Respiratory Motion Prediction with Random Vector Functional Link (RVFL) Based Neural Networks

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Abstract. Respiratory motion exhibits non-linear and non-stationary behavior in nature and this has been a great hindrance to the accurate prediction of tumor in motion adaptive radiotherapy. Accurate prediction of respiratory motion and subsequent tracking of tumor has been a challenge due to the irregularities and intra-trace variabilities. In order to overcome this issue, prediction models can be trained by using neural networks. However due to the burden of large training data, computational efficacy of existing neural networks can be affected. Moreover, training of neural networks using conventional methods like back-propagation (BP) may result in local minima and it may slow down the learning rate and convergence respectively. As a solution, in this paper, we employed random vector function link (RVFL) based neural networks to train the model in a very efficient way to achieve high accuracy in respiratory motion prediction. In RVFL, the direct link from input features to output layer acts as regularization to prevent the network from overfitting. The proposed method is tested with real respiratory motion traces acquired from 31 patients. Results show that RVFL with the use of direct link performs quite better than without direct link.

1. Introduction
Motion adaptive radiotherapy plays an important role in the prediction of real time position of the thoracic and abdominal tumors. For the patients diagnosed with these tumors, motion adaptive radiotherapy has been a promising way for the cure. Sometimes, tumors motion impeded by the respiratory movement mechanism exceeding 20 mm and significantly compromises the dose conformity in radiotherapy treatment[1, 2]. Motion adaptive radiotherapy tries to deliver the conformal dose precisely to the abdominal and thoracic regions where tumors are present with minimal exposure to the surrounding tissues by compensating the tumor motion [1, 3-5]. However, in equipments used to track tumors in real time like Cyberknife [6], there is an inherent latency up-to several milliseconds due to its limitation in data processing and mechanics. Eventually, this delay affects in targeting the beam to the target tumor [7]. To get rid of this latency, system’s known latency can be employed in the prediction the future tumor motion [7].

Several prediction methods [5,6,8] have been developed in the literature to solve this problem. Compared to model based methods[6, 8, 9], learning based methods such as, artificial neural networks (ANN) [10, 11], support vector regression (SVR) [5] provide better adaptability to predict respiratory motion especially at large prediction horizons [9]. Artificial neural networks (ANN) has been popular for solving classification and regression problems for bio-medical data, especially due to non-stationarity and non-linearity of such data [5]. Single hidden layer feedforward neural network (SLFN) is the simplest type of the feedforward neural network (FNN) and it can be trained with the traditional back propagation (BP). However, back propagation is a very slow process as it requires multiple
iterations besides having presence of multiple minima as its major drawback. Meanwhile, in a situation where training takes longer period of time and there is higher chance of getting trapped in multiple local minima, randomized neural network has been a better choice [13]. Random vector functional link neural network is categorized as a semi-random realization of functional link neural networks [13, 14], where the direct link as well as the closed form solution features make it an attractive approach for the prediction problem. In this paper, we employed RVFL to predict the respiratory motion for longer prediction horizons on respiratory motion data set containing 304 traces from 31 subjects.

2. Method

In this section, we first highlight the adaptation of neural network to the prediction of respiratory motion. Thereafter, we explain the implementation of our approach on a data set consisting of 304 respiratory motion traces obtained from a total of 31 patients at Georgetown University Hospital during CyberKnife treatments [15]. Fig. 1 gives the overview of the entire approach.

2.1. Single Layer Feedforward Neural Networks

Single layer feedforward neural network (SLFN) is a form of Artificial neural networks (ANN) which consists of an input layer, a hidden layer of neurons with non-linear activation function, and an output layer. In our architecture, the SLFN is constructed with adjacent layers containing adjustable weight, making them more robust in activation. The interconnection of neurons within the same layer were avoided aligning with the traditional approach of SLFN architecture. Outputs from all hidden nodes were calculated using the following equation as stated in [13]:

\[ v_j = f(\sum_{i=1}^{n} w_{ij}x_i + b_i) \]  

where \( f(.) \) representing non-linear activation function; \( x_i \) is the input to the neuron; \( w_{ij} \) is the weight of connection between the input \( i \) and hidden neuron \( j \) of the hidden layer and \( b_i \) represents the bias to the neurons at the hidden layer.

Our input matrix constructed from the respective respiratory motion traces with the use of sliding window of fixed length were fed into the SLFN so that on activation within the hidden layer, the final outputs are computed as follows:

\[ y = g(\sum_{j=1}^{h} w_{jo} v_j + b_j) \]
where \( g(.) \) is the non-linear activation function, \( v_j \) is the output of the hidden neuron; \( w_{ji} \) is the weight of connection between hidden layer neuron \( j \) and output and \( b_j \) is the bias of the neurons at the output layer. The weights in SLFN (\( w_{ij} \) and \( w_{jo} \)) are optimized by back propagation (BP) method.

2.2. Random Vector Functional Link

Random vector functional link (RVFL) network being a randomized form of FNN, a direct link is established between input and output neurons and this approach helps to avoid overfitting issues. In our implementation of RVFL architecture, we adopted the use of least square estimation in a closed form and fixed random weights and biases between input and hidden layers.

The basic architecture of RVFL is as shown in Fig. 2. Our RVFL design is such that the hidden layer weights \( \omega_h \) follow the uniform distribution whose values lie in between a given interval \([-S, +S]\), where \( S \) is the scaling factor determined during parameter tuning phase of the experimentation process. Therefore, we compute \( H \) at the hidden layer \( H \) with the use of the activation function \( f \) given in equation (3) as stated in [13]

\[
H = f(W_h \cdot X) \tag{3}
\]

where \( X \) is the training data. Thus, the only weights that need to be optimised are the output layer weights \( W_o \). \( W_o \) can be optimized through least square method as given in equation (4).

\[
W_o = (H^T H)^{-1} H^T Y \tag{4}
\]

Applying \( W_o \) and \( W_h \) on the testing data \( X_s \), the predicted values can thus be calculated as:

\[
\hat{Y}_s = W_o \cdot f(W_h \cdot X_s) \tag{5}
\]

where \( \hat{Y}_s \) denotes predicted values and \( X_s \) is the testing data.

![Figure 2. The structure of RVFL.](image)

2.3. Performance Measures

For analyzing the performance of the proposed approach, we employed root mean square error (RMSE) for different prediction lengths \( l \). If \( y_i(k) \) denotes the actual value for a trace \( i \) at discrete time index \( k \). Then \( y_i(k + l) \) represents the actual value at \( k + l \) for a trace \( i \) and \( \hat{y}_i(k + l) \) is representing its corresponding \( l \) steps ahead predicted value. Hence, the prediction error \( \hat{e}_i(k + l) \) in [8] could be easily computed as:

\[
\hat{e}_i(k + l) = y_i(k + l) - \hat{y}_i(k + l) \tag{6}
\]

Therefore, the RMS prediction error (RMSE\(_i\)) for a trace \( i \) can be computed as:

\[
RMSE_i = \sqrt{\frac{1}{N_i} \sum_{k} \hat{e}_i(k + l)^2} \tag{7}
\]

where \( N_i \) denotes the total number of samples in testing data of a trace \( i \).

Further, we also compute the average RMS prediction error for all traces for multiple steps ahead prediction as follows:
where $N_t$ denotes the total number of traces.

3. Results

3.1. Data Description

In this paper, we employed 304 traces of respiratory motion to evaluate the performance of the RVFL model. These traces were recorded from a category of 31 subjects while using the Cyberknife at Georgetown University Hospital at 26 Hz [15]. This data set contains both 3D and 1D respiratory motion traces which are obtained by applying the Principle Component Analysis (PCA) on 3D respiratory motion traces. The prediction performance obtained from 1D respiratory motion traces provides an approximate estimate of 3D respiratory motion traces. Further we down-sampled the traces to 5.2 Hz to satisfy the kV/MV image-guided treatment. The average length of the traces is 71.2 min.

3.2. Parameter Selection

For the proper initialization of the parameters, we did exhaustive grid search through out all 304 traces. For our prediction problem, we found minimum average $RMSE$ of testing data of 304 traces using equation (8) at 100 number of neurons. We compared different activation functions on this number and found that the most fitted function to our dataset is hardlim function as shown in Table. 1.

| Number of neurons | Activation functions | RMSE   |
|-------------------|----------------------|--------|
| 100               | Hardlim              | 0.7645 |
| 100               | Sigmoid              | 36.2506|
| 100               | Sine                 | 10.4409|
| 100               | Tribas               | 5.8337 |
| 100               | Radbas               | 9.56×10^4|
| 100               | Sign                 | 0.7698 |

3.3. Simulation Results

In this paper, the large database of 304 respiratory motion traces were used to evaluate the performance of the proposed RVFL model. The length of each trace was splitted into training and testing data. The first 54 min were used for training while remaining data were used for the testing.

Figure 3. RVFL prediction for trace-168 at 5.2 Hz with (a) Showing segment of the trace and the RVFL prediction at 384 ms (b) Showing the corresponding training and testing errors respectively. The RVFL model is trained for different prediction lengths to predict the respiratory motion. For instance, the prediction result obtained for trace-168 with ID (p22_f74_m3_proc2_pca) at the prediction lengths of 384 ms and 576 ms are shown in Fig. 3 and 4 respectively. The errors are also shown in the same figure.
We employed RMS value for quantification of the prediction errors for training and testing of all respiratory motion traces. We compared the RMSE values of different RVFL variants with the training and testing RMS values of prediction error for each trace. From Fig. 5 we can observe that the performance of RVFL with direct link is better than RVFL without direct link during both training and testing phases. In Fig. 6 and Fig. 7 the we can also notice that the training and testing RMSE values are lower for RVFL with direct link as compared to RVFL without direct link for prediction at 384 ms and 576 ms.

The statistical comparison of RVFL with and without direct link between input and output nodes in terms of RMSE is tabulated in Table 2. Using (8), we computed the RMSE average of 304 traces for three prediction lengths separately.

**Figure 4.** RVFL prediction for trace-168 at 5.2 Hz with (a) Showing segment of the trace and the RVFL prediction at 576 ms (b) Showing the corresponding training and testing errors respectively.

**Figure 5.** Comparison between RVFL with and without direct link at prediction length 192 ms (a) The RMSE of each trace during training (b) The RMSE of trace each during testing.

**Figure 6.** Comparison of RVFL with and without direct link at prediction length 374 ms (a) The RMSE of each trace during training (b) The RMSE of each trace during testing.
Figure 7. Comparison of RVFL with and without direct link at prediction length 576 ms (a) showing the RMSE of each trace during training (b) The RMSE of each trace during testing.

The statistical comparison of RVFL with and without direct link between input and output nodes in terms of RMSE is tabulated in Table 2. Using (8), we computed the RMSE average of 304 traces for three prediction lengths separately.

Table 2. Performance comparison between different activation functions at 100 number of neurons.

| Prediction length | With Direct Link | Without Direct Link |
|-------------------|------------------|---------------------|
|                   | Training         | Testing             | Training         | Testing             |
| 192 ms            | 0.3096           | 0.3753              | 1.0275           | 1.6615              |
| 376 ms            | 0.6335           | 0.7645              | 1.2098           | 1.8327              |
| 576 ms            | 0.8943           | 1.0818              | 1.3583           | 1.9908              |

4. Conclusion

In this paper, we implemented RVFL for the respiratory motion prediction. 304 respiratory motion traces were employed in evaluating the prediction performance of the RVFL model. Our analysis with different combinations of activation functions and number of hidden nodes in RVFL identified that the most fitted activation function for respiratory dataset is hardlim at 100 number of hidden neurons. We have observed from the RVFL performance that, optimal number of hidden neurons is necessary to avoid over-fitting. Prediction of respiratory motion has been performed for three different prediction lengths using RVFL with direct and without direct link between input and output nodes. By comparing the results of both variants of RVFL based on different prediction lengths, we found that the performance of RVFL with the direct link is better than the without direct link. In order to improve the robustness of the model for further steps ahead prediction of respiratory motion, the acquired weights from RVFL model need to be updated online, hence in the future work, we shall incorporate incremental learning to the model. The use of a larger dataset with more patients will also be considered for generalization of the approach.

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