



Bi-level Reliability-Based Optimization of Trusses via Competitive Distributed Genetic Algorithm

V. Kalatjari¹, P. Mansoorian²

1- Assistant Professor, Shahrood University of Technology

2- PHD Student, Shahrood University of Technology

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Corresponding Author's E-mail: p.mansoorian@gmail.com

Abstract

Optimization of structures under the constraint of structural system failure probability is a much time consuming process and thus many researchers have attempted to approximate the probability of structural system failure conservatively as the sum of the members' failure probabilities. In this paper optimization of the trusses is performed in two different levels using parallel genetic algorithm. In the first level, the optimization is done based on the members' failure probabilities to obtain initial population for the second level. Then in the second level, the optimization process is continued under the constraint of structural system failure probability. Using the first level, many inefficient chromosomes are discarded quickly and an initial population is generated for the second level, resulting in saving considerable computational time. In the present study a novel parallel genetic algorithm namely, competitive distributed genetic algorithm (CDGA) is also employed to speed up the optimization convergence. In this method, genetic algorithm parameters and operators are different in each island. Then islands compete to produce own next generations. During the first level of the optimization, the islands which have generated better individuals send their parameters and operators to unsuccessful ones along with their fittest chromosomes. Then the second level optimization process is performed by winner islands' parameters and operators.

Keywords: reliability analysis, reliability-based optimization, branch and bound method, structural system failure probability, distributed genetic algorithm.

1. INTRODUCTION

The applied loads, the strength of materials etc in real structures can not be recognized as deterministic quantities and thus they are usually considered in an approximate manner in the problems. These sources of uncertainty should be examined carefully and hence the random nature of these variables causes a probabilistic space in analysis and design. In this regard, in the most of problems *failure* is defined first and then based on the probability concepts, failure paths and probability of failure can be found.

One preliminary approach chosen to take into account these uncertainties by the designers was using the loads and the strength safety factors. This approach corresponds to the first level of reliability design. At the first level only a single member is designed and the structural elements interaction is not considered. Furthermore, only one value of random variables such as their mean value is used. Random variables are considered along with their mean value and variance (or probability density function) at higher levels (second and third levels). At these levels after definition the failure, *limit state function* is defined as difference between the strength and the applied load. Finally, considering the correlation between the problem variables, structural system failure probability is found.

The highest level of reliability-based design, namely the fourth level, is the reliability-based optimization. At this level, the designer's aim is to find a reliable structure with minimum weight.

One of the most popular approaches to evaluate the structural system failure probability is based on the failure paths. The *branch and bound method* [1] and the *truncated enumeration method* [2] are more common examples of such approach.

In these methods, upper and lower bounds are calculated for structural failure probability by discarding the failure paths with low probability and selecting *dominant failure paths*. In large real structures, there are usually numerous failure paths, while only some contribute to structural system failure probability, namely the dominant failure paths, and the others have negligible occurrence probability.

Despite all efforts, these methods have two main disadvantages. Firstly, wide bounds are usually determined for structural failure probability [3]. Secondly, much time is consumed to find the dominant