

A New Algorithm for Detection of Animal and Plant Ion Concentration Based on Gene Expression Programming

Kangshun Li, Dongguan City College, China*

Leqing Lin, South China Agricultural University, China

Jiaming Li, South China Agricultural University, China

Siwei Chen, South China Agricultural University, China

Hassan Jalil, South China Agricultural University, China

ABSTRACT

In order to accurately predict the concentration detection data of ion sensors for animal and plant, this paper proposes a gene expression programming (GEP) based concentration detection method. The method includes collecting ion concentration data as well as voltage timing data; preprocessing all the collected data to obtain an initial sample set; constructing a prediction model of ion concentration, which is an explicit functional relationship between voltage and the concentration of a specific ion. The Gene Expression Programming is used to train and evaluate the prediction model, and obtain a trained model. By comparing gene expression programming with other two modeling methods, it is found that the accuracy of the model established by gene expression programming has greater advantages than that established by polynomial fitting and neural network in processing animal and plant ion concentration data.

KEYWORDS

Gene Expression Programming, ion concentration, prediction model

INTRODUCTION

Inorganic ions are an important component of animals and plants and have the function of regulating physiological activities, which is a necessary condition for maintaining the normal growth of animals and plants. Obtaining the exchange and absorption information of inorganic ions in the environment during the growth of animals and plants is helpful to reveal the life activity mechanisms of animals and plants, assist agricultural scientific research, and promote agricultural production. In order to dynamically and accurately monitor the changes in ion content around the plant growth environment, the most suitable growth environment conditions for the plant can be obtained by comparing the

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*Corresponding Author

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growth status of the plant in different concentration environments of specific ions. As a result, it can provide a method for large-scale vegetable and fruit farms to accurately measure the suitable plant growth environment, thereby improving the yield and quality of vegetables and fruits. The authors conducted a large number of detection experiments on standard solution samples and mixed solution samples of eight ions, including Mn^{2+} , Ca^{2+} , K^+ , Na^+ , Mg^{2+} , Cl^- , NH_4^+ , and NO_3^- , and obtained a large amount of data. The authors will use gene expression programming to model the ion-selective membrane properties of these data detection results. On this basis, pattern recognition technology is used to achieve the automatic identification of these ions as well as the automatic concentration reading.

GENE EXPRESSION PROGRAMMING

Gene expression programming was created by Portuguese scientist Ferreira. It is a development of GA (genetic algorithm) and GP (genetic programming design). GEP combines the advantages of both, including the simple and fixed-length coding characteristics of GA, and the indefinite length and indefinite characteristics of the tree structure in GP. Therefore, gene expression programming is much faster than GA or GP.

Gene expression programming processes chromosomes, which consist of genes connected by linking functions. A gene consists of a head and a tail, and the head contains function sets and terminals, while the tail contains only terminals. Thereinto:

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

where t represents the length of the gene tail, h represents the length of the gene head, and n denotes the maximum number of parameters in the function set.

K-Expressions

Chromosomes are made up of one or more fixed-length, linear, equal-length genes, so genes are also linear and fixed-length. Chromosomes can determine the size and shape of the expression tree. For example, in this simple algebraic equation:

$$\sqrt{(a - b) \times (c - d)} \quad (2)$$

The expression tree of this equation is shown in Figure 1, where q represents the square root. Traversing the expression tree in Figure 1 from top to bottom and left to right yields the corresponding K-expression, as shown in equation (3). The genotype in gene expression programming is:

$$q * - a \ b \ c \ d \ 1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8 \quad (3)$$

Fitness Function

In order to obtain the best solution, the newly produced chromosomes need to be evaluated for environmental adaptability. In the application of functional modeling, the final result is to find an expression that fits the sample data well within the limits of the error. The evaluation of the pros and cons of the expression is based mainly on the degree of consistency between the results of the expression calculation and the training data. In gene expression programming, the coefficient of determination R^2 , root mean square error $RMSE$, mean absolute error MAE , etc. are usually used as evaluation criteria.

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