Using Machine Learning to Predict Hypertension from a Clinical Dataset

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Abstract— Hypertension is an illness that often leads to severe and life threatening diseases such as heart failure, thickening of the heart muscle, coronary artery disease, and other severe conditions if left untreated. An artificial neural network is a powerful machine learning technique that allows prediction of the presence of the disease in susceptible populations while removing the potential for human error. In this paper, we identify the important risk factors based on patients' current health conditions, medical records, and demographics. These factors are then used to predict the presence of hypertension in an individual. These risk factors are also indicative of the probability of a person developing hypertension in the future and can, therefore, be used as an early warning system. We present a neural network model for predicting hypertension with about 82% accuracy. This is good performance given our chosen risk factors as inputs and the large integrated data used for the study. Our network model utilizes very large sample sizes (185,371 patients and 193,656 controls) from the Canadian Primary Care Sentinel Surveillance Network (CPCSSN) data set. Finally, we present a literature study to show the use of these risk factors in other works along with experimental results obtained from our model.

Keywords — Artificial neural network; hypertension; backpropagation network; medical decision support systems.

I. INTRODUCTION

Hypertension is a common health condition in the modern world that can lead to a number of severe illnesses such as stroke, heart disease, and renal failure [10]. Fig. 1 shows the prevalence of hypertension compared to seven other chronic diseases based on a sample of Canadian Primary Care Sentinel Surveillance Network (CPCSSN) data set [28]. We describe the data set later in the paper and use it in this study. A diagnosis of hypertension is made when the diastolic or systolic blood pressure readings exceed 90 mm Hg or 120 mm Hg, respectively for at least two subsequent visits [10]. Risk assessment of the disease is significantly more complicated and depends on a multitude of factors and transient environmental conditions that can artificially raise blood pressure readings [15]. Commonly identified risk factors include age, gender, body mass index (BMI), obesity, stress, triglycerides, uric acid, lipoproteins, cholesterol, history of smoking habits, and family history of the disease [1][12][15][21][23][25]. Due to the complexity associated with disease prediction, evaluations by clinicians are prone to error especially in cases where the data is incomplete or noisy [15].

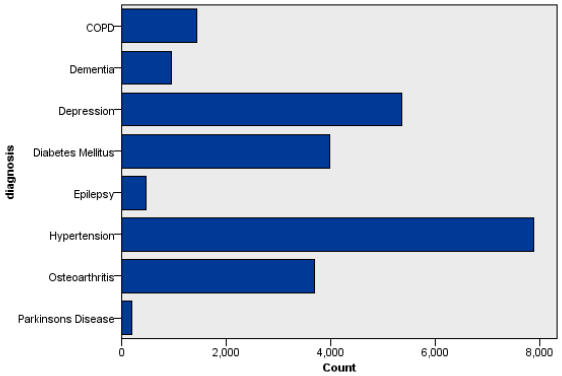

Fig. 1 Distribution of patients having one of the eight chronic diseases in a sample of the CPCSSN data set used in our study (COPD- chronic obstructive pulmonary disease).

Artificial Neural Networks (ANNs) are currently resurging in popularity across a variety of domains [3]. For example, ANNs are used to predict the stock market [17], detect objects and perceive scenes [22], or compress images [13]. Within the field of medicine in particular, ANNs are popular due to their ability to analyze medical imagery, design medications, and act as diagnostic systems [3][11]. Medical oriented systems must also achieve a high degree of efficiency, accuracy, and reliability in order to minimize harm to patients [3]. Machine learning serves as a viable option that allows clinicians to better identify patterns in data that are otherwise prone to human error and improve upon vital performance measures in medicine [2][9][21]. Therefore, medical decision support systems can integrate machine learning in order to provide efficient and accurate results that a doctor can then use to better diagnose and treat illnesses. Such technologies are also capable of providing timely interventions if coupled with data obtained early in a patient's treatment cycle. This is a priority for healthcare providers if they are to provide preventative care to these patients and reduce the overall costs. Neural networks are capable of meeting the high demands of medicine and serve as a powerful invaluable tool in the field.

To date, there has been little research on investigating the practicality of predicting hypertension risk using large datasets. The majority of studies from this area typically have quite low sample sizes. Our study focuses on the analysis data with an n > 100,000 per subject group [15]. Since our network is trained on a much broader range of subjects, we argue that the overall applicability of our network will be substantially more robust for use in the field. In this paper, we apply machine learning and data integration techniques to classify hypertension/non-hypertension patients given the anonymous electronic health records of the patients in the CPCSSN data set [28]. A three-layer ANN is developed as our predictive model which uses the backpropagation learning algorithm. Data is extracted from the CPCSSN data set for training and testing. Matlab was used as an analytic tool to develop the networks. We obtained an accuracy of about 82% which is quite good given the use of the integrated CPCSSN data set for the study.

The rest of this paper is organized as follows. In Section 2, we discuss related works. Section 3 describes the CPCSSN data set and the metrics used as the interesting input factors for our network. In Section 4, we first present the neural network approach in general and then explain our specific ANN model, the data preprocessing steps and the implementation details using the Matlab neural network toolbox. We discuss the results obtained in Matlab in Section 5. Finally, Section 6 concludes the paper and lists some ideas for the future work.

II. Related Work

The existing literature in the area of predicting hypertension within patient populations focus on several techniques such as statistical models [14], neural networks [20][21][24][25] and fuzzy models [1].

Echouffo-Tcheugui et al. [14] provide a comparative study and a summary of performances of the various statistical approaches that present risk models of hypertension. The paper presents 15 different hypertension prediction risk models from 11 studies which report on the development, validation, and impact analysis of hypertension risk prediction models. Some of the key comparison criteria include design and characteristics, predictors, model discrimination, calibration and reclassification ability, validation, and impact analysis. The common predictor variables used in most of the models are age, sex, body mass index (BMI), status of diabetes, and blood pressure. Some of the other variables used are smoking, family history, and physical inactivity. Most risk models have acceptable-to-good discriminatory ability (C-statistic 0.7 to 0.8). Some of these works focus on specific gender, age or racial group and use different sources of data to develop the models. None of these models, however, apply a neural network approach which has proven promising in many data domains. To better relate with our ANN approach presented in this paper, some of the existing ANN approaches are discussed below.

One of the earliest works in the area is by Poli et al. [20] which uses an ANN called Hypernet to diagnose and treat hypertensive patients. The network is split into multiple specialized feed-forward network modules of differing complexity in order to mimic the reasoning of physicians. The network takes anamnestic data as well as a time series of blood pressure monitoring data as inputs in order to arrive at outputs specifying the quantity of antihypertensive drugs to administer to each patient. An absence of output indicates that a patient is not hypertensive.

Samant and Rao [21] developed a Levenberg-Marquardt backpropagation neural network in Matlab consisting of 13 input nodes and 1 output node with multiple hidden layers to predict hypertension. Input factors consisted of blood pressure, serum proteins, albumin, hematocrit, cholesterol, triglycerides, and hemorheological parameters. The authors also evaluated differences in performance based on the number of hidden nodes and layers to determine optimal performance. They concluded that a deep network with 20 nodes in the first hidden layer and 5 nodes in the second hidden layer result in the best accuracy. The authors report to have achieved an accuracy of 92.85% with their approach using a rich data set collected over 10 years at the Hemorheology Laboratory of the Indian Institute of Technology Bombay (IITB) hospital in Mumbai, India. The data set consisted of 13 clinical, biochemical, and hemorheological data metrics of hypertensive and non-hypertensive patients.

Ture et al. [25] compare the performances of three decision tree models, four statistical algorithmic models and two ANN models, all of which predict the risk of essential hypertension disease. Predictor variables used in the models include age, sex, family history, smoking habits, lipoproteins, triglycerides, uric acid, cholesterol, and BMI. Based on the sensitivity and specificity analysis of the models, the study infers that the metrics used are good predictor variables for diagnosing hypertension and the ANNs are the best models which also have the incremental learning capability to complement the existing statistical models.

Srivastava et al. [23] demonstrate a fuzzy soft computing approach to classify five different grades of hypertension namely very low, low, moderate, high, very high. The input variables used in the study consist of age, systolic blood pressure (SBP), diastolic blood pressure (DBP), BMI, heart rate, low density lipoprotein (LDL), high density lipoprotein (HDL), triglyceride, smoking, and exercise. The approach is unable to learn as ANNs do and depends on the definition of the fuzzy utilities.

Sumathi and Santhakumaran [24] demonstrate that their feed-forward backpropagation network consisting of eight input variables, four hidden variables, and two output variables achieve results comparable to physicians. Accuracy and subject counts were not included in the study.

The comparison of the performances of our approach with some of these related works are summarized in TABLE II.

III. CPCSSN Data Set

We used the Canadian Primary Care Sentinel Surveillance Network (CPCSSN) data set [28] for our study which contains anonymous Electronic Medical Record (EMR) data of patients seeking aid from their primary health care providers. Patients

in this set are further classified into eight chronic disease groups based on clinician-developed CPCSSN diagnostic algorithms [7][16][26]. The hypertensive group consisted of 185,371 individuals identified as having hypertension [26]. The control group consisted of 193,656 patients not belonging to any of the eight chronic disease categories but still seeking medical aid for other reasons. We used this labelled data in our study for training and testing our machine learning model.

A. Factors of Interest

Based on the study of the related work and the available CPCSSN data set, we defined 11 factors of interest as input variables in our ANN model as described in Table 1. These included age, gender, BMI, systolic and diastolic blood pressure, high and low density lipoproteins, triglycerides, cholesterol, microalbumin, and urine albumin creatinine ratio. Patients were not excluded if they had missing data. We considered missing data for the above factors as an indicator that hypertension was not present because the relevant lab tests were not ordered by the physician. Some of these factors are described below.

1) Body Mass Index (BMI)

BMI refers to a height/weight ratio and is calculated as weight in kilograms divided by height in meters squared [27]. BMI values are classified into one the following four classes based on the BMI of the corresponding individual [27].

Underweight:	BMI < 18.5
Normal:	18.5 >= BMI >=24.99
Overweight:	BMI > 25
Obese:	BMI >30

2) Systolic and Diastolic Blood Pressure

Systolic blood pressure refers to pressure in the arteries when the heart beats (heart muscle contracts) which is the higher number, and diastolic blood pressure is the pressure between heart-beats (muscles relaxed) which is the lower number of a blood pressure reading [6]. Blood pressure measures are classified as follows [6] (S: systolic, D: diastolic).

Normal:	S < 120,	D< 80
Prehypertension:	120= < S < 139,	80 =< D < 89
Hypertension stage 1:	140= < S < 159,	90= < D < 99
Hypertension stage 2:	S >=160,	D > =100
Hypertensive crisis:	S >= 180,	D > =110

3) Lipoproteins, Triglycerides and Cholesterol

Cholesterol is transported in the blood by both high and low density lipoproteins [5]. An individual's total cholesterol count is made up of one fifth of their triglyceride level along with their HDL and LDL cholesterols [5]. HDL and LDL cholesterols differ in that HDL is considered "good cholesterol" and removes the bad LDL cholesterol that contributes to arterial plaque deposits from the body [5].

4) Albumin

Albumin is a protein made from the liver that prevents fluid from leaking from blood vessels [4]. It's often used to measure a patient's overall health status or their nutritional status [4]. A micro-albumin level higher than 30mg indicates an early kidney disease and a level higher than 300mg indicates a more advanced kidney disease [18].

5) Albumin/creatinine ratio (ACR)

The Albumin/Creatinine Ratio is used to screen people with chronic conditions, such as diabetes and high blood pressure and is, therefore, used as a factor in our model. Virtually no albumin is present in the urine when the kidneys are functioning properly. However, albumin may be detected in the urine even in the early stages of kidney disease. Creatinine is a byproduct of muscle metabolism which is normally released into the urine at a constant rate and indicates the urine concentration. A higher value of ACR, therefore, indicates deteriorating health condition for patients having diabetes, blood pressure and kidney disease.

TABLE I. NETWORK INPUT FACTORS

#	Variable (unit of measure)	Type (mean ± standard deviation)
1	Birth Year	Numeric (56.59±14.65)
2	Gender	Categorical (0,1)
3	Body Mass Index (kg/m^2)	Numeric (28.57±5.29)
4	Systolic Blood Pressure (mmHg)	Numeric (127.22±14.81)
5	Diastolic Blood Pressure (mmHg)	Numeric (78.39±9.08)
6	High Density Lipoprotein (mmol/L)	Numeric (1.40±0.33)
7	Low Density Lipoprotein (mmol/L)	Numeric (2.96±0.72)
8	Triglycerides (mmol/L)	Numeric (1.44±0.64)
9	Cholesterol (mmol/L)	Numeric (4.99±0.83)
10	Micro-albumin (mg/L)	Numeric (29.46±31.68)
11	Urine Albumin-Creatinine Ratio (mg/mmol)	Numeric (4.14±4.87)

IV. OUR APPROACH: A NEURAL NETWORK MODEL

Artificial Neural Networks (ANNs) have gained much success as incremental learners and predictors that mimic human intelligence. They can have different layouts and use many different learning algorithms. A commonly used ANN is the feedforward backpropagation neural network as shown in Fig. 2, which consists of nodes arranged into multiple layers (numbered 0 to N, where $N \geq 2$) [19]. These nodes are the basic processing units that roughly mimic the function of brain neurons. Layer 0 represents the input layer, layer N represents the output layer, and layers 1 to N-1 represent the hidden layer(s) [19]. Nodes in the neighbouring layers are connected by forward links through which information flows from the input towards the output layer. Each connection has an associated weight that is changed by the learning algorithm during the network training phase. A 3 layer 11-7-2 network with 11 input, 7 hidden and 2 output nodes would thus have a total of 91 weight values ((11*7) + (7*2)).

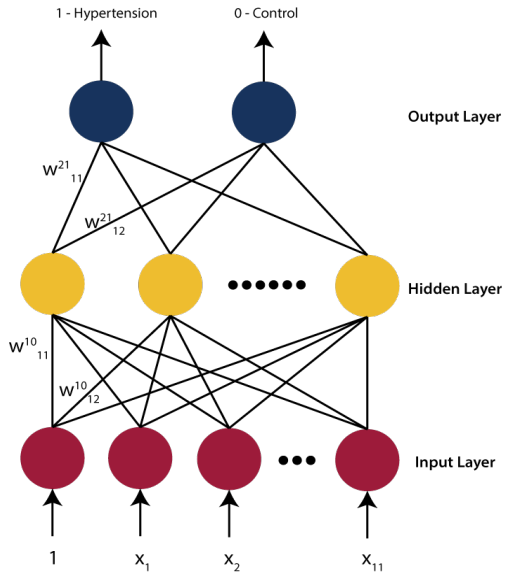

Fig. 2 ANN architecture. Information flows from the 11 input nodes (and 1 bias node) to the 7 hidden nodes, and finally to the 2 output nodes. $w^{ll'}_{ji}$ is the weight to node j in layer l from i^{th} input in layer l'.

As the training progresses using labeled data which has a set of input and the desired output values (d), network weights are adjusted in multiple iterations to align the outputs (y) more and more each time to the expected values until the error is reduced to an acceptable level or a threshold number of iterations is reached. So, in each iteration for the input vector p, the error (e) is calculated from the difference between the desired (d_p) and obtained (y_p) output values.

$$e = (d_p - y_p) \quad (1)$$

The backpropagation algorithm tries to minimize the error by following the downward slope of the error curve of the sum-squared error value, which is called the gradient descent approach as given below.

$$\sum_p (d_p - y_p)^2 \quad (2)$$

The sigmoid function is commonly used as the transfer function to generate node outputs.

$$S = 1 / (1 + e^{(-m * net)}) \quad (3)$$

where *net* is the total input signal of the node and m is the slope of the sigmoid function. For our network, we use $m = 1$.

A. ANN Architecture

We developed a backpropagation neural network composed of 11 input nodes, 7 hidden nodes, and 2 output nodes in order to classify the hypertensive and control patients as shown in Fig. 2. The 11 input nodes were used to represent the 11 factors of interest. The number of nodes in each layer is indicative of the overall complexity of the system and affects the required processing time [3]. More hidden nodes enable better mapping of the input to the output and often better accuracy of the results which also comes with the adverse effects of increased processing time and overfitting of the data. Overfitting makes the model less efficient for varying input data. Designing a model thus involves taking the above factors into consideration and achieving a balance of complexity, accuracy, flexibility and performance.

B. Data Preprocessing

We did a substantial amount of cleaning and preprocessing of the CPCSSN data prior to feeding it into our network. The data processing flow is shown in Fig. 3 below.

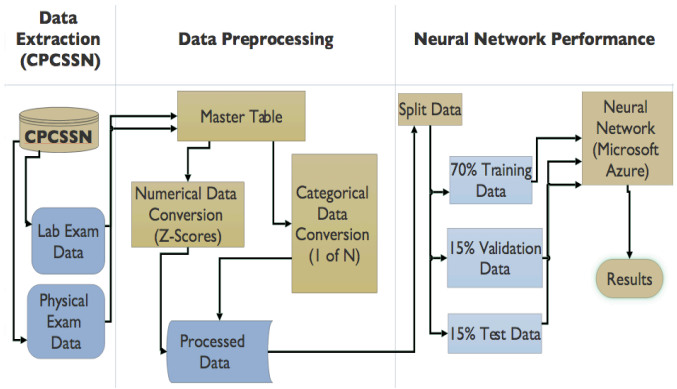

Fig. 3 Data processing flow of the project.

We began with the labeled CPCSSN data where patients are labeled with the detected types of chronic diseases if applicable. The data was anonymized and each patient was identified with a patient ID. Patients may be suffering from one or more of the eight chronic diseases of interest to the CPCSSN researchers. These eight diseases include: hypertension, diabetes, chronic obstructive pulmonary disease (COPD), dementia, depression, epilepsy, osteoarthritis, and Parkinson's disease. We considered the *control patients* as individuals who are not suffering from any of the aforementioned conditions but still seek medical treatments for other reasons. We then extracted the factors of interest from multiple tables within the CPCSSN database (Microsoft SQL Server) for both hypertensive and control patients for analytics.

First we selected the data items for analytics from the multiple set of tables and data items in the CPCSSN data which included patients' encounters with the physicians, doctors' comments, billing information etc. These data items were selected based on a comprehensive overview of the literature in order to ensure that all network variables were evidence-based.

Next we selected the period of data to include in the data extraction process because an individual may undergo a large number of tests and physical exams throughout their lifetime. For hypertensive patients, we selected the tests occurring within a close temporal proximity to the date of diagnosis. In order to do this, the total amount of days was calculated between each lab test and the date of diagnosis of each patient. The minimum value then determined selection of the lab test for extraction. For control patients, we selected the test closest to their date of registration in the CPCSSN data set since they lacked any identifying diagnosis dates.

We initially extracted diagnosis codes and medication data along with the demographic, lab and physical exam data from multiple CPCSSN tables into a master table for analytics. We got almost 100% accuracy as both the medication data and diagnosis codes are deterministic factors of a disease and incur *target leaks* during network training. Target leaks are any pieces of information hinting at patterns in the data. These factors also required a large number of input nodes to represent which also substantially reduces generalizability.

Our final data set included the 11 factors listed in Table I from the demographic, lab, and physical examination data. We aggregated the data into a master table for cleaning and preprocessing such as assigning class values as described in Section 3. The master table was then exported as a .csv file which was used as an input to our custom java application for further processing of the data. Our application took columns of interest from the .csv file and converted the data into a format that our ANN could process.

At this point we used the following criteria to clean the data.

a. Any patient missing all nine lab and physical exam tests as listed in Table I is removed from the data.
b. Patients born prior to 1940 are removed.
c. Remaining missing values in the data are then converted to 0's since the absence of a particular lab test may be indicative of the absence of hypertension.

The numerical data, which basically included all factors except the gender, was then converted into z-scores using Eq. 4 as given below. Here X represents each of the data items or factors, μ represents the mean of all the data values and σ represents the standard deviation.

$$\text{z-score} = (X - \mu / \sigma) \quad (4)$$

Traditionally max-min scores are used to convert this data into 0-1 ranges. However, we used Z-scores in order to identify outliers and also because we reasoned that extreme values could be considered important for a medical based network (i.e.: very high values typically indicate more severe symptomology). Gender, the only categorical variable, was encoded into 1-of-N vectors (where N = the number of unique values this factor can take). For example, [0,1] = male whereas [1,0] = female. 1-of-N vectors are important to ensure that the network can distinguish unique variables and prevent network bias [19].

We processed and stored the converted data into another .csv file to use as the input for the ANN. Records with a z-score higher than 5 or lower than -5 were excluded from the data set because they were considered to be extreme outliers and the results of miscoding of the data.

C. Implementation using Matlab

The pattern recognition tool in the neural network toolbox in Matlab was used to build our predictive diagnostic model to distinguish the hypertensive from the control patients. This tool utilizes a *scaled conjugate gradient* algorithm by default. We used the preprocessed consolidated data from the CPCSSN data set and split the data into 70% for training, 15% for validation, and 15% for testing samples as shown in Fig. 4. Network training is terminated when either the magnitude of the gradient falls below 1e-5 or the validation performance fails to decrease for a total of 6 iterations. Validation performance is based on *cross-entropy error*.

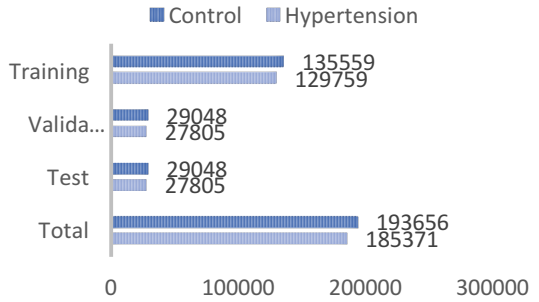

Fig. 4 Data split (70%, 15%, 15%) for training, validation, and testing phases. Also shows the total number of patients in each classification group.

V. RESULTS

Performance of the ANN model is measured in terms of the number of patients correctly identified as hypertensive patients in Matlab. Patients who do not have hypertension but are incorrectly classified as hypertensive patients constitute the false positive group and patients who have hypertension but are wrongly classified as non-hypertensive form the false negative group. Patients correctly classified as hypertensive patients are in the true positive group while those correctly classified as non-hypertensive patients are in the true negative group. A *Confusion Matrix* is commonly used to express the accuracy of classification in terms of the above four groups, and their sizes are compared to the total data. The other commonly used measure is the *Receiver Operating Characteristic (ROC)* curve which graphically illustrates the performance of a binary classifier system. The curve is created by plotting the *true positive rate (TPR)* against the *false positive rate (FPR)* at various threshold settings. The true-positive rate, also known as *sensitivity* or *recall* in machine learning, is the ratio of the number of true positives to the total number of data items in that class. The false-positive rate, also known as the fall-out, is calculated as (1–specificity), where *specificity* indicates the ratio of the number of true negatives to the total number of data items in that class. Each prediction result or instance of a confusion matrix represents one point in the ROC space. We discuss our results in this section using confusion matrix and ROC.

Fig. 5 shows the confusion matrix generated by Matlab where output class 1 represents the hypertensive patients and output class 0 represents the control patients. The green vertical striped blocks demonstrate correct classifications (42.4% true positives and 39.9% true negatives) and the red horizontal striped blocks show incorrect classifications (9% false positives or Type I error, and 8.7% false negatives or Type II error). In these four blocks, the numbers on the top denote the total number of patients in each class and the numbers on the bottom denote the same in percentage. Finally, the black box

on the bottom right corner shows overall classification accuracy of the network. Our network achieves 82.2%, 82.3%, and 82.5% accuracies in training, validation, and test phases, respectively. The confusion matrix only shows the combined overall accuracy of 82.3% at the bottom right corner. Therefore, the confusion matrix demonstrates that our network can predict both the presence and absence of hypertension across patient population with about 82% accuracy.

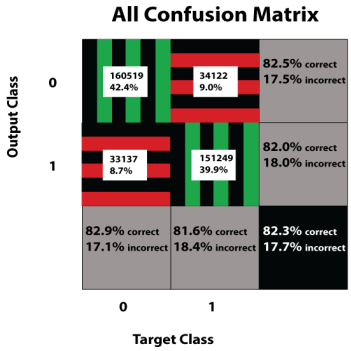

Fig. 5 Confusion matrix demonstrating 82.3% overall accuracy.

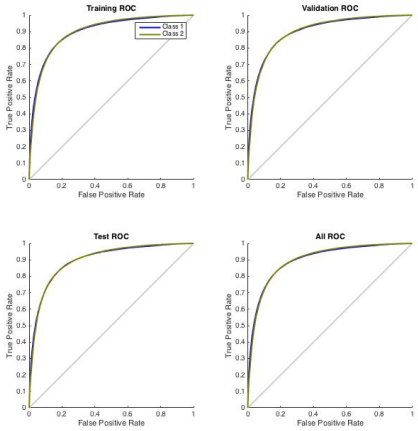

Fig. 6 ROC Curves from Matlab for training, test, and validation phases as well as the combined result (all ROC).

The ROC curves in Fig. 6 show smooth plots for the training, validation and test phases and the sharp rises of the curves depict a good TPR/FPR ratio. Points above the straight line, called the line of no-discrimination, implies good predictive outcomes and the upper left corner of the ROC space indicates the best possible prediction representing 100% sensitivity (no false negatives) and 100% specificity (no false positives). ROC curves are good for comparing the performances of multiple models.

A. Discussion

The typical performance for hypertension diagnosis ranges from about 80-90% accuracy depending on the data and the model. Table II compares our approach to two other approaches that achieve good accuracy using ANN models.

TABLE II. COMPARISON OF ANNS

Paper	Patients/ Control	Input factors	Hidden nodes	Output nodes	Accuracy
LaFreniere et al.	185,371/ 193,656	11	8	2	82.3%
Ture et al.	452/242	9	Unknown	2	81.48%
Samant et al.	981, split unknown	13	20 (L-1), 5 (L-2)	2	92.85%

Ture et al. developed a network that achieves greater than 90% of sensitivity, greater than 66% of specificity, and 81.48% accuracy during testing using only 452 patients and 252 controls. Samant and Rao achieved a 92.85% accuracy using a deep learning network with 2 hidden layers and a total of 981 subjects (the number of patients and controls was not reported). Both the above studies used data collected at a single medical facility unlike our data which is collected from many different EMR systems and from the offices of many different physicians. Also we use a much larger data sample compared to the other works. Sumathi and Santhakumaran [24] also developed a neural network model and reported that it has reliable performance when compared to a physician but did not report the accuracy or number of patients used in their study.

We achieve about 82% accuracy which is quite high considering the data used in the study and the varying health factors that influence the results. The versatility of the EMR systems from which the data is collected in the CPCSSN data bank and the large number of patient records in the data suggest a high degree of confidence in the results obtained and ensure that the model is more generalizable. However, the preprocessing of the lab and exam data may be improved further. Currently the missing diagnosis date for the control group (no disease) makes it difficult to select the lab results to compare with the hypertensive group. One option may be to either take an average of all the lab results or use a wide time window to select from for each patient. For example, it may be better to select up to three lab tests per patient. However, such adjustments come with the obvious disadvantages of increased inputs nodes (three times more), decreased generalizability, and increased processing time.

The network accuracy may also be further improved by including a wider range of evidence-based factors found in the literature. Several key demographic factors are currently unavailable within the CPCSSN database in a standardized format which limited the number of valuable factors that could be used for training the network. Access to information such as smoking history, family history of hypertension, alcohol consumption, and stress factors would be beneficial. The network must also be tried out in practice or real life to determine its usefulness in a healthcare setting.

VI. CONCLUSION

Real time predictive systems based on EMR data can assist preliminary diagnosis and eventually reduce hospital readmissions, cost, and prevalence of more severe illness. In

this paper, we propose a predictive ANN model to diagnose hypertension using the large integrated CPCSSN data which achieves an impressive 82% accuracy. Existing works use very small data samples collected at specialized centres which provide high accuracy but are impractical considering the many EMR systems in use by the physicians these days. Other approaches using statistical techniques do not support incremental learning as the neural networks do.

Apart from assisting physicians as a decision support tool, such predictive diagnostic tools can have a wide range of applications. These systems can be used in triage section in the hospitals to assist the nurse practitioners. Patients themselves can use these systems at home in the future instead of a simple blood pressure monitor to prevent critical situations. Wearable technology is gaining a lot of attention recently given the relatively simple means by which personal vitals can be monitored more frequently and continuously [8]. Home devices such as a Bluetooth enabled blood-pressure monitor can easily feed important information to a predictive system such as our ANN, which would provide real-time assessments to patients about their health conditions so that they can get medical help at the right time [8]. The data thus collected over a period can also be extremely useful for the physicians and researchers.

A. *Future Work*

As a future work, we would like to extend the ANN model to deep learning networks with multiple hidden layers to study more influencing factors and complex disease patterns [21]. According to the literature, family history and risk factors such as smoking and alcohol use are linked directly to hypertension. We need to collect this data and incorporate it in our network. We also like to categorize medications and include it as another input factor in the network.

ACKNOWLEDGMENT

We like to thank CPCSSN for providing the data used in this study.

REFERENCES

[1] Abdullah, A. A., Zakaria, Z., & Mohamad, N. F. (2011). Design and development of fuzzy expert system for diagnosis of hypertension. Proceedings of IEEE International Conference on Intelligent Systems, Modelling and Simulation, 2011, 113-17.

[2] Al-Shayea, Q. K. (2011). Artificial neural networks in medical diagnosis. International Journal of Computer Science Issues, 8(2), 150-154.

[3] Amato, F., López, A., Peña-Méndez, E. M., Vaňhara, P., Hampl, A., & Havel, J. (2013). Artificial neural networks in medical diagnosis. Journal of applied biomedicine, 11(2), 47-58.

[4] American Association for Clinical Chemistry. (2011, July 11). Albumin. Retrieved from https://labtestsonline.org/understanding/analytes/albumin/tab/test/

[5] American Heart Association. (2009, July 2). Good vs. bad cholesterol. Retrieved from http://www.heart.org/HEARTORG/Conditions/Cholesterol/AboutCholesterol/Good-vs-Bad-Cholesterol_UCM_305561_Article.jsp#.V0OY_JMrKDV

[6] American Heart Association. (2011, January 11). Understanding blood pressure readings. Retrieved from http://www.heart.org/HEARTORG/Conditions/HighBloodPressure/AboutHighBloodPressure/Understanding-Blood-Pressure-Readings_UCM_301764_Article.jsp#.V0OilZMrKDU

[7] Birtwhistle, R., Keshavjee, K., Lambert-Lanning, A., Godwin, M., Greiver, M., Manca, D., & Lagacé, C. (2009). Building a pan-Canadian primary care sentinel surveillance network: Initial development and moving forward. J Am Board Fam Med, 22(4), 412-22.

[8] Bonato, P. (2005). Advances in wearable technology and applications in physical medicine and rehabilitation. Journal of NeuroEngineering and Rehabilitation, 2(2).

[9] Brause, R., (2001). Medical analysis and diagnosis by neural networks. Proceedings of ISMDA 2001, Lecture Notes in Computer Science, 2199, 1-13

[10] Carretero, O., & Oparil, S. (2000). Essential hypertension part I: definition and etiology. Circulation, 101(3), 329-335.

[11] Cireşan, D. C., Giusti, A., Gambardella, L. M., & Schmidhuber, J. (2013). Mitosis detection in breast cancer histology images with deep neural networks. Proc. MICCAI, 2, 411–418.

[12] Das, S., Ghosh, P. K., & Kar, S. (2013). Hypertension diagnosis: a comparative study using fuzzy expert system and neuro fuzzy system. Proc. of IEEE International Conference on Fuzzy Systems (FUZZ-IEEE), 2013, 1-7.

[13] Daugman, J., (1988). Complete discrete 2-D Gabor transforms by neural networks for image analysis and compression. Acoustics, Speech and Signal Processing, IEEE Transactions on, 36(7), 1169-1179.

[14] Echouffo-Tcheugui, J., Batty, G., Kivima, M, Kengne, A., (2013) Risk Models to Predict Hypertension: A Systematic Review. PLoS ONE 8(7): e67370.

[15] Kaur, A., & Bhardwaj, A. (2014). Artificial Intelligence in Hypertension Diagnosis: A Review. International Journal of Computer Science and Information Technologies, 5(2), 2633-2635.

[16] Keshavjee, K., Chevendra, V., Martin, K., Jackson, D., Aliarzadeh, B., Kinsella, L., Turcotte, R., Sabri, S., & Chen, T. (2011). Design and testing of an architecture for a national primary care chronic disease surveillance network in Canada. Stud Health Technol Informat, 164, 341-5.

[17] Kimoto, T., Asakawa, K., Yoda, M., & Takeoka, M. (1990). Stock market prediction system with modular neural networks. Proceedings of the IEEE International Joint Conference on Neural Networks, 2, 11-16.

[18] Mayo Clinic. (2016). Microalbumin test. Retrieved from http://www.mayoclinic.org/tests-procedures/microalbumin/details/results/rsc-20169684

[19] Mehrotra, K., Mohan, C. K., & Ranka, S., (1997). Elements of artificial neural networks. Cambridge, MA: MIT press.

[20] Poli, R., Cagnoni, S., Livi, R., Coppini, G., & Valli, G., (1991). A neural network expert system for diagnosing and treating hypertension. *Computer*,*24*(3), 64-71.

[21] Samant, R., & Rao, S., (2013). Evaluation of Artificial Neural Networks in Prediction of Essential Hypertension. International Journal of Computer Applications, 81(12), 34-8.

[22] Schneiderman, H., & Kanade, T. (2000). A statistical method for 3D object detection applied to faces and cars. International Conference on Computer Vision, 1, 746-51.

[23] Srivastava, P., Srivastava, A., Burande, A., & Khandelwal, A., (2013). A note on hypertension classification scheme and soft computing decision making system. ISRN Biomathematics, 2013, 1-11.

[24] Sumathi, B., & Santhakumaran, A. (2011). Pre-diagnosis of hypertension using artificial neural network. Global Journal of Computer Science and Technology, 11(2).

[25] Ture, M., Kurt, I., Kurum, A. T., & Ozdamar, K. (2005). Comparing classification techniques for predicting essential hypertension. Expert Systems with Applications, 29(3), 583-5.

[26] Williamson, T., Green, M. E., Birtwhistle, R., Khan, S., Garies, S., Wong, S. T., Natarajan, N., Manca, D., & Drummond, N. (2014). Validating the 8 CPCSSN case definitions for chronic disease surveillance in a primary care databse of electronic health records. Ann Fam Med, 12(4), 367-72.

[27] World Health Organization. (2012, July 27). BMI classification. Retrieved from http://apps.who.int/bmi/index.jsp?introPage=intro_3.html

[28] CPCSSN available online at: http://cpcssn.ca/research-resources/cpcssn-data-for-research/ retrieved on May 25, 2016.