CHAPTER 7

ABLATION STUDY FOR OPTIMIZED MACHINE LEARNING AND DEEP LEARNING TECHNIQUES

7.1 INTRODUCTION

Ablation studies are commonly employed in the field of neuroscience to investigate complex biological systems. The ablation study involves removing a specific part of the network to gain a improved comprehension of the network's behavior. In addition, an ablation study in the framework of deep learning is a technique employed to recognize the importance or contribution of each component in a neural network model. This can help identify which parts of the model are most significant for a specific task and inform the design of more efficient or effective models. It involves removing or "ablating" certain parts of the model, such as a specific layer or neuron, and observing the resulting impact on the method result.

To analyze the importance of each contribution involved in the proposed predictive models, an ablation study is conducted. Here, the proposed research work is divided into three major parts: preprocessing, feature selection, and classification. With diverse contributions, disease prediction is achieved more accurately and in less time. First, preprocessing of the database is performed to remove noise and inconsistent data out of the dataset. The pre-processed data is provided as input in the feature selection process. In this step, the most relevant aspects are chosen, and irrelevant aspects are eliminated to predict the disease. From the chosen features, patient data classification is carried out to categorize the data accurately.

Initially, preprocessing is proposed using the ALRTOHE method and the Zero Mean Feature Normalized Encoding (ZMFNE) technique. The ALRTOHE Technique is designed to carry out data preprocessing in minimal time with higher accuracy, using a disease dataset as input. With this input, ALRTOHE model performs additive log-ratio transformation and one-hot encoding. Later, data encoding is performed to transfer the numerical data within binary coding. This helps to obtain the binary representation of data in the shortest time possible.

The proposed ZMFNE technique is designed to enhance the preprocessing of the input dataset with higher accuracy. ZMFNE technique executes the data normalization and encoding process. The input data samples and features are taken from the dataset. With this, the sample input matrix is created as rows and columns. Then, the zero mean feature scaling is applied to normalize input data. Subsequently, the information transformation process is performed via one-hot encoding. Here, the encoder converts the categorical features into a numeric array, where each feature is encoded to produce a binary column for each category. As a result, the data normalization and transformation process are executed to get the preprocessed output.

With the preprocessed data, Nonlinear Sammon Projective Pattern Selection (NSPPS) Model, Tversky Similarity-Indexed Distributive Feature Embedding (TSIDFE) Technique, and Statistical correlative targeted projection pursuit-based feature selection (SCTPP-FS) Technique are proposed for feature selection. First, the NSPPS Model is developed to select pertinent aspects to reduce error. The developed method utilizes Sammon projection, which projects the features of a high-dimensional space into a low-dimensional space. From this, the inter-pattern distances are managed to decrease the error rate while choosing pertinent features. Thus, the NSPPS model improves the result of feature selection.

Another feature selection method, called TSIDFE, is designed for predicting disease using feature selection. The preprocessed data is taken as input in TSIDFE. With this input, the Tversky index similarity coefficient between two features is determined. From this coefficient measure, the relevant and irrelevant features are identified. This is performed by using the similarity coefficient. The results of the similarity coefficient vary from 0 to 1. If the similarity coefficient provides the result as ‘1’, then the feature is pertinent; likewise If the similarity coefficient provides the result as ‘0’, then the feature is irrelevant. With this, the relevant aspects are selected with higher accuracy in less time.

SCTPP-FS Technique is developed to identify the selected pertinent features with better accuracy. The SCTPP-FS technique considers the different features as input to carry out the selection process. Then, the target features are mapped by calculating the correlation between the features. In the SCTPP-FS technique, the correlation between features is estimated using Kaiser–Meyer–Olkin correlative projection pursuit to select the main features for accurate disease prediction. From the correlation computation, relevant and irrelevant aspects are determined through minimum time analysis. Therefore, pertinent features are chosen with maximum accuracy and a lower error rate.

By considering selected features as input, classification is performed using Emphasis Perceptron Boosting Classification (EPBC) method, TCLMCNL Technique and Memetic Optimized U-Net Deep Learning (MO-UNetDL) classifier techniques. The proposed EPBC technique uses the patient data with selected features as input. With this, the perceptron binary classifiers are formed via weighted sum. The classifier spilt the features and their data with zero training error. As a result, the actual classification outcomes are acquired with accuracy.

The TCLMCNL Technique is developed for classifying patient data to forecast disease at the pre-emptive phase. Developed TCLMCNL utilizes the time-dependent Cox regression, which calculates the Cramér's phi correlation function. With these regression outcomes, precise classification is carried out. Additionally, the Huber loss is calculated for both forecasted and real outcomes, and the Levenberg–Marquardt method is applied to minimize the error. Finally, the classification result is acquired with low error and high accuracy.

MO-UNetDL classifier model is proposed to categorize information on disease forecast. MO-UNetDL technique determines Wilcox's index coefficient to find the similarity. Then, the index coefficient is provided to the soft step activation to compute the index coefficient value, which presents the outcomes as either ‘1 or ‘0’. When the result of the activation function provides ‘1’, then the disease is rightly diagnosed. Besides, the max-pooling operation is employed to minimize the dimension of data samples by applying the activation function. Upsampling is used to enhance the dimension of the data and provide more accurate classification outcomes. To decrease data classification, memetic optimization is employed in MO-UNetDL to tune the hyperparameters. With this, the error rate in the classification is minimized, as a result it improves the accuracy.

7.2 EXPERIMENTAL SETUP

An ablation study is conducted for seventeen predictive models, including proposed models and base models (existing models). First, ablation experiments are performed on proposed preprocessing models, such as ALRTOHE and ZMFNE, as well as existing CNN-GRU-based hybrid deep learning methods and VOC-DL models, to explore the significance of these models. Then, ablation experiments are conducted on proposed feature selection models, including the NSPPS Model, TSIDFE, SCTPP-FS, and existing AHEG-FS, as well as Chi^2-MI, using both with and without preprocessing methods to determine the best possible performance. In addition, ablation studies for the proposed classification models, namely EPBC, TCLMCNL, MO-UNetDL technique, an existing deep learning LSTM ensemble model, and DSPM, are carried out using both with and without preprocessing methods to obtain the best results with respect to disease prediction.

To examine the performance of the above predictive models, the COVID-19 Corona Virus India Dataset and the RSNA Pneumonia Detection Challenge dataset are used. In this work, the 10 cross-validation is employed. The datasets are gathered from Kaggle. The database is split into a training set and a testing set, where the training set comprises 90% of the data and the testing set comprises 10% of the data for performance analysis.

7.2.1 Ablation Study for Preprocessing Models

The ablation study for preprocessing models is conducted, and outcomes are confirmed with respect to preprocessing accuracy, Preprocessing Time (PT), Error Rate (ER), and Space Complexity (SC). Accuracy in the preprocessing models is calculated as a percentage of the amount of information that is properly preprocessed. PT is defined as the time taken to preprocess data samples. ER is computed as the incorrect preprocessing of data samples. Also, SC is calculated and depends on the amount of memory used for preprocessing.

Table 7.1 Ablation study results of proposed preprocessing models compared to the baseline models for COVID-19 and Pneumonia datasets

Models	**COVID-19 Dataset**				**Pneumonia Dataset**			
	Accuracy (%)	**PT (ms)**	**ER (%)**	**SC (KB)**	**Accuracy (%)**	**PT (ms)**	**ER (%)**	**SC (KB)**
Existing VOC-DL	71	6270	29	77	74	5020	26	71
Existing CNN-GRU based hybrid deep learning model	75	5930	25	69	79	4570	21	62
Proposed ALRTOHE	83	5430	17	65	88	3890	12	60
Proposed ZMFNE	**86**	**5060**	**14**	**60**	**90**	**3630**	**10**	55

Table 7.1 presents the ablation study outcomes of preprocessing models, including ALRTOHE, ZMFNE, and an existing CNN-GRU-based hybrid deep learning method, as well as VOC-DL models, for the COVID-19 as well as Pneumonia datasets. The significance of each pre-processed model is based on noise rate. In particular, if the noise rate is lesser in preprocessing, then the model is said to be more efficient. Therefore, noise elimination is performed. In an ablation study, parts of the input data sample (i.e., noise data samples) are removed to determine whether input parts are significant to the model output. After that, ablation study results are acquired and compared to the proposed ALRTOHE and ZMFNE models with conventional CNN-GRU-based hybrid DL method and VOC-DL models. As presented in the above table, the outcomes of the ZMFNE method with respect to accuracy, PT, ER, and SC are improved compared to the other models.

In an ablation study, portions of the data samples are consistently removed to find significant data in the dataset. Initially, data samples from the given database are taken as input. Then, the input samples undergo the preprocessing process. During the preprocessing, the noise in the dataset is eliminated using the proposed preprocessing models. However, the normalization was not carried out to convert data into a structured format. Unlike other preprocessing models, the ZMFNE model performs normalization first using zero-mean feature scaling. Then, a one hot encoding approach is employed to preprocess the data, effectively eradicate the noise data present in the dataset. Therefore, the dataset is obtained in a structured format for easy interpretation. This helps the proposed ZMFNE model achieve high accuracy with fewer errors during the preprocessing process.

From the Table 7.1, the results of preprocessing accuracy for the COVID-19 dataset using ALRTOHE, an existing CNN-GRU-based hybrid deep learning method, and VOC-DL models are achieved at 83%, 75%, and 71%, respectively. In contrast, the proposed ZMFNE model achieved a higher preprocessing accuracy of 86%. This is observed as the greatest percentage accuracy in comparison with other proposed models. Likewise, the error rates of the proposed ALRTOHE, the existing CNN-GRU-based hybrid DL method, and VOC-DL models are computed as 17%, 25%, and 29%, respectively. In contrast, the proposed ZMFNE model achieved an error rate of 14%. The space complexity of ALRTOHE is obtained as 65 KB, whereas the CNN-GRU-based hybrid deep learning model achieves it at 69 KB. VOC-DL is obtained at 77 KB, and the ZMFNE model at 60 KB. It needs to be observed that the proposed ZMFNE model achieves 90% accuracy, a preprocessing time of 3630ms, an error rate of 10%, and a space complexity of 55 KB for the Pneumonia dataset. As stated in the above discussion, it can be determined that the ZMFNE model yields better results in terms of accuracy, error rate, and space complexity by removing a certain portion of data samples from the dataset.

7.2.2 Ablation Study for Feature Selection Models

Ablation study for five feature selection models is estimated with respect to feature selection accuracy, Feature selection time (FT), error rate, and space complexity. The ablation study results for Chi^2-MI, AHEG-FS, NSPPS, TSIDFE, and SCTPP-FS are presented in the table below.

Table 7.2 Ablation study results of proposed feature selection models with pre-processing (ZMFNE) methods for COVID-19 and Pneumonia datasets

Models	COVID-19 Dataset				Pneumonia Dataset			
	Accuracy (%)	FT (ms)	ER (%)	SC (%)	Accuracy (%)	FT (ms)	ER (%)	SC (%)
Existing Chi^2-MI	81	6900	19	76	83	6870	17	72
Existing AHEG-FS	84	6400	16	70	85	6360	15	65
Proposed NSPPS	86	5800	14	66	88	5760	12	60
Proposed TSIDFE	89	5320	11	61	91	5260	9	55
Proposed SCTPP-FS	**91**	**4950**	**9**	**55**	**93**	**4900**	**7**	**50**

Table 7.3 Ablation study results of proposed feature selection models without pre-processing methods compared to the baseline models

Models	COVID-19 Dataset				Pneumonia Dataset			
	Accuracy (%)	FT (ms)	ER (%)	SC (%)	Accuracy (%)	FT (ms)	ER (%)	SC (%)
Existing Chi^2-MI	75	7200	25	82	77	7170	23	77
Existing AHEG-FS	78	6800	22	77	80	6770	20	72
Proposed NSPPS	80	6100	20	73	82	6060	18	67
Proposed TSIDFE	83	5600	17	68	86	5550	14	61
Proposed SCTPP-FS	**85**	**5300**	**15**	**62**	**88**	**5260**	**12**	**56**

In the above ablation study, the irrelevant features among all other aspects are isolated, which helps identify the chosen relevant aspects to improve the method's results. Table 7.2 reports the outcomes of feature selection methods with preprocessing methods on diverse evaluation metrics, including accuracy, feature selection time (FT), error rate (ER), and specificity (SC), for COVID-19 and Pneumonia datasets. Table 7.3 shows the feature selection methods without preprocessing methods for two datasets. Here, accuracy is calculated as per the quantity of aspects exactly chosen, which totals the aspects in the dataset. FT is computed on the basis of time taken for relevant feature selection. The incorrect selection of features from the dataset measures ER. Additionally, the space complexity is estimated as the memory required to perform the feature selection process.

Different Machine Learning methods are employed for feature selection in ablation studies. Existing studies remove features, but the selection of the most informative feature for performance has failed. For this reason, the proposed SCTPP-FS model is designed to remove all irrelevant and least informative features among the independent variables. It also chooses the more significant features that contribute to the disease detection process. From the selected features, the SCTPP-FS model with the preprocessing method improves feature selection performance in relation to accuracy, FT, ER, SC.

As noted above ablation study models, part of irrelevant features among the other features in the dataset is removed. The input dataset comprises various files. Based on this, the patient data file is considered for the feature selection process. The patient data file consists of 9 features. From these input features, five significant features for the COVID-19 dataset (Latitude, Longitude, Cured/Discharged/Migrated, New cases, and New Deaths) and the Pneumonia dataset 6 significant features (Patient Id, Boxes, Target, class, Lung Capacity/not normal, No Lung Capacity/not normal) are selected using proposed SCTPP-FS model. This is due to the application of Kaiser–Meyer–Olkin correlative projection pursuit in the SCTPP-FS model. It computes the correlation among features in the database. Then, the feature that is more correlated for disease prediction is chosen to improve the feature selection performance. This, in turn, improves the accuracy of feature selection in the SCTPP-FS model with the preprocessing technique, resulting in lower error.

From the Table 7.2 and 7.3 the results of feature selection accuracy using existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS with preprocessing methods are achieved at 81%, 84%, 86%, 89%, and 91%, respectively. The ablation study outcomes demonstrate that the proposed SCTPP-FS model gained the greatest accuracy while selecting nine significant features. Without preprocessing, the accuracy results of the existing Chi^2-MI, AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS are obtained as 75%, 78%, 80%, 83%, and 85%, respectively.

Additionally, the error rates of the existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS with preprocessing methods were 19%, 16%, 14%, 11%, and 9%, respectively. The error rate of Chi^2-MI, AHEG-FS, NSPPS, TSIDFE, and SCTPP-FS without preprocessing methods was obtained as 25%, 22%, 20%, 17%, and 15%, respectively. Moreover, the space complexity of existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS with preprocessing method is obtained as 76 KB, 70 KB, 66 KB, 61 KB, and 55 KB, respectively. Furthermore, the space complexities of existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS without preprocessing are obtained as 82 KB, 77 KB, 73 KB, 68 KB, and 62 KB, respectively. The ablation study results of feature selection confirm that the proposed SCTPP-FS model, with the preprocessing method, attained improved results compared to other methods while removing irrelevant feature parts from the dataset.

By using the Pneumonia dataset, the existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS achieve accuracies of 83%, 85%, 88%, 91%, and 93%, respectively, with preprocessing models. Existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS with preprocessing models achieve space complexities of 72 KB, 65 KB, 60 KB, 55 KB, and 50 KB, respectively. The feature selection times are 6,870 ms, 6,360 ms, 5,760 ms, 5,260 ms, and 4,900 ms, respectively, for the Pneumonia dataset. Also, without preprocessing models, existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS attains 77%, 80%, 82%, 86%, and 88% accuracy for the Pneumonia dataset. Besides, the existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS without preprocessing models achieve space complexities of 77KB, 72KB, 67KB, 61KB, and 56KB, respectively. In contrast, feature selection times are 7170ms, 6770ms, 6060ms, 5550ms, and 5260ms, respectively, for the Pneumonia dataset.

Through the above comparative ablation study, the proposed SCTPP-FS model, which utilizes the preprocessing method, selects pertinent features from the database in the minimal time. The proposed SCTPP-FS maps the target features by identifying the association between them. The maximum correlated features are chosen as the target feature for disease detection.

The results of feature selection time using existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS with preprocessing methods are measured at 6900ms, 6400ms, 5800ms, 5320ms, and 4950ms, respectively, for the COVID-19 dataset. The results of feature selection time using existing Chi^2-MI, existing AHEG-FS, proposed NSPPS, proposed TSIDFE, and proposed SCTPP-FS without preprocessing methods are measured at 7200ms, 6800ms, 6100ms, 5600ms, and 5300ms, respectively, for the COVID-19 dataset.

7.2.3 Ablation Study for Classification Models

In this section, ablation studies for eight different classification models, i.e., predictive models, are discussed utilising accuracy, precision, recall, F-measure, and precision.The ablation study for EPBC, EPBC without Boosting, TCLMCNL, TCLMCNL without Levenberg–Marquardt (w/o LM) algorithm, MO-UNetDL technique, UNetDL without MO (w/o Memetic Optimization), deep learning LSTM ensemble model and DSPM are given in below table.

The ablation study examines the diverse assessment parameters. The accuracy is computed as the count of data samples exactly classified divided by the overall count of data samples. Precision is referred to as the ratio of properly forecasted samples of class to total forecasted samples of class. In contrast, Recall is referred to as the ratio of properly forecasted samples of class to every sample in the expected class. The F1 score integrates precision and recall values. PT is determined as the time spam used to categorize data samples.

Different classification models are employed in the ablation study. Conventional classification methods categorize data to predict whether patients are normal or abnormal. However, classification based on the most informative features was not performed. With this intent, the proposed models, such as EPBC, TCLMCNL, and MO-UNetDL technique, are developed to categorise the data grounded on the selected important features for disease prediction. This, in turn, the ablation study results in accuracy, precision, recall, F-measure, and specificity, being found to be better in the proposed MO-UNetDL technique with the preprocessing method.

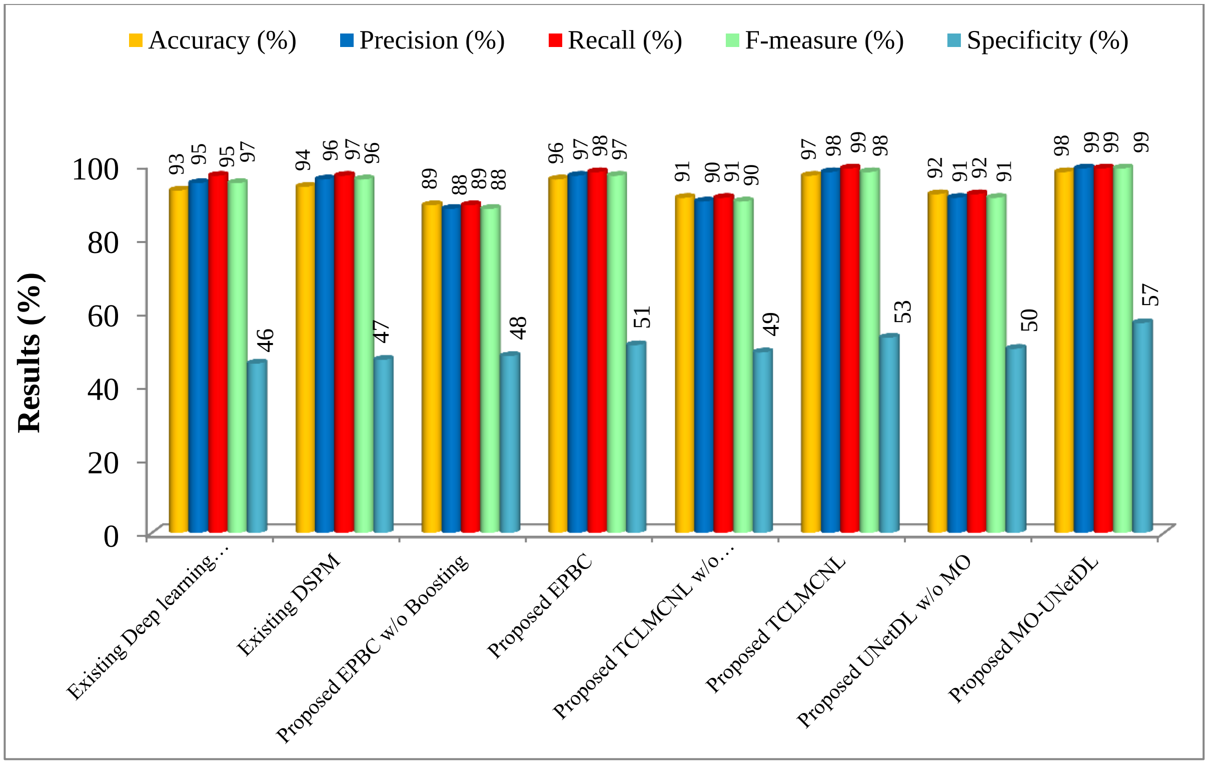

Figure 7.1 (a) Ablation study visualization of classification models with pre-processing (ZMFNE) method for COVID-19 dataset

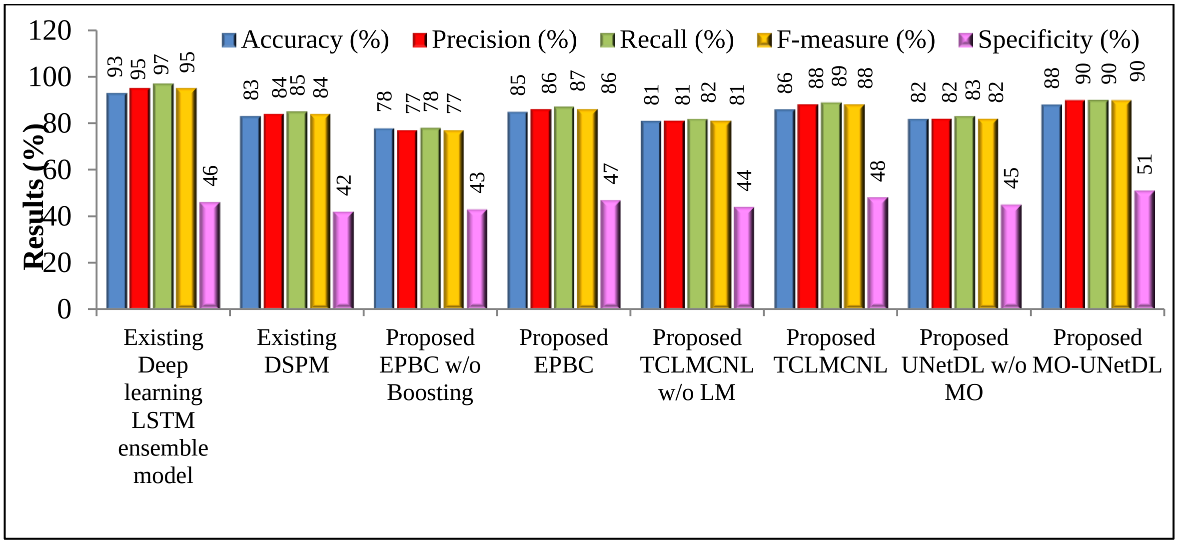

Figure 7.1 (b) Ablation study visualization of classification models with pre-processing (ZMFNE) method for Pneumonia dataset

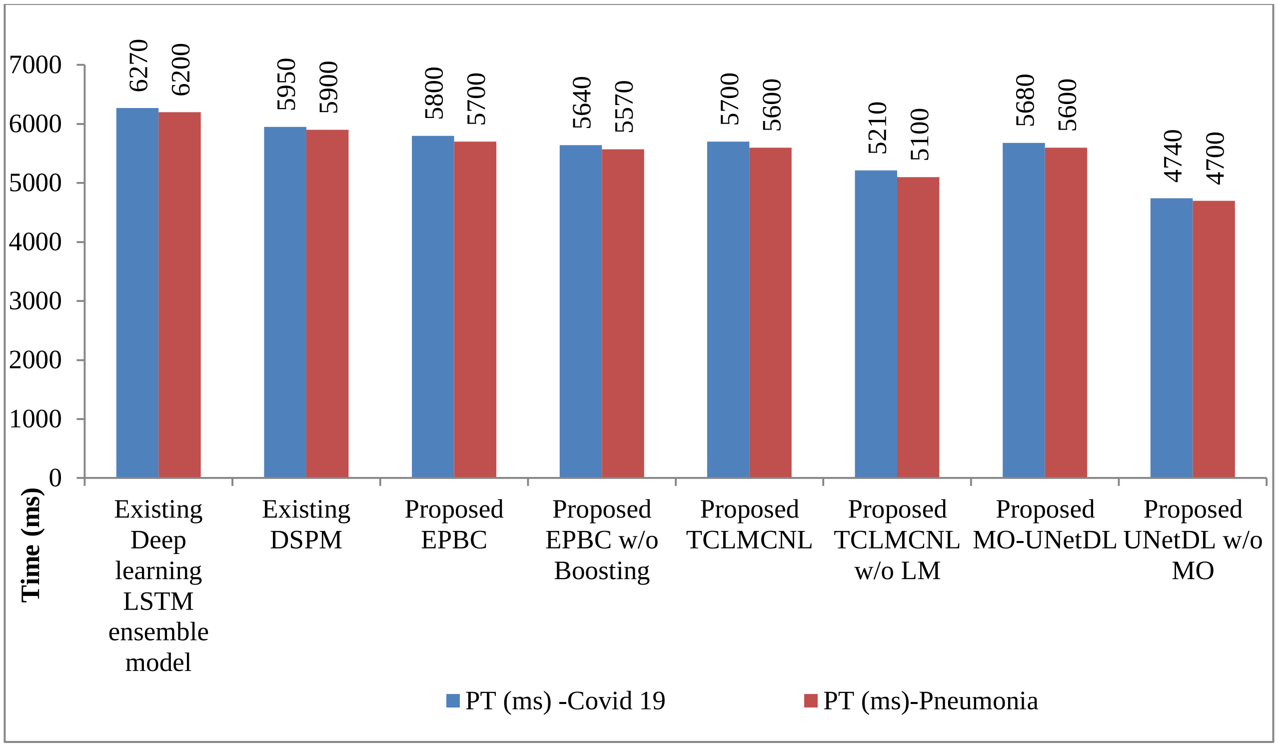

Figure 7.1 (c) Ablation study visualization of Time for classification models with pre-processing (ZMFNE) method for COVID-19 and Pneumonia datasets

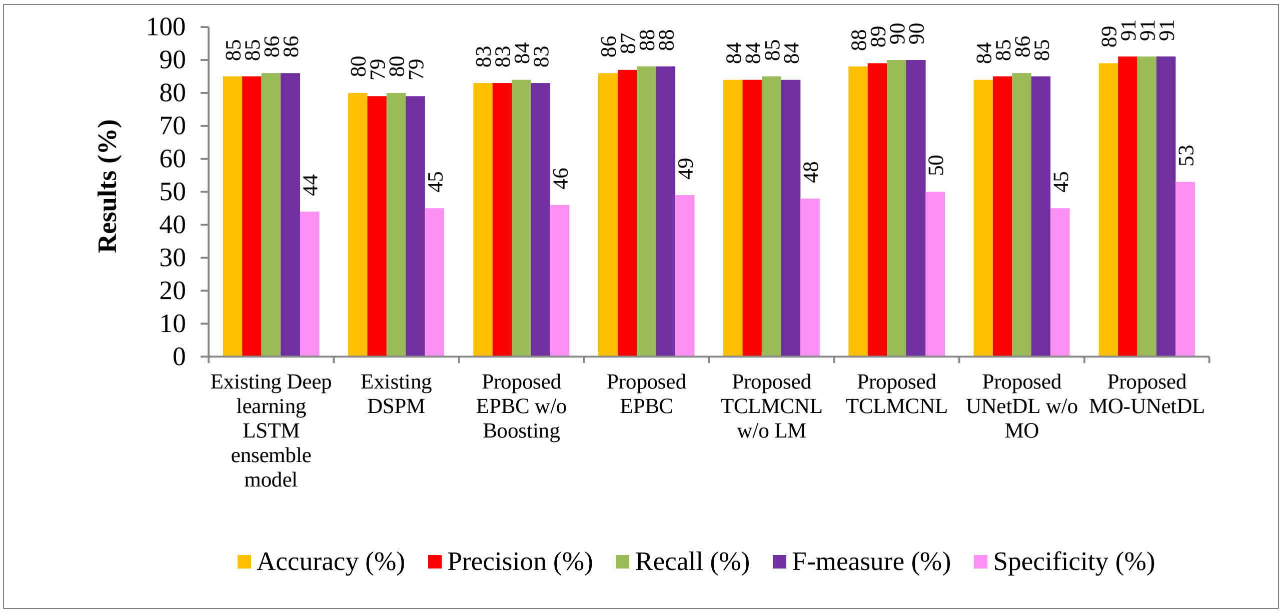

Figure 7.1 (d) Ablation study visualization of classification models without pre-processing methods for COVID-19 dataset

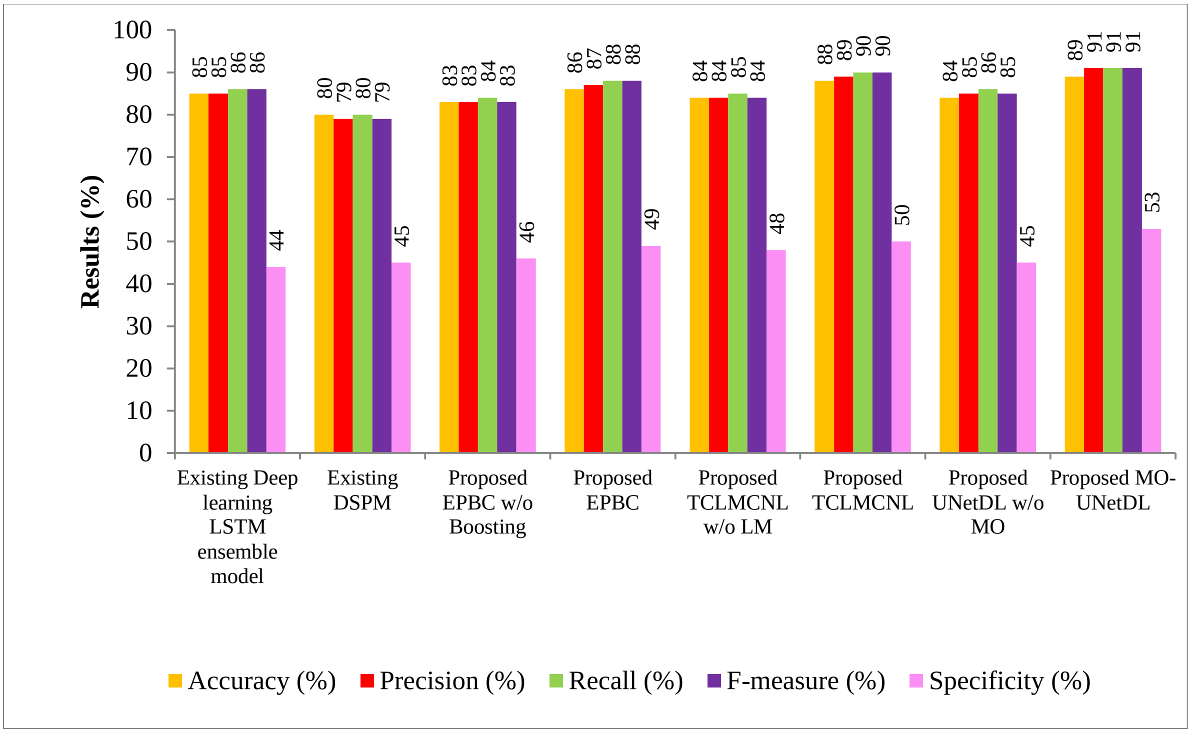

Figure 7.1 (e) Ablation study visualization of classification models without pre-processing methods for Pneumonia dataset

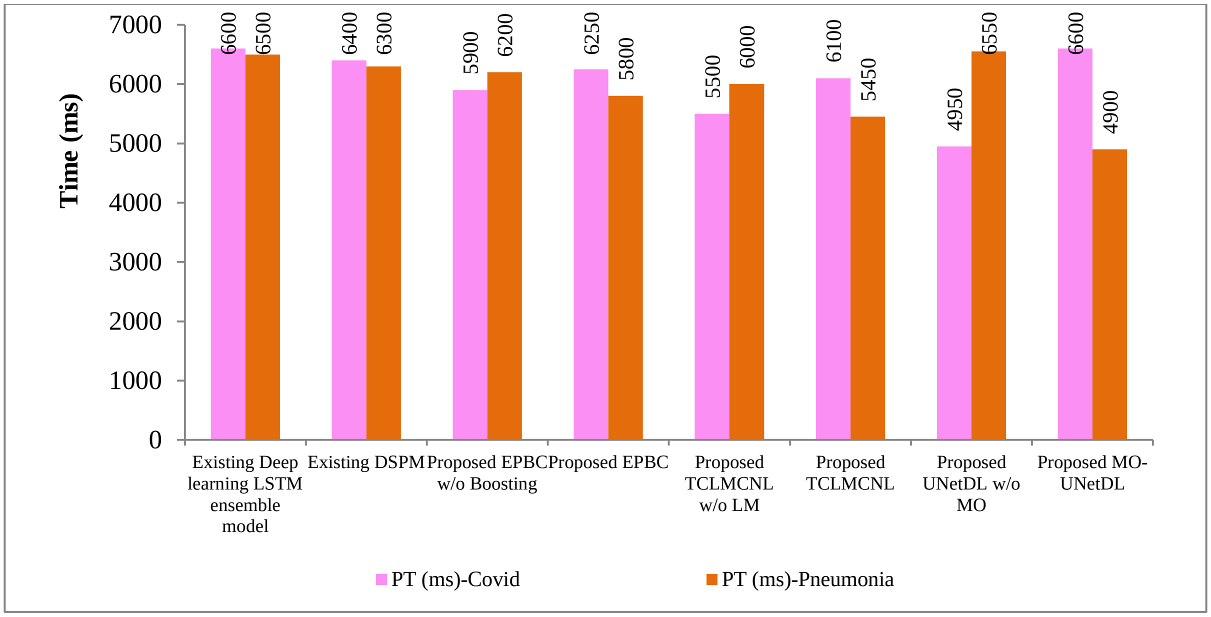

Figure 7.1 (f) Ablation study visualization of classification models without pre-processing methods (Time) for COVID-19 and Pneumonia dataset

Figure 7.1 (a) and (f) depict the ablation study visualization of accuracy, precision, recall, f-measure, and specificity using proposed classification models with and without pre-processing methods for two datasets. Initially, the importance of EPBC lies in classifying the data into diverse classes. Without using a boosting classifier in the COVID-19 dataset, the accuracy is degraded to 91% in EPBC. By implementing the boosting process in EPBC, an accuracy of 96% is achieved in the prediction. Therefore, the process of boosting is important in the EPBC model, where it finds a strong classifier to give better classification outcomes. Moreover, the execution of the suggested TCLMCNL technique without using the Levenberg–Marquardt algorithm (LM) degrades to 92%, whereas implementing LM yields a complete model accuracy of 97%. Thus, the process of the Levenberg–Marquardt algorithm is significant in the TCLMCNL model that minimizes the error rate in the classification process. Additionally, without implementing the Memetic optimization algorithm, the accuracy degrades to 94%. By integrating memetic optimization into the proposed MO-UNetDL model, an accuracy of 98% is achieved. Thus, the application of Magnetic optimization is important to enhance the accuracy of prediction. The comprehensive method achieves maximum accuracy and outperforms all baselines.

Similarly, for other parameters without implementing boosting (EPBC w/o Boosting), the results are degraded as 88%, 89%, 88%, and 48%, respectively. By using the boosting process, the EPBC achieves precision, recall, F-measure, and specificity of 96%, 95%, 96%, and 51%, respectively. Without implementing the LM algorithm (TCLMCNL w/o LM), precision, recall, f-measure as well as specificity is degraded to 91%, 92%, 91%, and 50%, respectively. By implementing a complete TCLMCNL, precision, recall, F-measure, and specificity are achieved at 97%, 96%, 97%, and 53%, respectively. In addition, the proposed UNetDL without MO yields degraded results, with precision, recall, F-measure, and specificity of 95%, 94%, 95%, and 47%, respectively. Additionally, the complete proposed MO-UNetDL model, combined with the pre-processing method, yields results of 98%, 98%, 98%, and 57%, respectively. Furthermore, the proposed MO-UNetDL model, without a pre-processing method, achieved precision, recall, F-Measure, and specificity of 90%, 90%, 90%, and 51%, respectively. Thus, the complete MO-UNetDL model, combined with the pre-processing method, improves performance related to other models.

In the ablation study, the proposed MO-UNetDL model, combined with a pre-processing method, takes less time for disease prediction during the classification process. The complete MO-UNetDL model classifies the data samples and also finds the error rate using the Magnetic optimization algorithm. With this, the time needed for the MO-UNetDL model with the pre-processing method is reduced. Without implementing the MO algorithm (UNetDL w/o MO), the prediction time is improved to 5680 ms. In contrast, by implementing the complete MO-UNetDL model with the pre-processing method, the PT is reduced to 474 ms. The complete MO-UNetDL model, without the pre-processing method, takes 4950ms as the processing time. Thus, the complete MO-UNetDL model, combined with the pre-processing method, minimizes PT and outperforms all the baselines.

Table 7.4 Ablation study results of proposed classification models with feature selection (SCTPP) methods for COVID-19 and Pneumonia datasets

Models	COVID-19 dataset						Pneumonia dataset					
	Accuracy (%)	Precision (%)	Recall (%)	F-Measure (%)	Specificity (%)	PT (ms)	Accuracy (%)	Precision (%)	Recall (%)	F-Measure (%)	Specificity (%)	PT (ms)
Existing Deep learning LSTM ensemble Model	93	94	95	95	52	5100	94	95	96	96	54	5000
Existing DSPM	90	90	91	89	50	5300	91	91	92	90	52	5200
Proposed EPBC w/o Boosting	92	91	92	91	53	4850	93	92	93	93	55	4750
Proposed EPBC	96	97	98	97	60	4700	98	98	94	93	63	4600
Proposed TCLMCNL w/o LM	94	92	93	92	56	4800	96	93	94	93	58	4700
Proposed TCMMCNL	97	98	98	98	62	4600	97	95	96	99	65	4500
Proposed UNetDL w/o MO	95	96	95	96	58	4750	97	97	96	97	60	4650
Proposed MO-UNetDL	98	99	99	99	65	4500	98	98	98	99	69	4400

Table 7.5 Ablation study results of proposed classification models without feature selection methods for COVID-19 and Pneumonia datasets

Models	COVID-19 dataset						Pneumonia dataset					
	Accuracy (%)	Precision (%)	Recall (%)	F-Measure (%)	Specificity (%)	PT (ms)	Accuracy (%)	Precision (%)	Recall (%)	F-Measure (%)	Specificity (%)	PT (ms)
Existing Deep learning LSTM ensemble Model	92	93	94	94	48	5200	93	94	95	95	45	5100
Existing DSPM	89	89	90	88	46	5400	90	90	91	89	53	5300
Proposed EPBC w/o Boosting	91	90	91	90	49	4950	92	91	92	91	56	4900
Proposed EPBC	96	96	95	96	55	4800	97	97	96	97	53	4700
Proposed TCLMCNL w/o LM	94	92	93	92	52	4900	95	93	94	93	50	4800
Proposed TCMMCNL	95	94	95	95	58	4700	96	95	96	96	56	4650
Proposed UNetDL w/o MO	92	93	92	93	52	4850	93	94	93	94	50	4800
Proposed MO-UNetDL	96	95	96	96	60	4600	97	96	97	97	58	4550

Tables 7.4 and 7.5 describe the ablation study visualization of classification models with feature selection methods for the COVID-19 dataset and the Pneumonia dataset. The performance of classification is improved with feature selection methods compared to without them. In addition, the proposed MO-UNetDL method achieved better results, in accuracy, precision, recall, F-measure, specificity and PT in both COVI-19 and Pneumonia datasets.

7.3 CHAPTER SUMMARY

As described in the above sections, an ablation study for different models, namely preprocessing, feature selection, and classification methods, is conducted to identify the importance of the proposed models. The ablation studies using proposed Machine Learning and Deep Learning methods for disease recognition give insights into how different parts of the method contribute to its overall functionality. Understanding which components are crucial for disease detection helps in diagnosing issues and refining model architecture. Ablation studies help to recognise the most crucial features for disease detection. The feature selection with preprocessing models effectively chooses the relevant features than when it is used without preprocessing models. In classification, the ablation study tests the model’s performance with and without preprocessing and feature selection components, ensuring its robustness and ability to generalize across different datasets.

Ablation studies for ALRTOHE, ZMFNE, and the existing CNN-GRU-based hybrid deep learning method, as well as VOC-DL models, are conducted. The outcomes confirm that the initiated ZMFNE model substantially eliminates noisy data in the dataset, and the elimination process improves the overall ablation results with respect to other baseline models, with an average accuracy of 86%, an error rate of 14%, a space complexity of 60KB, and a preprocessing time of 5060ms. In another ablation study, SCTPP-FS with a preprocessing method significantly removes the irrelevant aspects of the database than other models. This removal procedure helps to determine the crucial features. The selected features of the proposed SCTPP-FS model with the preprocessing method outperformed the without preprocessing method in terms of higher accuracy at 91%, FT at 4950ms, error rate at 9%, and SC at 55KB. Later, an ablation study is conducted for classification models, including EPBC, EPBC without Boosting, TCLMCNL, TCLMCNL without the Levenberg–Marquardt (w/o LM) algorithm, MO-UNetDL technique, UNetDL without MO (w/o Memetic Optimization), deep learning LSTM ensemble model, and DSPM. The complete MO-UNetDL technique with the preprocessing method significantly improved the outcomes of the ablation study compared to the method without a preprocessing, by increasing the accuracy to 98%, precision to 98%, recall to 98%, f-measure to 98%, and specificity to 57%, while decreasing the processing time to 4740ms. The outcomes highlight the significance of proposed models in disease prediction. The next chapter presents the detailed investigation on preprocessing, feature selection and classification techniques using both the COVID-19 and Pneumonia datasets.