runs) was computed that is required to cross the saddle for a population located initially on the top of the lower of the two adaptive hills. This was done in function of number of trials for three population sizes and two
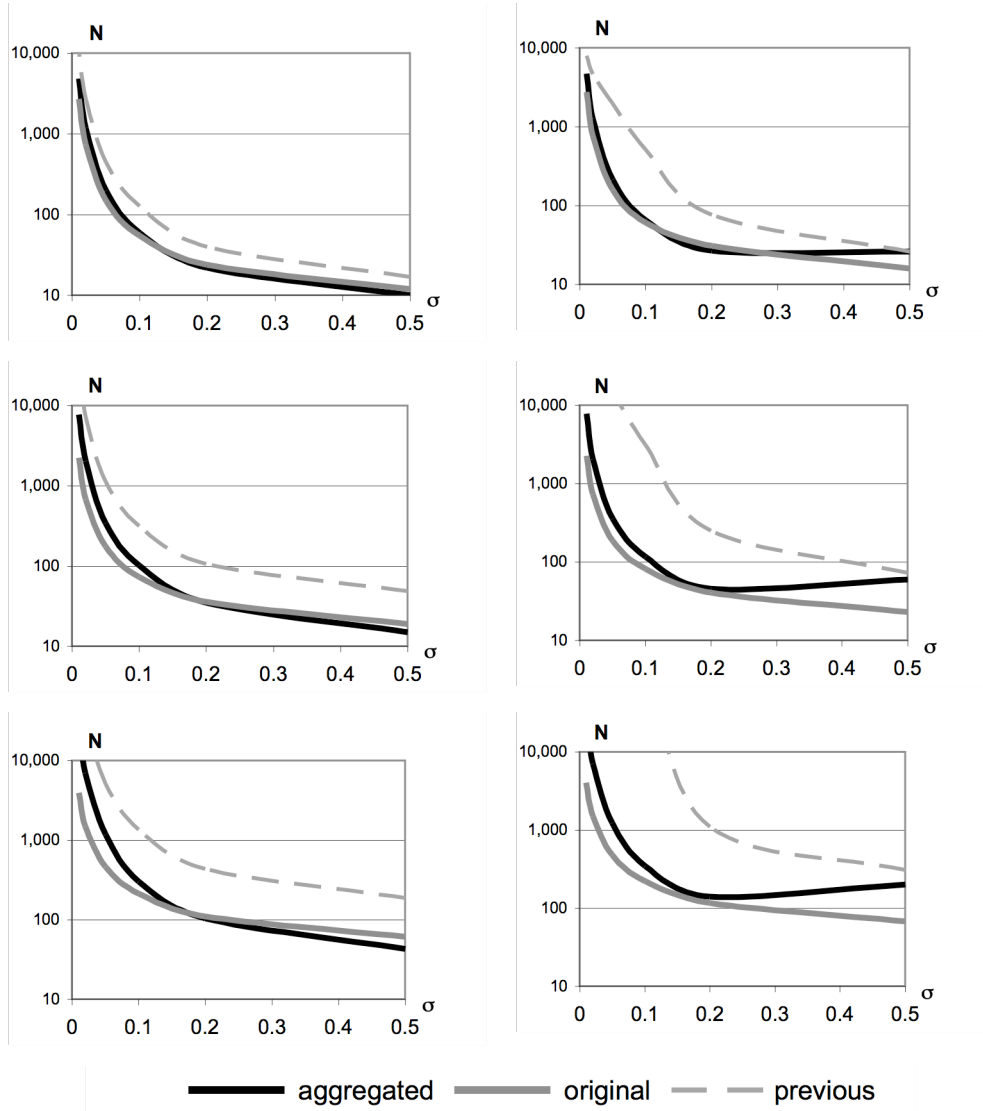

Figure 2. Number of trials (*N*) needed to move the population at the distance 0.8; the starting point is set at [-1, 0,…, 0]. The dimensionality of the landscape *n* is 2 (first column) and 6 (the second column), respectively. The population size *m* is equal to 2 (first row), 5 (second row) and 20 (third row). Dashed lines represent results from previous aproach and were taken from [3] without scaling of σ.

Figure 3. Number of trials N needed to cross the saddle. The dimensionality of the landscape *n* is 2 (first column) and 6 (the second column), respectively. The population size *m* is equal to 2 (first row), 5 (second row) and 20 (third row). Dashed lines represent results from previous aproach and were taken from [3] without scaling of σ.
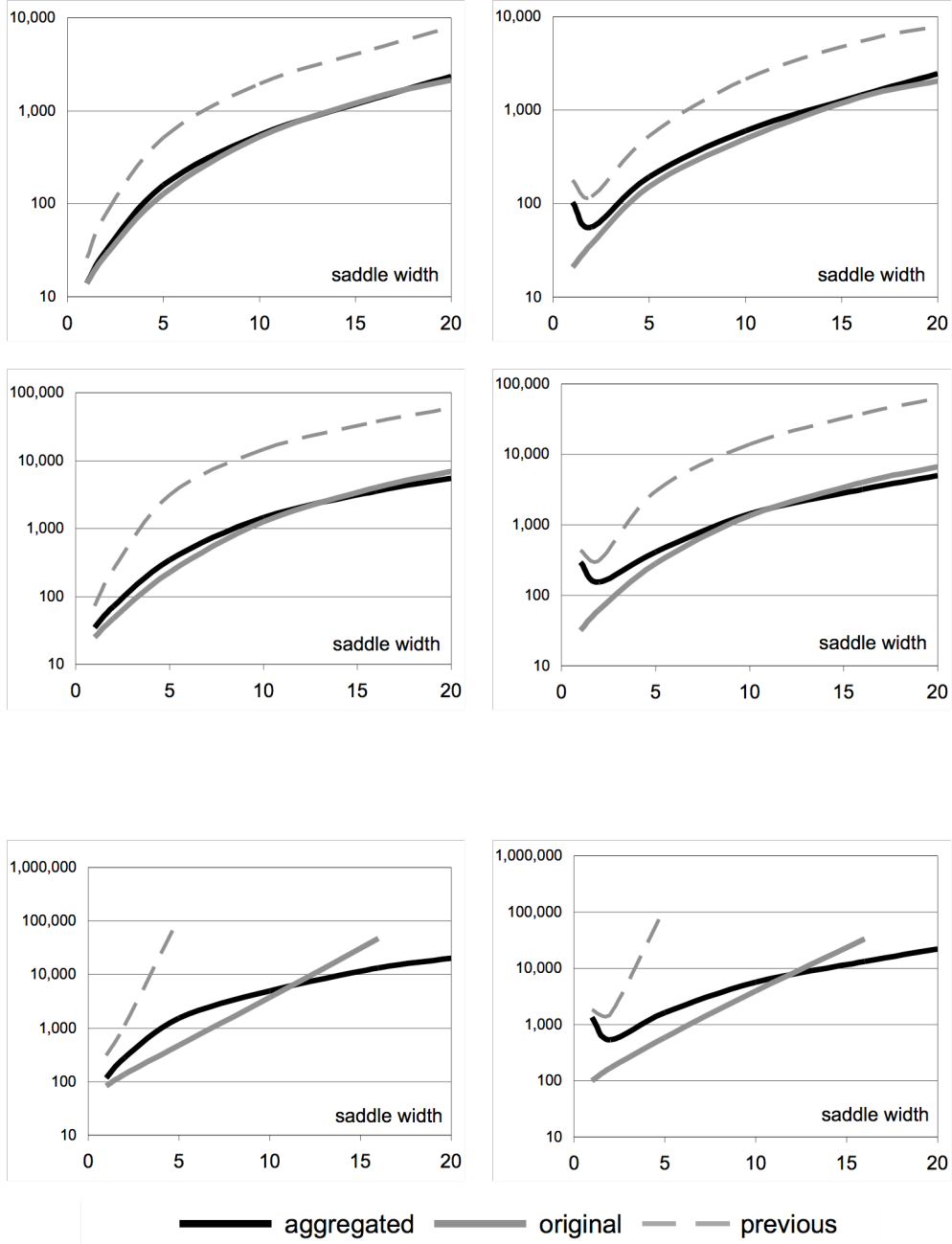
dimensions of the search space. The results are presented on Fig. 2 and 3, respectively. The characteristics for "aggregated" evolution are drawn against similar characteristics obtained using the original method.

4   Conclusions

The proposed "aggregated model" assumes that the population represented by the base point is replaced (in case of success) by the probe point that is equivalent to most of individuals within a population. For small population sizes this assumption may be acceptable because individuals are equally spread around gravity center. In case of larger populations certain differences in properties that are observable in both, original and "aggregated" model, indicate that this assumption is not true.

Concluding, the replacement of the probe point with the base point simplifies the model description and requires fewer selection steps. Moreover, the presented model requires no scaling of the mutation, thus fewer model parameters are required.

The evolution in two scenarios has shown similar characteristics to the standard algorithm for different dimensional landscapes and population sizes. Therefore, the model is more precise for smaller populations.

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