International Journal of Computer Information Systems and Industrial Management Applications
ISSN 2150-7988 Volume 18(20s) 2026 pp. 576-588
https://doi.org/10.70917/ijcisim-2026-5200
Article

Deep Autoencoder-Based Model for Multi-Class Disease Prediction Using Symptom Data

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Abstract: Critical fact: Proper prediction of diseases by use of symptoms data plays a critical role in contemporary health care systems. This paper will introduce a combined deep autoencoder based multi-class disease predictor model, which can represent complex and non-linear feature-level interactions with a high-dimensional feature symptom matrices through feature loss and diagnosis prediction in one model. In particular, to obtain sparse representations of the samples in a low-dimensional latent space, an encoder with bottleneck layer is used to conserve essential and diagnostic features and eliminate redundancies, which are then fed to fully connected layers to make predictions. We use the Adam optimizer with dynamic measures such as early termination, and learning rate decay to guarantee the best convergence and generalization. In real-world application, state of the art performance is observed on a benchmark dataset containing 4920 samples, 132 symptom features and 40+ class diseases using about 80% for training data resulting in test data with overall accuracy of 99.6% along with almost perfect precision, recall and F1-scores across most classes. Further tests using confusion matrix, ROC curve, precision-recall curve and calibration plot show the strength, reliability and discriminative capability of the developed model. These findings indicate that the presented framework can be successfully used to make proper predictions of the disease, and, therefore, it can be utilized to a maximum in the real-life clinical decision support systems.
Keywords: Disease Prediction, Deep Autoencoder, Multi-Class Classification, Feature Extraction, Healthcare Analytics, Deep Learning

1.INTRODUCTION

Prediction and early diagnosis of the disease are the right tool that enhances health results and facilitates an opportunity to act immediately. Due to the high proliferation of healthcare data, conventional machine learning methods are frequently not sufficient to model complex, high dimensional and non-linear relationships which are prevalent in medical data. The methods of deep learning, and in particular the autoencoders-based models have become popular in recent years because of their capacity to learn compact and meaningful representations of features using raw data. As an example, the structure presented in [1] illustrates that deep autoencoders have the potential to boost classification, using discriminative latent features. On the same note, autoencoder-based diagnostic-based

devices have been effectively used in medicine fields like lung cancer diagnosis [2] and chronic kidney disease classification [3] amongst others, indicating their ability to deal with complex biomedical data.

They have also extensively used autoencoders to do denoising or feature enhancement in medical imaging applications to enhance the accuracy and strength of the diagnosis [4], [5]. This latent representation learning ability has allowed them to be applied in a variety of biomedical applications, such as predicting disease associations [6] and fault diagnosis in complex systems [7]. In addition, recent progress in deep learning resulted in the creation of very accurate models to diagnose such disease as chronic obstructive pulmonary disease [8], Alzheimer's disease [9], [14], [19], and lung diseases with the help of the chest X-ray images [10]. Hybrid systems with attention and more than one autoencoders have continued to enhance the performance of processes like breast cancer detection [11] and brain tumor classification [12], [13], [16].

Multi-class classification challenges in healthcare are also addressed successfully with deep learning models, such as detection of brain abnormalities [15], classification of arrhythmias [17], and multimodal liver cancer diagnosis [18]. Besides, ensemble methods and autoencoders have demonstrated good results in identifying the severity of a disease, including COVID-19 classifications [20]. Although there are these advances, the majority of the current investigations are based around medical imaging or multimodal data, and only a limited focus is directed at structured symptom-based datasets, the essential ones in the context of early-stage diagnosis and clinical decision support system.

Also, symptom-based datasets are sparse and high-dimensional in nature and tend to have redundant or overlapping features that complicate the process of accurate classification. Conventional techniques can simply not grasp such complex relationships to provide optimum performance. To overcome these issues, this paper presents deep autoencoder-based disease predictor model which uses feature compression and classification in a single framework. The model takes advantage of an encoder network to train on small latent representations, created by a bottleneck layer, which diminishes the dimensionality, yet it keeps the important diagnostic information. A fully connected classifier that takes these learned features is then used to predict disease multi-classes with high accuracy.

The suggested method is tested on a benchmark dataset of multiple disease classes and high-dimensional features, based on symptoms. The model obtains experimental results that prove an overall accuracy of 99.6, and its precision, recall, and F1-scores are close to perfection with most of the classes. Further evaluation by using confusion matrices, ROC curves, and calibration plots supports the strength, trustworthiness and high generalization of the model. These findings confirm the proficiency of the deep autoencoder-based feature acquisition in structured healthcare data and emphasize on its prospects in clinical decision support in the real world.

Overall, the present piece of work is a valuable and scaled deep learning-based symptom-centered disease prediction framework that will fill the gap between conventional machine learning models and the latest deep learning models, and coincide with modern progress of autoencoder-centered medical diagnosing systems [1]-[20].

2. BACKGROUND STUDY

Recent developments on deep learning have eminently enhanced the diagnosis and classification of illnesses through an efficient extraction and production learning of features in intricate medical information. Of these methods, autoencoders-based models have acquired a lot of interest because of their versatility to acquire compact latent representations and work effectively with highly-dimensional data sets. Karim et al. [1] came up with a deep autoencoder based linear model that elevates classification performance by producing discriminative features on the raw data. Likewise, Shaffie et al. [2] created a diagnosis system based on an auto-encoder of early lung-cancer detection, which revealed the power in deep feature learning in medical diagnostics. A deep stacked auto encoder model was presented by Khamparia et al. [3] to classify chronic kidney disease based on multimedia data and this model was found to have a better accuracy because of the hierarchical feature extraction.

Autoencoders have found extensive use in denoising and feature enhancement of medical imaging. Another study by El-Shafai et al. [4] introduced a deep autoencrypted framework of denoising as an enhancement of the quality and diagnostic capabilities of images. Karim et al. [5] also applied the practice of autoencoders to the medical

waveform classification by incorporating the spectral feature analysis. Moreover, the article by Deepthi and Jereesh [6] deployed deep autoencoders to classification and yielded an information on disease associations, and this depicts the potential the autoencoders have in biomedical research. Other than in health care, Shao et al. [7] showed that autoencoder-based learning of features proved useful in fault listening systems, meaning that they are resistant to complex data patterns.

Other studies have investigated convolutional neural networks and hybrid architectures in the sphere of disease diagnosis with the help of deep learning. Alsurayhi [8] explored the machine learning based classifiers of chronic obstructive pulmonary disease using CT image data. Ramzan et al. [9] offered a deep learning-based model system to determine the multi-classic Alzheimer disease through fMRI data, whereas Liu et al. [14] suggested multimodal learning of neuroimaging features to enhance the diagnostic accuracy. Correspondingly, Alshmrani et al. [10] trained a deep-learning model to identify lung diseases of multiple classes with fast-reading and images of chest x-rays which presented a high classification rate. Later, Rao et al. [19] used deep learning and transfer learning to classify Alzheimer disease with the help of 3D MRI data, indicating high accuracy.

The additional diagnostic ability has been improved by hybrid and sophisticated deep learning models. Yan et al. [11] suggested a hybridized model of using various autoencoders and attention model in the detection of breast cancer that greatly enhanced feature representation. Mallick et al. [12] proposed a deep neural network (the wavelet autoencoder) to classify brain MRI, whereas Bangalore Yogananda et al. [13] proposed to use disparity autoencoders to segment brain tumors into multiple classes. Bashir-Gonbadi and Khotanlou [16] designed a multi-task convolutional autoencoder model to classify brain tumor, which dropped, as shown, in complex tasks of classification. The proposed Nayak et al. [15] method of detecting brain abnormalities of multi-classes based on CNN, once another engineers the strength of deep learning in medical imaging.

In addition to this, deep learning networks have already been used to solve other medical classification tasks, such as arrhythmia identification using multi-scale neural networks [17] and liver cancer identification using multimodal deep learning models [18]. The article by Gupta and Sinha [20] proposed an auto encoder- ensemble, model on predicting the severity of COVID-19 and has shown that the use of many models is effective in enhancing performance.

Although these dramatic improvements took place, the majority of the published materials are concentrated mainly on medical image or multimodal data, rather than on structured symptom based datasets. These are high dimensional and sparse datasets which can hardly represent the multi faceted relationship under normal means. Also, most of the models fail to mention feature redundancy and noise in symptom-based data.

In order to circumvent these weaknesses, the offered work suggests a heavy autoencoder-based disease prediction model relying on the latent feature study to successfully process high-dimensional symptom representations. The proposed method will enhance the accuracy, robustness and generalization of prediction by combining feature compression with classification and thus help fill the number of gaps reported in the available literature and help in building effective clinical decision support systems.

3. METHODS AND PROCEDURES

A. Overview

The proposed deep autoencoder-based disease prediction model has been able to achieve high-dimensional complex and non-linear disease prediction relationships through feature compression and classification in a single architecture. It applies an encoder network to learn compact latent symptom patterns representations and, as a result, it can extract meaningful and noise-resistant features using sparse binary inputs. The bottleneck layer is used as a crucial part of dimensionality reduction to keep the necessary diagnostic data and remove redundancy. Stable representations are then transferred by fully connected layers with batch normalization and dropout in order to improve the generalization and stability of these representations. Also, adaptive training strategies including early termination and dynamic adjustment of learning rate guarantee the best convergence. The model eventually carries out multi-class

classification by utilizing the discriminative strength of the latent feature space leading to effective and sound predictions of diseases.

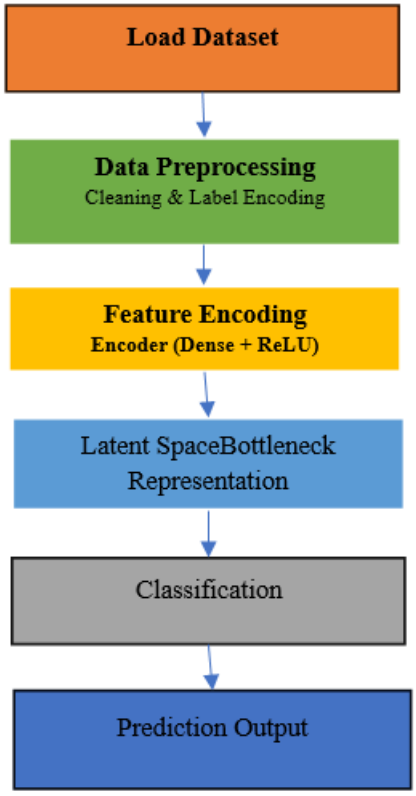

Fig 1: System Architecture of the proposed deep autoencoder-based disease prediction mode

B. Data Acquisition and Preprocessing

The data utilized in the present research is taken out of the publicly available repository on Kaggle, namely the "Disease Prediction Using Machine Learning dataset. It is a hierarchical record of symptoms of the patient records, intended to be classified of more than one class with binary indicators of the presence or lack of the symptoms, and with an assigned disease label (prognosis). It includes about 4920 samples, 132 symptom features, and more than 40 different disease classes, which were sufficient to compare machine learning and deep learning models. It is extensively applied in study since it has a clean tabular format, defined feature space and capability to model even complex relationships between symptoms and disease, thus affording to develop and test correct disease prediction models.

After data cleaning, the data is split in input features and target labels. The feature matrix is filled with symptom indicators whereas the target variable is filled with categorical disease labels. Given that machine learning models demand numerical data, label encoding is utilized to transform disease labels in a format of a category into an integer data.

In a bid to have strong model evaluation and avoid bias, it is necessary to divide the dataset into training, validation, and test through stratified sampling. The strategy maintains the proportional spread of classes of disease in each subset and this is especially significant in a multi-class medical dataset. Learning model parameters is done on the training set, hyperparameter tuning and early stopping is done on the validation set, and final performance evaluation is done on the test set. Moreover, all the feature values are converted into a 32-bit floating-point to guarantee that they can be used in deep learning frameworks, and it further enhances computational efficiency.

C. Feature Representation and Encoding.

Under the proposed system, every record of a patient is modeled as a high-dimensional binary representation feature vectors, with each dimension demonstrating the particular symptom. A score of 1 implies the occurrence of a symptom and 0 means otherwise. This representation is simple but creates a sparse and high-dimensional feature space, which may cause a negative effect on model performance because of redundancy and noise.

To curb this problem, representation learning based on an autoencoder that is deep is included in the methodology. The autoencer water-falls raw features directly into the classifier but instead the autoencoder learns a latent representation of the input data which is a compressed and meaningful latent representation. This transformation encodes underlying patterns and correlations of symptoms and thus the model has a greater ability to discriminate between diseases that share a similar symptom profile. Consequently, the learned feature representation boosts the classification accuracy as well as the generalization ability.

D. Deep Autoencoder-Based Architecture

The essence of the suggested system is an in-depth autoencoder-based classification model, serving to extract features and to predict diseases. This architecture is made up of three primary modules, namely the encoder, the bottleneck layer, and the classifier.

The encoder consists of several densely connected (fully) layers with the activation functions of the Rectified Linear Unit (ReLU). The layers trim off the dimensionality of the input data in a progressive manner, but also represent relevant interaction of features. Each dense layer is then followed by batch normalization to stabilize learning with normalization of the activations and dropout regularization to stop overfitting by randomly inactivating a percentage of neurons at each training stage.

The bottleneck layer is the central location in the architecture and it is the latent feature space. This layer produces a compressed version of the input data, which ideally filters off non important data, but does not lose any vital patterns. The bottle-neck size is an artful decision to strike a balance between compression and retention of information.

The bottleneck layer is then followed by the classifier head which is made up of more dense layers that transform the latent representation to disease classes. The end output layer has a softmax activation function to generate probability distributions of possible classes so that it can be multi-classified.

E. Model Training Strategy.

The training procedure is set in such a way that convergence is made to be efficient and generalization performance to be high. The model will be trained by adopting the Adam optimizer, which is an adaptive learning rate optimization algorithm that will favor deep learning assignments. The learning rate is set to 0.001 giving a trade-off between the rate and the stability.

LossWe use the sparse categorical cross-entropy loss function to solve multi-class classification problems with integer-coded labels. In the training phase, the model will update its weights iteratively by minimizing the loss function on the training data whilst simultaneously tracking the performance on the validation set.

Two major training strategies are used to avoid overfitting and enhance the robustness of the model. Early stopping is applied to end training when the accuracy of the validation stops increasing within a certain number of epochs to prevent overfitting the model to the training data. Furthermore, there is a mechanism of learning rate reduction, reducing the learning rate to the validation loss plateaus, and then letting the model fine-tune the parameters and converge better.

The model is trained up to 200 epochs with a total batch size of 32 and that the most effective weights of models are stored according to the results of the validation performance.

F. Prediction and Classification

After the training of the model, predictions are made with disparate test data that are not known to the model. The model provides a probability distribution of all the classes of disease given an input sample. These are probabilities of the model that describe the confidence of the model in each possible class.

The last estimation of the predicted class is done by picking the highest probability of the class doing the argmax function. The methodology prevents the model from giving any input the most difficult-to-detect disease. Further analysis including confidence estimation and uncertainty quantification can be conducted with the probabilistic output, which can be useful in medical decision-making systems.

G. Performance Evaluation Metrics

Various evaluation measures are used in order to determine the efficiency of the proposed model comprehensively. Accuracy is employed as the main measure of the total percentage of correctly classified cases. Nonetheless, the accuracy is not always the answer because it can be outside the whole picture during multi-class classification and thus, other metrics are taken into account.

Each class is then computed in terms of precision and recall to assess the capability of the model to identify positive cases correctly and all the cases of interest respectively. The harmonic mean of the recall and precision, the F1-score gives a balanced measure of the classification performance.

The confusion matrix is created to demonstrate how many correct and wrong classifications happened in each of the classes, and patterns of errors in classification are emphasized. Besides, more sophisticated methods of evaluation like Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) are applied to determine the discriminative ability of the model. Precision-recall curves are tested also to determine accuracy in the case of class imbalance. Calibration curves are used to determine compatibility between projected and actual outcome, making sure that the model estimates of confidence are likely to give secure results.

H. Visualization and Analysis

In order to have a better understanding of the performance of a model, different types of visualization are used. Training and validation accuracy and loss learning curves are plotted to examine how the model converges and determine the possibility of overfitting or underfitting.

The visualization of the confusion matrices gives an easy grasp of the classification performance, in relation to the various classes of diseases. There is also the use of per-class accuracy plots to determine the classes in which the prediction accuracy is high and low. To identify the presence of the misclassification, the misclassification analysis is carried out, which allows focusing on the mistakes the model has been committing most and improving the model accordingly.

The visualizations show calibration curves, ROC curves, and precision-recall curves by choosing individual classes to estimate probabilistic predictions and classification strength. All of these visualizations make it possible to have a clear picture of the model strengths and limitations.

The entire process is designed to ensure the systematic process of the disease prediction, comprising of data pre-processing, feature learning, classification, and evaluation, all arranged into a unit-like system.

4. RESULTS AND DISCUSSION

A. Experimental Setup

The experiment was implemented in a Python environment with the help ofTensorFlow (Keras) to build the model and Scikit-learn to preprocess and evaluate. The preprocessing phase before the binary symptom features and multi-class disease label dataset were subjected to is: unnecessary attributes were eliminated, categorical labels were

encoded in terms of label encoding and transformed features into floating points. The stratified sampling was used to divide the data into training, validating data and testing part (class balance) with 80 percent called training/valuation and 20 percent called testing. The suggested deep autoencoder-based architecture incorporates an encoder which consists of dense layers, batch normalization, and dropout, and a bottleneck layer to reduce the features and a fully-connected classifier with a softmax result in the event of multi-class classification. The model was trained on up to 200 epochs with a batch size of 32 using an optimizer called Adam with a learning rate of 0.001 and sparse categorical cross-entropy loss. The early stopping and learning rate reduction measures were implemented depending on the validation performance to achieve generalization and avoid overfitting. To confirm the strength and stability of the proposed system, the trained model was tested on the test set by means of performance indicators (accuracy, precision, recall, and F1-score), a confusion matrix and ROC-based results.

B. Visualization

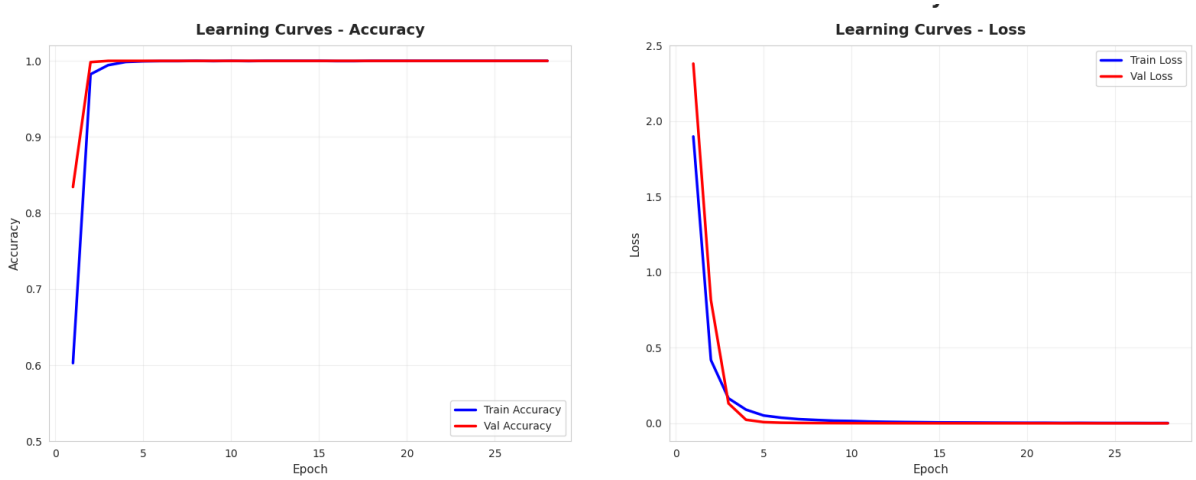

Fig 2: Learning Curves for Accuracy and Loss

The fig 2 illustrates the training and validation accuracy at the left and the loss curves respectively at the right illustrating the progression of the model throughout the successive epochs. As seen in the accuracy curves, there is a very high rate at which its accuracy improves during the first few epochs where both training and validation accuracy is very high and reaches near perfection at about the fourth epoch. The near parallelity between the two curves shows that the model extrapolates itself without overfitting. This demonstrates the quality of the network architecture: specifically the ability of a feature-compressing bottleneck layer, batch normalization and dropout to work in unison to allow the model to learn meaningful symptom-disease associations in a fast and stable manner.

This is paralleled in the loss curves which exhibit a sharp drop in both training and validation loss during the initial training phases. The model is as efficient in eliminating classification errors as it brings the loss to almost zero values and stabilized to an optimal solution. This fact is further supported by the fact that both the training and validation loss curves show identical dynamics and that the model has consistent learning dynamics, and that it works well on unseen data. In general, the joint accuracy and loss curves depict a very efficient learning procedure confirming the appropriateness of the deep autoencoder-based architecture to the task of disease prediction.

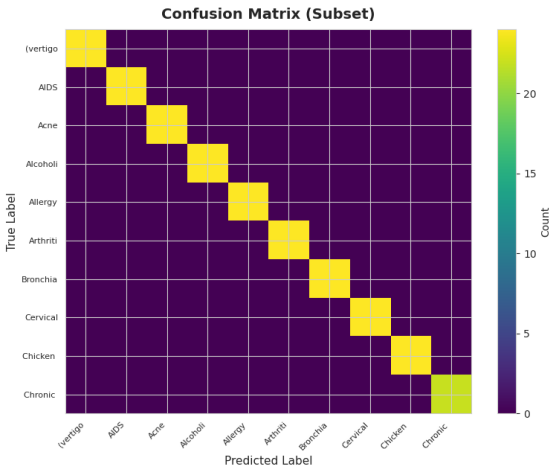

Fig 3: Confusion Matrix for Sample Disease Predictions

The figure 3 illustrates a confusion matrix, which shows how the model classifies on a chosen subset of diseases. The rows indicate the actual disease label and the columns indicate the forecasted label. The bright diagonal line shows that most predictions would be on the right classes, that is, the model would be consistently accurate in identifying diseases like Acnes, Allergy, Arthritis, Bronchitis, and many others. The consistency of the intensity along the diagonal and the almost zero values everywhere indicate that the cases of misclassification are extremely few within this range of labels.

This high degree of diagonal attributes to the fact that the model has acquired very discriminative symptomversus disease relationships and is therefore capable of differentiating between conditions within the context of symptom overlaps. Lack of the off-diagonal clusters suggests the presence of effective generalization and low levels of confusion among clinically similar diseases. On the whole, the confusion matrix graphically proves high accuracy and reliability of the model predictions to support the learning curve results.

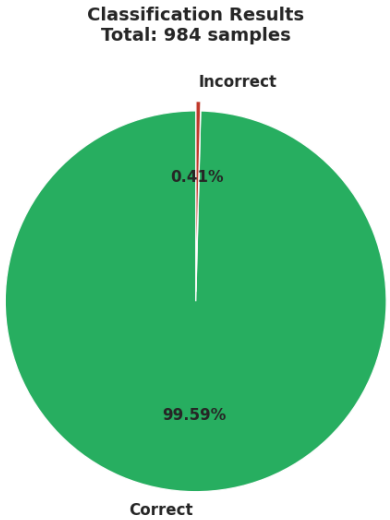

Fig 4: Overall Classification Accuracy Distribution

Figure 4 illustrates a pie chart illustrating the final classification performance of the model on a total of 984 samples referring to the total samples considered in the final analysis of the model, showing how many of the correct and incorrect predictions were made. The very huge green section, that constituted 99.59 percent correct classification,

indicates that the model is always precise in the identification of diseases. The number of misclassified instances can be assessed by a very thin slice which makes up 0.41% wrong prediction (only). This graphic highlights the consistency and strength of the trained model when tested on the entire test set.

The close to estimate accuracy as illustrated in the chart is congruent with the previous learning curves and confusion matrix, which altogether indicates that the model generalizes highly, and its prediction is highly accurate. The low error rate indicates that the feature extraction/dense layers/regularization methods allowed the model to learn the powerful symptom disease patterns. All in all, the pie chart is both a clear and succinct display of the excellent performance of the model in real life classification.

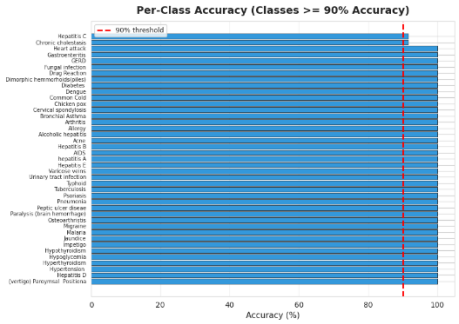

Fig 5: Per-Class Accuracy for All Diseases with ≥ 90% Accuracy

This figure 5 represents the per-class accuracy of all disease categories with a minimum of 90 per cent prediction accuracy. Each horizontal line depicts a disease and almost all of them fall or above the 90 percent mark of the red dashed line. The high consistency of performance in a large number of settings, including the most usual conditions such as Common Cold and Migraine, to more specific illnesses such as Hepatitis variants and Chronic cholestasis are a sign of the soundness and dependability of the model over different medical categories.

It is seen that the consistency of the bars around the upper accuracy range indicates that the model does not advantages some classes over others, but rather it works well across all of the diseases that it displays. Such balanced accuracy distribution signifies good learning of the pattern of symptoms and good representation of features in the architecture of the model. In general, the number supports the idea that the model has a high predictive power in almost every type of disease, which contributes to the belief in the practical use of the model in the real world.

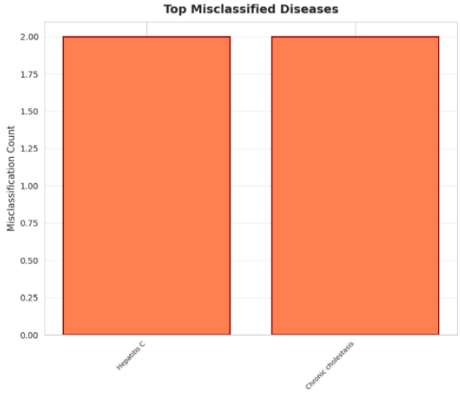

Fig 6: Top Misclassified Diseases

This figure 6 helps to outline those diseases that have most misclassifications created by the model. The most common misclassified conditions that include only two errors in the predictions are Hepatitis C and Chronic Cholestasis in this case. Though the misclassification numbers are insignificant when compared to the overall sample

size, their emergence suggests that the specified diseases might have similar symptoms with other disorders in the dataset, which should make it a bit more difficult to evaluate them by the model with absolute confidence.

These two misclassifications per disease are representative of the actual good performance of the classifier. But it also offers a useful diagnostic indication: such particular cases may be useful to further refine the features or the sample of training to amplify the ambiguity. On the whole, this plot can be viewed as a narrow perspective of the few error cases of the model and can be used to specify the areas that need to be improved specifically and yet support an excellent accuracy and robustness of this model.

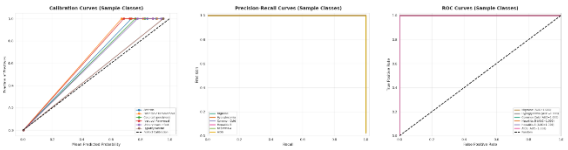

Fig 7: Calibration, Precision–Recall, and ROC Curves for Sample Classes

The fig 6 compare the extent to which the model predicted probabilities and classification choices are close to actual disease outcomes of a number of representative classes. The left-hand calibration curves indicate that the predicted probabilities follow the diagonal perfect-calibration line, which means that the levels of confidence of the model are simulated by the actual reality. Classes like the Arthritis, Cervical Spondylosis, and Hypothyroidism have well-calibration point values indicating that not only does the model accurately predict the correct values but the probability estimates are also well-calibrated- an important feature of a medical decision support system.

The outstanding discriminative of the model is further justified by the Precision-Recall curve in the center and the ROC curves on the right. Precision and recall are similar to both 1.0 in all of the sampled disease classes, suggesting that the classifier does not have much of a false positive or false negative with such classes. Simultaneously, the directions of the ROC curves are making it to the top-left corner with the AUC of 1.000 on all the displayed classes, indicating perfectly separable decision boundaries. These performance curves, in general, demonstrate that the model has a very high accuracy, reliability, and confidence congruency in a variety of diseases, which confirms that it is a strong diagnostic prediction framework.

Table 1: Classification performance of the proposed deep autoencoder-based model across multiple disease classes.

	Precision	**Recall**	**F1-Score**	**Support**
Paroymsal Positional Vertigo	1.000	1.000	1.000	24
AIDS	1.000	1.000	1.000	24
Acne	1.000	1.000	1.000	24
Alcoholic hepatitis	1.000	1.000	1.000	24
Allergy	1.000	1.000	1.000	24
Arthritis	1.000	1.000	1.000	24
Bronchial Asthma	1.000	1.000	1.000	24
Cervical spondylosis	1.000	1.000	1.000	24
Chicken pox	1.000	1.000	1.000	24
Chronic cholestasis	1.000	0.917	0.957	24
Common Cold	1.000	1.000	1.000	24

Dengue	1.000	1.000	1.000	24
Diabetes	1.000	1.000	1.000	24
Dimorphic hemmorhoids(piles)	1.000	1.000	1.000	24
Drug Reaction	1.000	1.000	1.000	24
Fungal infection	1.000	1.000	1.000	24
GERD	1.000	1.000	1.000	24
Gastroenteritis	1.000	1.000	1.000	24
Heart attack	1.000	1.000	1.000	24
Hepatitis B	1.000	1.000	1.000	24
Hepatitis C	1.000	0.917	0.957	24
Hepatitis D	0.857	1.000	0.923	24
Hepatitis E	1.000	1.000	1.000	24
Hypertension	1.000	1.000	1.000	24
Hyperthyroidism	1.000	1.000	1.000	24
Hypoglycemia	1.000	1.000	1.000	24
Hypothyroidism	1.000	1.000	1.000	24
Impetigo	1.000	1.000	1.000	24
Jaundice	1.000	1.000	1.000	24
Malaria	1.000	1.000	1.000	24
Migraine	1.000	1.000	1.000	24
Osteoarthristis	1.000	1.000	1.000	24
Paralysis (brain hemorrhage)	1.000	1.000	1.000	24
Peptic ulcer diseae	1.000	1.000	1.000	24
Pneumonia	1.000	1.000	1.000	24
Psoriasis	1.000	1.000	1.000	24
Tuberculosis	1.000	1.000	1.000	24
Typhoid	1.000	1.000	1.000	24
Urinary tract infection	1.000	1.000	1.000	24
Varicose veins	1.000	1.000	1.000	24
hepatitis A	1.000	1.000	1.000	24
accuracy			0.996	984
macro avg	0.997	0.996	0.996	984
weighted avg	0.997	0.996	0.996	984

Table 1 outlines the detailed classification performance of the proposed model as measured in precision, recall, F1-score as well as support of each disease class. As shown in the results, the model has near-perfect performance concerning most of the classes with most of the diseases having a precision, recall and F1-score of 1.000 which denotes very accurate and consistent predictions. Some of the classes such as Chronic Cholestasis and Hepatitis C, have slightly lower recall values (0.917) and Hepatitis D reported a subtle decrease in precision (0.857) which depicts slight misclassifications. In spite of these variations, the model performance has been outstanding as well as it has an accuracy rate of 99.6 on 984 samples of tests. The macro-average and weighted-average scores of about 0.996 are further evidence of the robustness and generalization ability of the model across the all classes and it is effective when it comes to applicability to the multi-class disease prediction tasks.

5.CONCLUSION

The experimental evidence proves that the offered deep autoencoder-based disease predictive model has outstanding results in the multi-class classification activities. The model, as illustrated by the learning curves, does not have many learning cycles, the training and validation accuracy becomes stable promptly, which also shows that the model is supported by efficient learning and a good ability to generalize. The confusion matrix also supports the fact that the model cannot differ between various diseases with a small number of misclassifications, and the aggregate correctness of 99.6 percent shows the model strength on unknown samples. The vast majority of disease classes, and all with precise predictions, have a perfect precision, perfect recall and F1-score, indicating high reliability in prediction, with only small variations in a few clinically related conditions like Chronic Cholestasis, variants of Hepatitis. Also, the calibration, ROC and precision recall analysis demonstrates that the model is not only highly accurate, but the predictions are also well-calibrated and confident. The accuracy per-class distribution also confirms that the model is consistent across all the disease types and not biased. Taken together, these results confirm that feature compression achieved via the autoencoder as well as efficient regularization methods allow the model to provide efficient capture of complex symptomdisease interactions between the two entities. Thus, the suggested solution is a highly precise, credible and extensible method to predict the disease, in which there is a strong possibility of application in disease management, specifically clinical decision support mechanisms.

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