

DIAMETRAL CREEP PREDICTION OF THE PRESSURE TUBES IN CANDU REACTORS USING A BUNDLE POSITION-WISE LINEAR MODEL

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The diametral creep of pressure tubes (PTs) in CANDU (CANada Deuterium Uranium) reactors is one of the principal aging mechanisms governing the heat transfer and hydraulic degradation of the heat transport system (HTS). PT diametral creep leads to diametral expansion, which affects the thermal hydraulic characteristics of the coolant channels and the critical heat flux (CHF). The CHF is a major parameter determining the critical channel power (CCP), which is used in the trip setpoint calculations of regional overpower protection (ROP) systems. Therefore, it is essential to predict PT diametral creep in CANDU reactors. PT diametral creep is caused mainly by fast neutron irradiation, temperature and applied stress. The objective of this study was to develop a bundle position-wise linear model (BPLM) to predict PT diametral creep employing previously measured PT diameters and HTS operating conditions. The linear model was optimized using a genetic algorithm and was devised based on a bundle position because it is expected that each bundle position in a PT channel has inherent characteristics. The proposed BPLM for predicting PT diametral creep was confirmed using the operating data of the Wolsung nuclear power plant in Korea. The linear model was able to predict PT diametral creep accurately.

KEYWORDS : Bundle Position-wise Linear Model, Genetic Algorithm, Uncertainty Analysis, Pressure Tube, Diametral Creep Prediction

1. INTRODUCTION

A heat transport system (HTS) is responsible for heat removal from the nuclear fission process in CANDU (CANada Deuterium Uranium) reactors, which are pressurized heavy-water reactors (PHWR). HTS aging has the potential to adversely affect the safety margins. Diametral creep of the pressure tube (PT) is one of the principal aging mechanisms governing the heat transfer and hydraulic degradation of an HTS. The HTS of CANDU

nuclear reactors experience time-dependent dimensional changes in the PTs through a creep mechanism. In particular, PT diametral creep leads to diametral expansion, which affects the thermal hydraulic characteristics of the coolant channels and the critical heat flux (CHF) (refer to Fig. 1). The CHF is a major parameter determining the critical channel power (CCP), which is used in the trip setpoint calculations of regional overpower protection (ROP) systems. Therefore, it is essential to predict the PT diametral creep in CANDU reactors, which is caused mainly by fast neutron irradiation, temperature and applied stress.

The currently used PT diametral creep prediction model considers the complex interactions between the effects of temperature and fast neutron flux on the deformation of PT zirconium alloys [1]. The model assumes that long-term steady-state deformation consists

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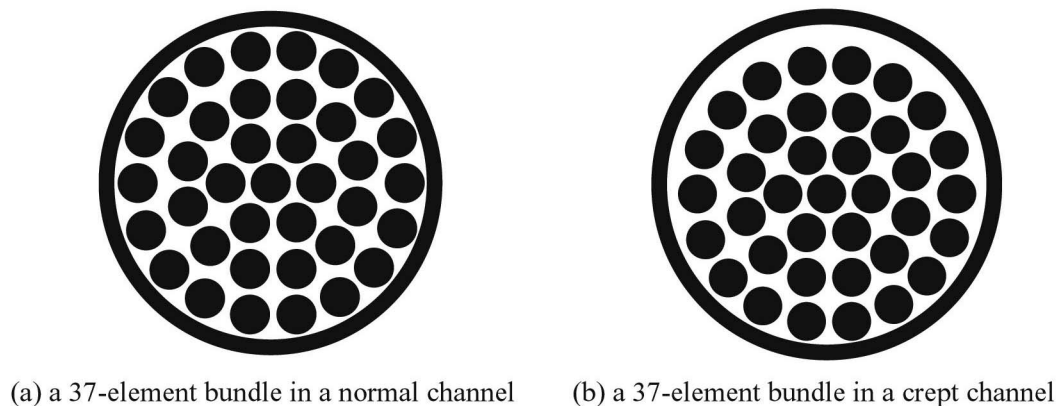


Fig. 1. Fuel Channel Configuration in a Normal and Crept Pressure Tube

of separable, additive components from thermal creep, irradiation creep and irradiation growth [1]. This is a mechanistic model based on measured data. However, this model has high prediction uncertainty. Recently, a statistical error modeling method was developed using plant inspection data from the Bruce B CANDU reactor [2]. Owing to the significant effect of diametral creep on the safety margin in CANDU reactors, many studies have examined methods for predicting PT diametral creep.

The Wolsung nuclear power plant has very good field data, which is not data of a laboratory level, to estimate the PT creep. The aim of this study was to develop a bundle position-wise linear model (BPLM) to predict PT diametral creep employing previously measured PT diameters and HTS operating conditions. The BPLM was optimized using a genetic algorithm. A variety of measured or estimated data including the neutron flux, effective full power days (EFPDs), HTS temperature and other parameters were considered as input data to the BPLM. The proposed BPLM used to predicting PT diametral creep was verified using the operating data of the Wolsung nuclear power plant in Korea.

2. GENETIC OPTIMIZED BUNDLE POSITION-WISE LINEAR MODEL (BPLM)

2.1 Linear Model

A linear model is a flexible generalization of ordinary least squares regression. In this paper, the linear model was optimized using a genetic algorithm in order to easily impose some constraints on the regression coefficients and to accomplish global minimization. The linear model is generally described as follows:

$$y = a_o + a_1x_1 + \cdots + a_px_p + \varepsilon_{ij} \quad (1)$$

where p is the number of input variables. Variables x_1 to x_p are the input signals that represent the fast neutron fluence, temperature, EFPD, etc. y is the output signal, which indicates the PT diametral creep or PT diameter. ε_{ij} is a random error for bundle i and channel j . Eq. (1) can predict PT diametral creep or the PT diameter at all bundle positions and channels using a single model.

The estimated output from the linear model is expressed as follows:

$$\hat{y} = \hat{a}_o + \hat{a}_1x_1 + \cdots + \hat{a}_px_p \quad (2)$$

The BPLM was also used to predict the PT diametral creep. This BPLM was devised because it is expected that the bundle position affects the diametral creep. The BPLM is described as follows:

$$y_i = a_{io} + a_{i1}x_1 + \cdots + a_{ip}x_p + \varepsilon_{ij} \quad (3)$$

where i indicates the bundle position in a PT channel.

The estimated output from the BPLM is expressed as follows:

$$\hat{y}_i = \hat{a}_{io} + \hat{a}_{i1}x_1 + \cdots + \hat{a}_{ip}x_p \quad (4)$$

Since a CANDU PT channel has 12 bundles, 12 linear models will be developed.

The appropriate selection of training data is very important because it can affect the optimization of the BPLM model. The input and output training data is expected to be in the form of clusters and the data in these cluster centers is more informative than the neighboring data. A BPLM model can be well trained using informative data.

It is assumed that M input/output data ($\mathbf{z}_k = (\mathbf{x}_k, y_k)$, $k=1,2,\dots,M$) is available and the data points are normalized in each dimension. The subtractive clustering (SC) scheme begins by generating a number of clusters in $m \times M$ dimensional input space, where m is the number of input variables. The SC scheme uses a measure of the potential of each data point, which is a function of the Euclidean

distances to all other input data points [3]:

$$P_1(k) = \sum_{j=1}^M e^{-4\|\mathbf{x}_k - \mathbf{x}_j\|^2 / r_\alpha^2}, \quad k = 1, 2, \dots, M \quad (5)$$

where r_α is the radius defining a neighborhood, which has considerable influence on the potential. Obviously, the potential of each data is high when it is surrounded by a considerable amount of neighboring data. After the potential of each data point is calculated, the data point with the highest potential is selected as the first cluster center.

In general, after determining the i^{th} cluster center \mathbf{c}_i and its potential value P_i^c , the potential of each data point is revised using the following equation:

$$P_{i+1}(k) = P_i(k) - P_i^c e^{-4\|\mathbf{x}_k - \mathbf{c}_i\|^2 / r_\beta^2}, \quad k = 1, 2, \dots, M \quad (6)$$

where r_β is also the radius, which is usually greater than r_α in order to limit the number of clusters generated. When the potential of all data points has been revised according to Eq. (6), the data point with the highest potential is selected as the next cluster center. These calculations stop if the inequality $P_i^c < \varepsilon P_i^c$ is true. Otherwise, these calculations are repeated.

The data positioned at the cluster centers is used as selected training data to develop the BPLM model.

2.2 Genetic Algorithm

John Holland formally introduced genetic algorithms for optimization in the 1970s [4]. Compared to conventional optimization methods, which move from one point to another, genetic algorithms begin from many points, simultaneously climbing many peaks in parallel. Therefore, genetic algorithms are less susceptible to being stuck at local minima than are conventional search methods [5,6]. Although a genetic algorithm has the disadvantage of being computationally expensive, it is the most useful method for solving optimization problems with multiple objectives. In genetic algorithms, the term chromosome refers to a candidate solution that minimizes the cost function and is 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 require a fitness function that assigns a score to each chromosome (candidate solution) in the current population, and maximizes the fitness function value. The fitness of a chromosome depends on how well that chromosome solves the problem at hand [6].

After an initial population of chromosomes is generated randomly, the typical genetic algorithm evolves the population through three operators; selection, crossover and mutation. 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 reproduce. After two individuals are chosen

from a population using the selection operator, the crossover operator chooses a crossover site randomly 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 placed into the next generation of the population. This process is likely to create even better individuals by recombining portions of good individuals. With some low probability, a portion of new individuals will have some of their bits flipped. A mutation can occur at each bit position in a string with some probability, normally 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 a small overall error. The fitness of an individual (chromosome) is calculated using the energy of an individual. Each chromosome contains the coefficients a_{ij} of the linear model. A chromosome with a lower energy has higher fitness. The energy functions are defined using the following two equations.

$$E_1 = \sqrt{\frac{1}{N} \sum_{k=1}^N \left(\frac{y_{rk} - \hat{y}_k}{y_{rk}} \right)^2} \quad (7)$$

$$E_2 = \max \{ |y_{r1} - \hat{y}_1|, |y_{r2} - \hat{y}_2|, \dots, |y_{rN} - \hat{y}_N| \} \quad (8)$$

E_1 and E_2 are the root mean squared errors and maximum absolute error, respectively. The subscript 'r' indicates the 'reference' or 'target' values. The fitness function is given as follows:

$$F = \exp(-\alpha E_1 - \beta E_2) \quad (9)$$

Three schemes were applied to increase the efficiency of the conventional genetic algorithm [7]. Initially, the proposed genetic algorithm has initial coarse tuning characteristics by first representing each parameter in a chromosome by a small bit number. If the parameters in a chromosome are represented by large bit numbers, the genetic algorithm can find the accurate optimal points in the limit of resolution but requires much more time to reach a convergence point. Therefore, it is essential to represent by a large bit number because many chromosomes gradually approach optimal points. Using this scheme, the genetic algorithm has initial coarse tuning and final fine tuning characteristics. The crossover site is selected in two ways. In the first the crossover site is selected randomly in a chromosome. In the second the crossover site is selected only between the parameters in a chromosome. This scheme slows premature convergence without reaching optimal solutions and speeds up the final convergence. In addition, a portion of the population of chromosomes with greater fitness in a priori generation is added to the new generation.

The same portion of the population of chromosomes with lower fitness in the total new generation is then removed to inhibit final drifting without convergence. Also, the other coefficients of Eq. (4) except for the bias term a_{i0} are bound to be positive values.

2.3 Uncertainty Analysis

The BPLM, which is a data-based model, requires uncertainty analysis to determine the accuracy of predictions. After uncertainty analysis, a prediction interval can be calculated such that the exact value exists in the prediction interval at a specified confidence level.

The BPLM has several possible sources of uncertainty in the predicted values; selection of training data, model structure including complexity, and noise in the input and output variables [8]. Since a BPLM is developed using a given training data set, each possible training dataset selected from the entire population of data will generate a different model and there will be a distribution of predictions for a given observation. In addition, model misspecification occurs when the model structure is not correct, thereby introducing bias. Analytical methods were used in this study [8-12].

A regression model for a specific i^{th} bundle position in Eq. (3) can be established from the N training data points $\{(\mathbf{x}_1, y_1), (\mathbf{x}_2, y_2), \dots, (\mathbf{x}_N, y_N)\}$:

$$y_k = f(\mathbf{x}_k, \boldsymbol{\theta}) + \varepsilon_k, \quad (10)$$

where

$$\boldsymbol{\theta} = [a_{i0} \quad a_{i1} \quad \dots \quad a_{ip}]^T.$$

For a regression model of an observation \mathbf{x}_0 , which is not part of the training data, the output prediction is given by

$$\hat{y}_0 = f(\mathbf{x}_0, \hat{\boldsymbol{\theta}}). \quad (11)$$

Using the Taylor series expansion of the output prediction to the first order, the output prediction can be approximated as follows:

$$\hat{y}_0 \approx f(\mathbf{x}_0, \boldsymbol{\theta}) + \mathbf{f}_0^T \cdot [\hat{\boldsymbol{\theta}} - \boldsymbol{\theta}], \quad (12)$$

where

$$\mathbf{f}_0^T = \left(\frac{\partial f(\mathbf{x}_0, \boldsymbol{\theta})}{\partial a_{i0}} \quad \frac{\partial f(\mathbf{x}_0, \boldsymbol{\theta})}{\partial a_{i1}} \quad \dots \quad \frac{\partial f(\mathbf{x}_0, \boldsymbol{\theta})}{\partial a_{ip}} \right) = [1 \quad x_1 \quad \dots \quad x_p].$$

The prediction error of the BPLM can be calculated as

$$y_0 - \hat{y}_0 = \varepsilon_0 - \mathbf{f}_0^T \cdot [\hat{\boldsymbol{\theta}} - \boldsymbol{\theta}]. \quad (13)$$

The variance of the prediction error can be expressed as

$$\text{Var}(y_0 - \hat{y}_0) = \text{Var}(\varepsilon_0) + \text{Var}(\mathbf{f}_0^T \cdot [\hat{\boldsymbol{\theta}} - \boldsymbol{\theta}]), \quad (14)$$

where

$$\varepsilon_0 \sim N(0, \sigma^2) \quad \text{and} \quad [\hat{\boldsymbol{\theta}} - \boldsymbol{\theta}] = N(0, \mathbf{S}).$$

In the BPLM, the variance-covariance matrix \mathbf{S} cannot be calculated because the parameter $\boldsymbol{\theta}$ is optimized with a genetic algorithm. However, the optimized parameters are not expected to be largely different from the parameters determined from the minimization of squared errors. Therefore, if the parameter is assumed to be estimated explicitly with the well-known squared error minimization technique, the variance-covariance matrix can be estimated as follows [12]:

$$\mathbf{S} = s^2 (\mathbf{F}^T \mathbf{F})^{-1}, \quad (15)$$

where

$$s^2 = \frac{1}{N - p - 1} \sum_{k=1}^N (y_k - f(\mathbf{x}_k, \hat{\boldsymbol{\theta}}))^2,$$

$$\mathbf{F} = \frac{\partial \mathbf{y}}{\partial \boldsymbol{\theta}} = \begin{bmatrix} \frac{\partial y}{\partial a_{i0}} & \frac{\partial y}{\partial a_{i1}} & \dots & \frac{\partial y}{\partial a_{ip}} \end{bmatrix},$$

$$\frac{\partial y}{\partial a_{ij}} = \left[\frac{\partial y_1}{\partial a_{ij}} \quad \frac{\partial y_2}{\partial a_{ij}} \quad \dots \quad \frac{\partial y_N}{\partial a_{ij}} \right]^T, \quad j = 0, 1, \dots, p.$$

The matrix \mathbf{F} is called the Jacobian matrix of first order partial derivatives with respect to the parameters determined from the minimization of squared errors.

The variance of the predicted output can be estimated as follows [12]:

$$\text{Var}(y_0 - \hat{y}_0) \approx \sigma^2 + \mathbf{f}_0^T \mathbf{S} \mathbf{f}_0 \approx s^2 + s^2 \mathbf{f}_0^T (\mathbf{F}^T \mathbf{F})^{-1} \mathbf{f}_0. \quad (16)$$

The estimate with a 95% confidence interval is expressed as

$$\hat{y}_0 \pm 2s \sqrt{1 + \mathbf{f}_0^T (\mathbf{F}^T \mathbf{F})^{-1} \mathbf{f}_0} = \hat{y}_0 \pm \delta. \quad (17)$$

3. APPLICATION TO THE DIAMETRAL CREEP PREDICTION

The data used consisted of a total of 588 input-output data pairs (x_1, \dots, x_3, y) taken from the Wolsung nuclear power plant units 2, 3 and 4 (WS2, WS3 and WS4). This data was acquired at 1501.04, 1943.71 and 3255.53 effective full power days (EFPDs) from unit 2, and 1324, 2183 EFPDs from unit 3, and 937, 2154 EFPDs from unit 4. Table 1 shows the PT channel identification name and EFPD of the acquired data. In this paper, all units are considered to have the same type (material and composition) of pressure tubes.

Table 2 compares the results of the BPLM using Eq. (4) and those of a general linear model using Eq. (2). The BPLM is superior to the general linear model. The general linear model predicts diametral creep at 12 bundle positions

using only one model. On the contrary, the BPLM predicts diametral creep using 12 different equations corresponding to 12 different bundle positions. Seventy percent (408 training data) of the acquired data was used to optimize the regression coefficients in Eqs. (2) and (4) using the genetic algorithm. One hundred and eighty test data points were used to independently verify the models. From this point, the BPLM will be examined in detail.

Table 3 lists the diametral creep prediction of the pressure tubes according to the usage of the EFPD value as an input. These results show that the RMS error and maximum error of the BPLM with EFPD value as an

input are smaller than those of the BPLM without the EFPD value as an input. Therefore, the BPLM model with the EFPD as input is better for predicting diametral creep.

Figures 2 and 3 show the estimated RMS errors and maximum errors for the 12 bundle positions. Fig. 2 shows the estimated RMS errors and maximum errors when the EFPD is used as an input. Fig. 3 shows the estimated RMS errors and maximum errors when the EFPD is not used as an input. As shown in Table 3, Figs. 2 and 3 explain that the estimated RMS errors and maximum errors of the BPLM with the EFPD as an input were smaller than

Table 1. PT Channel Identification Name and EFPD of the Acquired Data

unit	channels	EFPD
2	L09, L13, M11, N03, N21, O08, O14, Q06, Q11, S07, S15	1501.04
2	L13, N21, O08, O14, Q11, S07, T08	1943.71
2	L13, N21, O08, O14, Q11, S07	3255.53
3	L13, M11, N03, O08, O14, Q06, Q11, Q18, S07, T10, U11	1324
3	O08, O14, Q11, U11	2183
4	L13, M11, N03, O08, O14, Q06, Q11, U11	937
4	O08, O14	2154

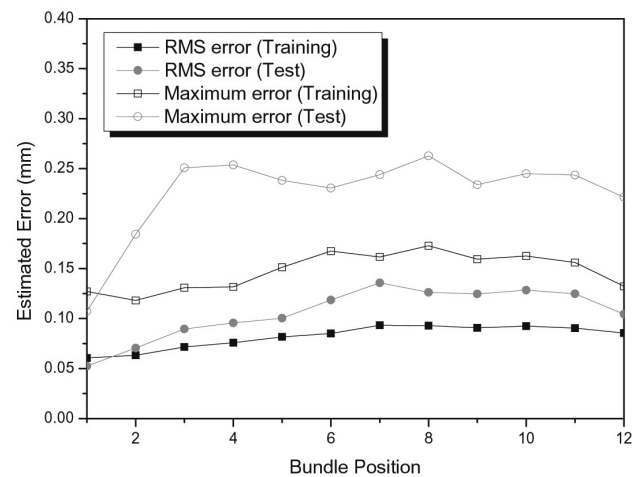


Fig. 2. Estimated RMS Errors and Maximum Errors as a Function of the Bundle Position of the BPLM with EFPD Value as an Input

Table 2. Comparison of the BPLM and a General Linear Model

Data Type	Data points	BPLM		General Linear Model	
		RMS error (mm)	Max. Error (mm)	RMS error (mm)	Max. Error (mm)
Training data	408	0.0827	0.1728	0.1051	0.2534
Test data	180	0.1087	0.2626	0.1818	0.5368

Table 3. Diametral Prediction of Pressure Tubes According as Whether or not the EFPD Values Are Used as an Input

Data Type	Data points	Usage of EFPD		No Usage of EFPD	
		RMS error (mm)	Max. Error (mm)	RMS error (mm)	Max. Error (mm)
Training data	408	0.0827	0.1728	0.0835	0.2040
Test data	180	0.1087	0.2626	0.1112	0.3954

those of the BPLM without the EFPD as an input. The case in which the error of the test data is smaller than that of the training data, as shown at the inlet bundle position in Figs. 2 and 3, occurs too much frequently. It seems that the condition of the training data sufficiently covers the condition of the test data because the creep at the inlet bundle position is relatively lower than at any other bundle position. In addition, as shown in Figs. 2 and 3, the RMS error at the 8th, 9th, 10th and 11th bundle positions starting from the PT inlet is higher than at other bundle positions because the fuel bundles at those positions are expanded more diametrically than the fuel bundles at the other positions due to the combined effect of high coolant temperature at the PT outlet-side and high neutron flux at the midpoint of the PT.

Since the estimated diameters of the current design model are given at 1500 EFPD, very near to 1501.04 EFPD where measured data exist, the results of the proposed BPLM and the current design model were compared (refer to Table. 4). The current design model is explained in [1], which is used to predict the diametral creep in the Wolsung nuclear power plants. The proposed BPLM is superior to the current design model.

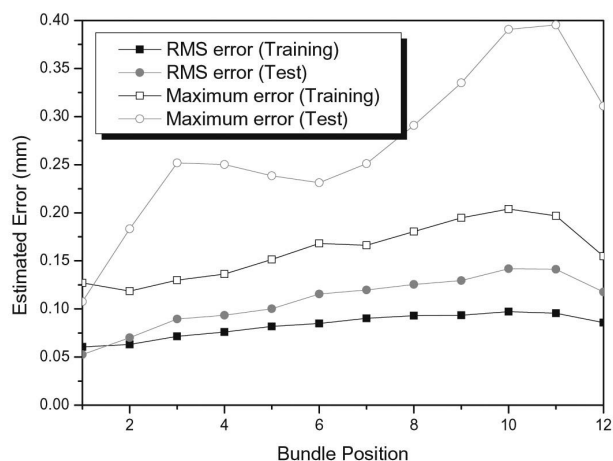


Fig. 3. Estimated RMS Errors and Maximum Errors as a Function of the Bundle Position of the BPLM without EFPD Value as an Input

To examine the prediction performance of a future PT creep based on previously measured data, the data, except for 3255.53 EFPD in Wolsung unit 2, were used for training and data at 3255.53 EFPD, which are the highest EFPD, were used for the test. The operating time point, 3256.53 EFPD, is the latest (longest) operation point. Therefore, that operation point is used for testing the prediction (kind of extrapolation) performance of the BPLM by developing the BPLM model using old operating data. Table 5 shows the diametral creep prediction of the pressure tubes for this case. As can be seen in Table 3, the BPLM can predict future PT creep well. The error tends to increase slightly but it is not so large as to degrade the prediction capability of the BPLM model.

All the acquired data included the data of the channels that had been measured repeatedly under different age conditions (EFPD). It was possible to develop a linear fitting model according to the EFPD for these repeatedly measured channels. The PT diameter of the channels, measured repeatedly by the linear fitting model, can be considered as a measured (target) diameter for future EFPD values. Fig. 4 shows the estimated errors as a function of the EFPD for the Wolsung unit 2 (WS2) and the errors increase globally according to EFPD. Fig. 5 compares the RMS errors estimated by the proposed BPLM and by the current design model for 10 repeatedly measured channels of Wolsung units 2, 3 and 4. The error is based on the maximum bundle diameter in a channel and also based on the values averaged upon 1500 EFPD interval from 3000 EFPD to 9000 EFPD. The diameters estimated by the linear fitting model using the repeatedly measured channel data were considered as target values. The results show that the BPLM can predict future PT diameter well. Also, it is shown that the prediction

Table 4. Comparison of the Proposed BPLM and the Current Design Model at 1501 EFPD

Model	RMS error (mm)	Max. Error (mm)
BPLM	0.0681	0.1587
Current Design Model	0.1503	0.2899

Table 5. Diametral Prediction Performance of the Pressure Tubes by BPLM

Data Type	Data points	RMS error (mm)	Max. Error (mm)
Training data (except for 3255.53 EFPD data)	490	0.0882	0.2197
Test data (3255.53 EFPD data)	72	0.1248	0.1994

capability of the BPLM is superior to that of the current design model.

Figures 6 and 7 show the target and estimated diameters in the L13 and O08 channels, respectively, along with the prediction intervals for the corresponding channel. The data at 3255.53 EFPD consists of 6 sets of channel data. Results similar to the L13 and O08 channels were obtained for the N21, Q11, O14 and S07 channels. All the measured diameters exist in the prediction interval, which means that the coverage is 100%. This complete coverage originates from the BPLM, which was developed using available data with the exception of 3255.53 EFPD data points in unit 2 (training data) and the 3255.53 EFPD data points (test data).

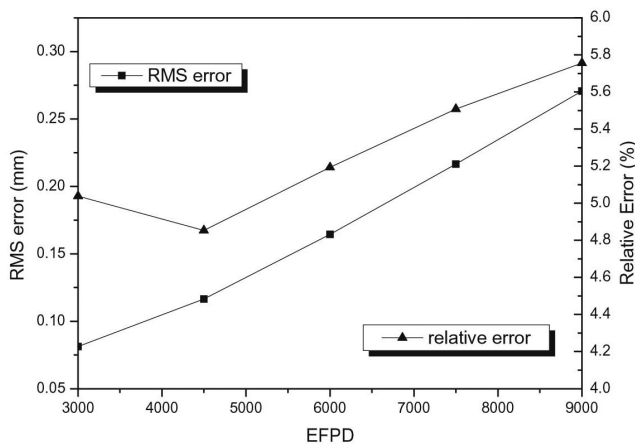


Fig. 4. Estimated RMS Errors and Relative Errors as a Function of the EFPD for WS2

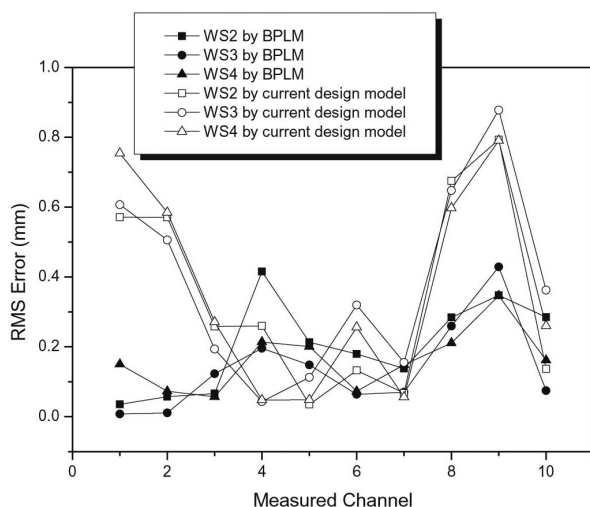


Fig. 5. Estimated RMS Errors by the BPLM and the Current Design Model for 10 Repeatedly Measured Channels of Wolsung Unit 2, 3 and 4

4. CONCLUSIONS

A BPLM was developed to predict PT diametral creep using the previously measured PT diameters and the HTS operating conditions in CANDU reactors. The linear model was devised based on bundle position and was optimized by a genetic algorithm because it is expected that each bundle position in a PT channel has inherent characteristics. A range of measured or estimated data, including the neutron flux, effective full power days (EFPDs), HTS temperature and other parameters were considered as input data to the BPLM. Finally, the fast neutron fluence, HTS temperature and EFPD were used as inputs to the BPLM.

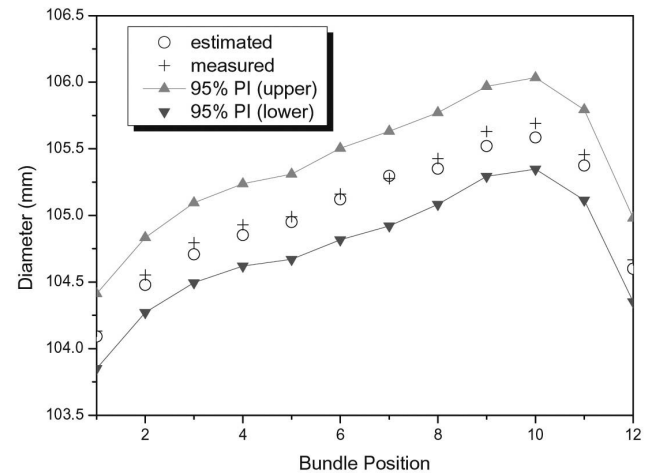


Fig. 6. Prediction Intervals of the BPLM Model in the L13 Channel at 3255.53 EFPD

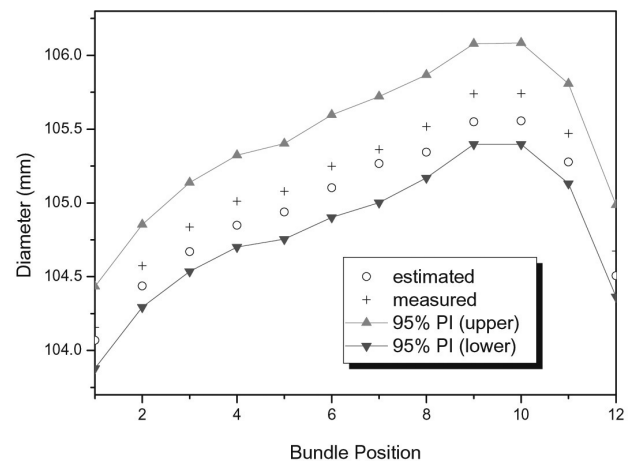


Fig. 7. Prediction Intervals of the BPLM Model in the O08 Channel at 3255.53 EFPD

The proposed BPLM for predicting PT diametral creep was verified using the operating data of the Wolsung nuclear power plants in Korea. The BPLM was able to predict the PT diametral creep accurately (with an accuracy of $\sim 0.1\text{mm}$ RMS error). In addition, since the development of a BPLM requires uncertainty analysis to determine how accurate the predictions are, estimates with a 95% confidence interval were obtained for 72 test data points (6 channels used as test channels) by performing analytical uncertainty analysis. The coverage of the prediction interval was 100%.

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