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Diametral Creep Prediction of the Pressure Tubes in CANDU Reactors Using a Genetic Optimized Linear Model

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1. Introduction

Pressure tube (PT) creep is one of the principal aging mechanisms governing the heat transfer and hydraulic degradation of the heat transport system (HTS) in CANada Deuterium Uranium (CANDU) reactors. PT diametral creep affects the thermal hydraulic characteristics of coolant channels and the critical heat flux (CHF). CHF is a key parameter in determining the critical channel power (CCP), which is used in the trip setpoint calculations of regional overpower protection (ROP) systems. Therefore, it is important to predict the PT diametral creep in CANDU reactors. PT diametral creep is mainly caused by fast neutron irradiation, applied stress, pressure and temperature.

The objective of this paper is to predict the PT diametral creep using the measured signals of the HTS by applying a genetic optimized linear model according to fuel bundle positions in a channel.

2. Genetic Optimized Linear Model

2.1 Genetic Optimized Linear Model

A linear model is a flexible generalization of ordinary least squares regression. In this paper, the optimization of the linear model is accomplished by a genetic algorithm in order to impose some constraints to regression coefficients. The genetic optimized linear model is described as follows:

$$\hat{y} = a_1 x_1 + a_2 x_2 + a_3 x_3 + a_4 x_4 + a_o \qquad (1)$$

The variables x_1 through x_4 are input signals that represent the fast neutron fluence, EFPD, temperature and pressure, respectively. y is the output signal which indicates the PT diametral creep.

Also, we also used bundle position-wise linear model based on linear model to predict the PT diametral creep. This bundle position-wise linear model was devised because it is expected that the bundle position affects the diametral creep. The bundle position-wise linear model is described as follows:

$$\hat{y}_i = a_{i1} x_1 + a_{i2} x_2 + a_{i3} x_3 + a_{i4} x_4 + a_{io} \qquad (2)$$

where i indicates a bundle position in a channel.

In genetic algorithms, the term chromosome typically refers to a candidate solution to a problem, often encoded as a bit string. Each chromosome can be thought of as a point in the search space of candidate solutions. The genetic algorithms process populations of chromosomes, successively replacing one such population with another. The genetic algorithms require a fitness function that assigns a score to each chromosome in the current population. The fitness of a chromosome depends on how well that chromosome solves the problem at hand [1].

After an initial population of chromosomes is randomly generated, the typical genetic algorithm evolves the population through the three operators; selection, crossover and mutation operators. The selection operator selects individuals (chromosomes) in the population for reproduction. The goodness of each individual depends on its fitness. The fitter the chromosome, the more times it is likely to be selected to be reproduced. After two individuals are chosen from the population using the selection operator, the crossover operator randomly chooses a crossover site along the bit strings and exchanges the subsequences before and after that crossover site between the two individuals to create two offspring. The two new offspring created from this mating are put into the next generation of the population. By recombining portions of good individuals, this process is likely to create even better individuals. With some low probability, a portion of the new individuals will have some of their bits flipped. Mutation can occur at each bit position in a string with some probability, usually very small. Its purpose is to maintain diversity within the population and inhibit premature convergence.

A genetic algorithm uses a cost function that evaluates the extent to which each individual is suitable for the given objectives such as maximum error together with small overall error. The fitness of an individual (chromosome) is calculated by means of the energy of the individual. Each chromosome contains the antecedent parameters c_{ij} and s_{ij} . The chromosome that has lower energy has higher fitness. The energy functions are defined by the following two equations.

$$E_1 = \sqrt{\frac{1}{N}\sum_{k=1}^{N}\left(\frac{y_{rk} - y_k}{y_{rk}}\right)^2} \qquad (3)$$

$$E_2 = \max\left\{\left|y_{r1} - y_1\right|, \left|y_{r2} - y_2\right|, \cdots, \left|y_{rN} - y_N\right|\right\} \qquad (4)$$

E_1 and E_2 are root mean squared errors and maximum absolute error, respectively. The fitness function is given as follows.

$$F = \exp\left(-\alpha E_1 - \beta E_2\right) \qquad (5)$$

3. Application

The used data consist of a total of 400 input-output data pairs $(x_1, \cdots, x_4, y)$ which were taken from the Wolsung nuclear power plant unit 1. These data were acquired at 2136, 2967, 3383 and 5726 effective full power days (EFPDs). 70% (280 training data) of the data were used to obtain the regression coefficients of Eqs. (1) and (2) by using the genetic algorithm.

The verification data consist of a total of 400 input-output data. Also, the test data1 and test data2 of 280 data sets were acquired at 6577 and 7336 EFPDs, respectively. These test data were prepared to verify the prediction performance of the linear models.

Table 1 compares the diametral creep prediction performance of the pressure tubes by both the linear model and the RC-1980 model to be being used currently. The linear model is inferior to the current RC-1980 model. Table 2 compares the bundle position-wise linear model and the RC-1980. The bundle position-wise linear model is superior to the RC-1980. Figures 1 and 2 show the position-wise RMS errors and the position-wise maximum errors of the predicted values using a bundle position-wise linear model.

Table 1. Diametral Prediction of the Pressure Tubes Using a linear model (Wolsung Unit 1)

Data Type	Data points	Linear model		RC-1980	
		RMS error (mm)	Max. Error (mm)	RMS error (mm)	Max. Error (mm)
Training data	280	0.2142	0.7446	0.1785	0.7091
Verification Data	400	0.1910	07446	0.1685	0.7091
Test data1	120	0.4512	0.8836	0.2218	0.4841
Test data2	160	0.5057	1.0513	0.2320	0.5171

Table 2. Diametral Prediction of the Pressure Tubes Using a bundle position-wise linear model (Wolsung Unit 1)

Data type	Data points	Linear model		RC-1980	
		RMS error (mm)	Max. Error (mm)	RMS error (mm)	Max. Error (mm)
Training data	280	0.1214	0.5078	0.1785	0.7091
Verification data	400	0.1135	0.5078	0.1685	0.7091
Test data1	120	0.1763	0.3992	0.2218	0.4841
Test data2	160	0.1960	0.6123	0.2320	0.5171

4. Conclusions

In this study, a genetic optimized linear model was developed to estimate the PT diametral creep in CANDU reactors. The proposed genetic optimized linear model was applied to the Wolsung nuclear power plants in Korea.

The RMS error of the bundle position-wise linear model was slightly greater than RC-1980 model which is currently being used to predict the diametral creep of the pressure tubes in the Wolsung nuclear power plants. However, the performance of the genetic optimized bundle position-wise linear model was more superior to the RC-1980 model. Therefore, it is expected that the genetic optimized bundle position-wise linear model can replace the existing RC-1980 model to predict the diametral creep of the pressure tubes in CANDU reactors.

REFERENCES

[1] M. Mitchell, An Introduction to Genetic Algorithms, The MIT Press, Cambridge, Massachusetts, 1996.

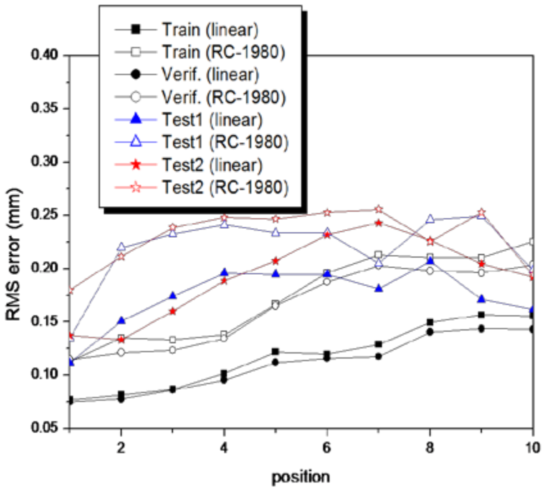

Fig. 1. Bundle position-wise RMS errors using a bundle position-wise linear model (Wolsung unit 1)

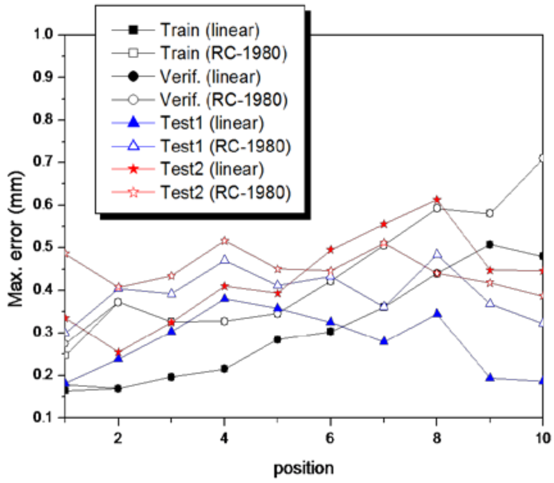

Fig. 2. Bundle position-wise maximum errors using a bundle position-wise linear model (Wolsung unit 1)