

## CIVIL ENGINEERING

# Soft computing for modeling punching shear of reinforced concrete flat slabs



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**Abstract** This paper presents applying gene expression programming (GEP) approach for predicting the punching shear strength of normal and high strength reinforced concrete flat slabs. The GEP model was developed and verified using 58 case histories that involve measured punching shear strength. The modeling was carried out by dividing the data into two sets: a training set for model calibration, and a validation set for verifying the generalization capability of the model. It is shown that the model is able to learn with high accuracy the complex relationship between the punching shear and the factors affecting it and produces this knowledge in the form of a function. The results have demonstrated that the GEP model performs very well with coefficient of determination, mean, standard deviation and probability density at 50% equivalent to 0.98, 0.99, 0.10 and 0.99, respectively. Moreover, the GEP predicts punching shear strength more accurately than the traditional methods.

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## 1. Introduction

Punching shear is considered to be one of the major criteria that control the design of concrete members such as flat slabs, spread footing or raft footings. This type of shear usually exists in the vicinity of slab column connections due to the high concentration of stress. The brittle nature of punching shear failure in structures made it very dangerous; when shear failure

occurs, the resistance of the structure tremendously reduced and consequently collapse takes place because of separation of column and slab. Therefore, design methods and codes of practice have paid great interest to account for such kind of failure.

Determining the punching shear strength is a complex design problem owing to the influence of numerous factors involved. Because of the complexity of the problem many researchers have attempted to model the punching shear phenomenon using different assumptions (e.g. [1–3]). As a result, different methods have been proposed to predict the punching shear strength of concrete members. However, considering the results obtained from applying these methods on same problem reveals different results depending on the method employed. Moreover, in several instances comparing these results with experimental data shows over-prediction by 20–50%. Consequently, more

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accurate methods are needed for better prediction of punching shear strength. Artificial intelligence techniques can represent a potential option to be explored.

The main concept behind the use of these techniques is that they learn adaptively from experience and extract various functions each appropriate for its purpose. Artificial intelligence systems have the ability to operate on large quantities of data and learn complex model functions from examples by training on set of input and corresponding output. The greatest advantage of the artificial intelligence over the traditional modeling techniques is their ability to capture a nonlinear and complex interaction between variables of a system without having to assume the form of the relationship between the input and the output variables. Artificial intelligence techniques have been applied to solve many problems in the field of engineering (e.g. [4–7]).

In this paper, the punching shear strength of flat slabs is modelled using a developed form of artificial intelligence techniques that is gene expression programming (GEP). Recently, GEP has been applied with success in solving engineering problems (e.g. [8–10]). The paper aimed to investigate feasibility of using GEP to determine a model relating punching shear strength with its significant factors; evaluate the performance of the model in training and validation sets and via sensitivity analysis; compare the predictions of the model with predictions of number of commonly adopted methods.

## 2. Overview of gene expression programming

GEP is an instance of an evolutionary algorithm from the field of evolutionary computation, invented by Ferreira [11] as a global optimization algorithm. It has similarities to other evolutionary algorithms such as the genetic algorithms (GAs), as well as other evolutionary automatic programming techniques such as genetic programming (GP). Similar to the GAs, GEP uses the evolution of computer programs (individuals or chromosomes) that are encoded linearly in chromosomes of fixed length, and likewise the GP the evolved programs are expressed nonlinearly in the form of expression trees (ETs) of different sizes and shapes. However, GEP implements different evolutionary computational method. The GEP distinguishes itself from GAs in that the evolved solutions are expressed in the form of parse trees of different sizes and structures and unlike the GP, genetic variations are performed on chromosomes before they are translated into ETs.

The GEPs chromosomes can be composed of single or multiple genes; each gene is encoded in a smaller sub-program. Every gene has a constant length and includes a head that contains functions (e.g. +, -) and terminals (e.g. d1, d2, which are the symbolic representation of the input variables), and a tail composed of terminals only. The genetic code represents a one-to-one relationship between the symbols of the chromosome, the functions or terminals. The process of information

decoding from chromosomes to ETs is called translation, which is based on sets of rules that determine the spatial organization of the functions and terminals in the ETs and the type of interaction (link) between the sub-ETs [12]. The principal terms of the GEP are described in the following subsections.

### 2.1. Initial population

In GEP, the search for a solution begins when a number of computer programs (individuals or chromosomes), referred to as the initial population, are randomly created from the set of functions and terminals defined by the user. Each program is expressed, evaluated and assigned fitness according to how well it performs towards the desired objective.

### 2.2. Chromosome gene and expression trees

The chromosome is a linear symbolic string of fixed length composed of one or multiple genes of equal size. A typical GEP chromosome is presented in Fig. 1.

The gene is a sub-program encoded in the chromosome and it consists of a head and a tail. The length of the head is usually predefined by the user during data setting, while the length of the tail is determined by the following:

$$t = h(n - 1) + 1 \quad (1)$$

where  $t$  is the tail length;  $h$  is the head length and  $n$  is the number of function's arguments.

Although the genes of the GEP have all the same size, they code for different expression trees of different sizes. The trees represent a spatial illustration demonstrating the interactions among the gene's components on the map of solution. Fig. 2 shows expression trees of the genes of the chromosome in Fig. 1.

### 2.3. Mutation

In GEP, mutation means randomly selecting any component of the gene's head or tail and replacing it with any other randomly selected component from the function or terminal set. In the heads, any component can change into another (function or terminal), whereas in the tails terminals can only change into terminals. The mutation may take place at one or two points within the chromosome and there are no constraints, neither in the kind of mutation nor in the number of mutations. In all cases, the newly created individuals are syntactically correct programs.

### 2.4. Recombination

The last significant step during each cycle of program evolution includes introducing genetic variation by recombination. The variations take place when two chromosomes are paired

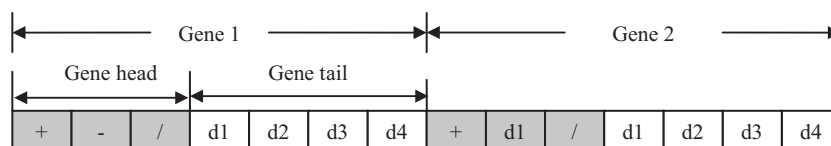


Figure 1 GEP chromosome.

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