Dynamic segregative genetic algorithm for assembly lines balancing

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Abstract — This paper presents a segregative genetic algorithm for “I”/“U”-shaped assembly line balancing problem. It uses a basic genetic algorithm and a feature function that associates a time profile of the workstations to each chromosome. The similarity based clustering in the feature space induces subpopulations of chromosomes. The segregative genetic algorithm acts both on representation and feature space. A similarity based communication preserves the clustering structure. Each subpopulation completely exploited sends its centroid to an associative tabu search mechanism. Some selected new individuals are used to create clusters that represent unexplored parts of search space. The exhausted subpopulations are replaced by new ones during the evolution. The resulted dynamic segregative genetic algorithm leads to a better trade-off between exploration, made by many clusters, and exploitation, done by the focusing on each subpopulation.

Experimental investigations show that the segregative approach is more stable and systematically produces better results than the basic genetic algorithm. A distributed implementation of the segregative approach is presented and its performance is reported.

Keywords — segregative genetic algorithm, associative tabu search, similarity preserving communication, distributed implementation, extensive exploration, novelty detecting, intensive exploitation.

I. INTRODUCTION

Assembly line balancing (ALB) is one of the important problems in the production management area. Exhaustive descriptions of the typology of ALB problems and enumerating of different solving tools can be found in the excellent monograph [1] and in [9]. The use of new intelligent and soft computing techniques extends the types of high complexity ALB problem variants that can be efficiently modeled and solved. In this context, the genetic algorithms (GA) have a high flexibility to incorporate the problem specific characteristics [2]. The GAs are adaptive methods based on a mechanism of natural selection and evolution, working in parallel with a number of chromosomes, or even populations of chromosomes, that are potential solutions. Even if a lot of evolutionary algorithms for different types of ALB problems have been proposed ([3], [4]), all these methods explore a unique set of solutions candidates. The implicit potential of the genetic algorithms (GA) for a parallel or distributed implementation can be exploited if an adequate organization of multiple populations is adopted ([Aff01]). A segregative approach is often superior to other ways to organize the search space, but its success highly depends on the available similarity measure. The main idea of this algorithm ([5]) is to divide the whole population into many subpopulations of similar individuals at the beginning of the evolutionary process. They evolve by using a similarity preserving protocol until the fitness improvement stagnates. Then, a reunification of all subpopulations is made.

In this paper, a dynamic segregative genetic algorithm (SGA) for “I”/“U”-shaped ALB problems is proposed. A vector of features is associated to each individual. This captures the processing time profile of the solution built on the chromosome, its components being the terms of the objective function of the ALB model. The features space is used to organize the search space in subpopulations. On each subpopulation, a basic genetic algorithm is applied. A simple clustering algorithm makes a partitioning of the initial population in an adequate number of clusters. The subpopulation structure is maintained through a communication protocol that preserves the similarity within each subpopulation. It contains an associative tabu search memory, and a component for the management of the unexplored regions of the search space.

Section II presents the mathematical model for ALB. The basic GA for ALB is presented in section III. The mapping from genotype to phenotype, the control components, the communication within the system and the activity of the BGA and SGA are described in section IV. The result of the experimental evaluation done for difficult ALB instances, the illustration of the activity of the main components and the performance of a distributed implementation are presented in section V. Last section summarizes the work and presents further research directions.
Fig. 7 represents the evolution of the best-found solution. The high capacity of the algorithm to escape from local optima has to be noted. Even after many evolution stages, when the solution seems to have converged, the algorithm is capable of improvements. These improvements were stable over all executions of the algorithm, which demonstrates that cases like this one are not simple random instances.

D. Segregative vs Single Population Genetic Algorithm

In this section some important characteristics and advantages of the segregative algorithm are underlined:

a. SGA usually obtains better results than the single population GA. The results are more stable and replicable in a high proportion of independent executions. Experiments were made with the simple GA too, in the same conditions. For example, in the case of ARC111.IN2, C = 5785, the segregative algorithm obtains a better solution (one workstation less) in 4% of the executions and for C = 6267 in 16% of the executions. On the instance SCHOLL.IN2, C = 1394, the BGA reaches error 3 in 63% of the executions, and 4 in the remaining 37%. The segregative algorithm doesn’t obtain a better solution, but reaches error 3 in all runs.

b. The SGA can compensate for an eventual weak performances of the basic population based heuristic. The genetic algorithm used in this paper (BGA) already performs very well on the presented data sets. Even so, the SGA has improved the performance of the solution in many cases.

c. It explores the search space more systematically. The exploration is guided by well-defined characteristics of the search space.

d. It systematically avoids being trapped in local optima.

e. It is designed for a distributed implementation, which makes it scalable to very large instances of the problem, given the needed computation resources.

VI. CONCLUSIONS AND FURTHER RESEARCH DIRECTIONS

In this paper, a high performance segregative genetic algorithm with dynamic subpopulations for ALB was presented. The method is capable of exploring many subpopulations and of organizing the new genetic material into clusters. It acts in both representation and feature spaces and uses an associative memory tabu search component based on the features of the solutions to avoid being trapped in local optima. The scheme of the segregative genetic algorithm is general and can incorporate different single population genetic algorithms.

The main practical result consists in a reliable method for optimizing the number of workstations for the “I”-shaped and the “U”-shaped determinist assembly lines balancing problems. The method was tested on classical benchmarks available in the balancing literature, and gives very good results. It offers much better performance and stability in terms of solution replicability than the single population algorithms.

An issue worthy of improvement pertain to addressing a better ability of the feature function to discriminate between very similar structures of the chromosomes.

The presented method is the first segregative approach working in feature space designed for ALB paradigm. Further research is envisioned to the extending of the algorithm to solve other types of ALB problems, including different constraints, multiple objectives, and problems where different parameters are no longer determinist. It can be easily extended to support different population based heuristics for a large class of optimization problems for which a feature function exists.

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