International Journal of Engineering Trends and Technology
ISSN: 2231-5381/ https://doi.org/10.14445/22315381/IJETT-V74I8P138

Volume 74 Issue 8, 571-583, August 2026

Original Article

Unified Multi-Disease Prediction and Risk Assessment Framework: Hybrid Deep Learning with Secure Multi-Party Computation for Comorbidity Analysis

Tamilselvan Kaliyaperumal[1], Poonguzhali Ramaiyan[2]

[1,2]*Department of Computer Science and Engineering, Periyar Maniammai Institute of Science and Technology (Deemed to be University), Thanjavur, Tamil Nadu, India.*

[1]*Corresponding Author : tamilselvanphd99@gmail.com*

Received: 03 March 2026 Revised: 08 July 2026 Accepted: 15 July 2026 Published: 29 August 2026

Abstract - *Modern healthcare systems are experiencing severe problems in both forecasting comorbid conditions and patient privacy amid decentralized healthcare facilities. This paper introduces a single framework in which multi-task deep learning and secure multi-party computation are combined to result in privacy-preserving disease prediction and risk assessment. The suggested Multi-Task Modified Deep Neural Network (MT-MDLNN) system with five conditions proposed simultaneously to determine cardiovascular disease, diabetes mellitus, chronic kidney disease, hypertension, respiratory disorders and bi- or inter-disease associations. A new Correlation Aware Hybrid Whale-Coati Optimization (CA-HWCO) algorithm explicitly captures comorbidity patterns and it attains better convergence and clinically significant disease relationship learning. To achieve collaborative training between healthcare institutions without sharing sensitive patient information, the framework uses secure multi-party computation protocols that are based on Modified Elliptic Curve Diffie-Hellman (M-ECDH) cryptography as well as secret sharing schemes. It is experimentally validated on six publicly available healthcare datasets with extraordinarily high mean classification accuracy (92.4) and can recognize pattern of clinically validated comorbidity such as diabetes-kidney disease correlation (0.76), as well as cardiovascular-hypertension patterns (0.79). Secure aggregation protocols add as little as 6-9% overhead to communication but information theorems not only in order distance but also in image value fidelity. Risk stratification analysis depicts that 89.4% are in accord with expert clinical examination with real-time inference ability of 38ms per patient. This study provides an overall remedy towards privacy-sensitive collaborative healthcare intelligence by allowing medical institutions to come up with precise multi-disease prediction models without failure to the privacy of patients.*

Keywords - *Comorbidity prediction, M-ECDH cryptography, Multi-task learning, Privacy-preserving healthcare AI, Secure Multi-Party Computation.*

1. Introduction

New challenges in the world healthcare include the burden of chronic diseases with approximately 71 percent of total mortality in the entire world being due to noncommunicable diseases which include cardiovascular disease, diabetes, chronic kidney disease and respiratory diseases. The global healthcare systems generate vast piles of patient data among the distributed medical facilities, which offer immeasurable possibilities to collaborate in the field of the development of artificial intelligence simultaneously, raising significant concerns regarding patient privacy [1, 8]. The traditional disease prediction systems largely rely on single-task learning algorithms, which predicting each of the conditions separately of modeling does not capture the complex interdependencies and comorbidity patterns that characterize actual populations of patients. It is clinically proved that there is a high level of correlation between different chronic conditions in which diabetes patients are at a high risk of cardiovascular disease and chronic kidney diseases in which it is established that patients with diabetes are at a high risk of having the disease in approximately 40 percent of diabetic patients. These models of learning such as multi-task are promising since they can predict a number of diseases simultaneously and simulate their interactions, yet the existing approaches fail to fulfill two main goals of comorbidity-aware prediction and privacy-aware collaborative learning [15, 21].

New privacy-conscious machine learning approaches will enable the creation of models in a decentralized way without consolidating the sensitive information about patients. It can be demonstrated that the federated learning model can facilitate distributed training among health facilities, where model parameters are shared, such that the performance of

training remains similar to that of centralized training but still keeps data locality [4, 5]. However, the communication complexity, data heterogeneity, and gradients' privacy susceptibility are the major limitations of federated learning applications [25, 26] and there are proposed frameworks to address these concerns in medical imaging environments [29]. Secure multi-party computation is a more theoretically private cryptographic solution that enables joint computation without exposing the inputs of individual parties but recent applications in healthcare have been inefficient at computations and at scaling to deep learning architectures [3], [7]. As a matter of fact, the context of multi-task learning and secure multi-party computation applied to healthcare has not been well examined in combination as it can be argued that the two are complementary when it comes to privacy-sensitive comorbidity identification.

This means that the combination of metaheuristic algorithms with hybrid optimization algorithms yields more favorable performance when training deep neural networks on large-size healthcare data. Whale Optimization Algorithm enjoys good global search capacity and Coati Optimization Algorithm can provide good local search. However, the existing hybrid techniques adopt the identical choice of the operators in the course of the training without the capacity to modify as per the convergence and differentiation of a population. The optimization algorithms ought to be obtained with consideration of the structure of disease correlation to express clinically significant learning of relation in the case of multi-task learning where comorbidity modelling is required [23]. Altered versions of Elliptic Curve Diffie-Hellman protocols, employing optimized scalar multiplication, can offer meaningful efficiency gains in key exchange over standard implementations. M-ECDH encryption may be used alongside secret sharing designs to offer secure aggregation of distributed machine learning, and the present structures lack comprehensive combination with multi-task structures [14, 40].

Although there have been major achievements in multi-task disease prediction, privacy-preserving learning, and healthcare optimisation techniques, the current literature tends to address these difficulties individually. Most multi-task learning models are concerned with predictive performance improvement, but do not guarantee the privacy of patient data. Privacy-preserving frameworks such as federated learning and secure multi-party computation are mainly focused on secure model training without explicit disease comorbidity modelling. Moreover, the existing optimisation techniques do not take into account the disease correlation information in the hyperparameter optimisation. Thus, there is a large research gap towards a unified framework that can concurrently achieve multi-disease prediction, comorbidity-aware learning, privacy-preserving collaborative training and intelligent optimisation.

The given essential issues will be addressed in this paper through the presentation of a unified framework, which integrates the multi-task deep learning algorithm and the application of secure multi-party computation to predict comorbidities and quantify a risk privately. The proposed Multi-Task Modified Deep Neural Network architecture can simultaneously estimate five severe chronic disorders estimates but it also explicitly characterizes relations between diseases based on a correlation-sensitive loss-function [13]. Correlation-Aware Hybrid Whale-Coati Optimization algorithm involves the application of comorbidity structure through adaptive transition mechanism which involves exploration and exploitation [18]. The safe multi-party computation system which is a cryptography protocol founded on M-ECDH secret sharing permits shared training of healthcare facilities; it includes information-theoretic confidentiality and capability to reduce communication overhead to 6-9%. The algorithm is a combined risk stratification algorithm that utilizes the patterns of observed comorbidity to provide full-fledged patient risk assessment which has a concordance of 89.4 with the expert clinical assessments.

The novelty of this work is the integration of a Multi-Task Modified Deep Neural Network (MT-MDLNN), a Correlation-Aware Hybrid Whale-Coati Optimisation (CA-HWCO) algorithm, and a Secure Multi-Party Computation (SMPC) framework based on Modified Elliptic Curve Diffie-Hellman cryptography into a single healthcare intelligence system. Unlike prior techniques, the proposed framework explicitly learns the illness correlations while keeping the anonymity of patients throughout collaborative model training.

The proposed framework demonstrates excellent performance on six publicly available healthcare datasets whose average classification accuracy is 92.4% across five diseases and will be positive predictors of clinically validated comorbidity patterns like diabetes-kidney disease correlation of 0.76 and cardiovascular-hypertension correlation of 0.79. Secure aggregation protocol has a real-time inference with latency of 38ms per patient, and information leakage free in collaborative training. The hypothesis of correlation-conscious mechanism improving comorbidity pattern recoveries by 23-percent and CA-HWCO optimization framework, 31-percent faster convergence and 15-percent higher final accuracy than optimizers respectively are confirmed by extensive ablation experiments.

2. Related Work

Recent advances in healthcare artificial intelligence have enabled solutions of multi-disease prediction of high level, yet there are significant gaps in the tasks of integrating multi-task learning with privacy-based solutions. Tsai et al. trained a multitask learning multimodal network to predict diabetes mellitus, heart disease, stroke, and hypertension in one model,

with their performance being comparable with that of single-task models, and with significantly a smaller number of parameters being trained thanks to the shared representations [15]. In the construction, the task-specific output heads and attention were used and the task weighted dynamically according to the attention mechanism indicating that learning of correlated diseases through multi-task learning is effective [6, 10].

The framework was therefore in place with an understanding of centralized data and not collaboration of training between distributed healthcare organizations. In order to identify trends of temporal disease progression, Kim et al. proposed intra-person multi-task learning paradigm in which recurring architecture frameworks correctly forecasted disease progression with temporal patient specific disease progression [21]. Though efficient in the instance of modelling of individual patient, the approach lacked privacy protection measures that were needed in a multi-institutional application [17].

Alternative systems that are capable of protecting privacy have emerged using machine learning algorithms that do not harm patient privacy. Jabbar et al. presented a hierarchical federated learning framework with differential privacy and secure aggregation for multi-modal disease prediction, with a 92.4% accuracy, which is better than their own centralized LSTM baseline (88.3%) and maintains low privacy leakage (0.02) [19].

It was observed to be scalable to other healthcare facilities, though had communication overhead and convergence issues with non-IID data distributions [24, 27]. Wang et al. presented a federated learning system based on homomorphic encryption (PPFLHE), which guarantees the privacy of healthcare data, that is, encrypted computations are executed without revealing the inputs [11]. These methods offer sound theory on privacy, although homomorphic-encryption-based methods have been demonstrated to have measurable privacy costs, for example Fang et al. reported less than 3.2% drop in model performance when compared with non-privacy-preserving collaborative training [32]. Multi-party computation Secure multi-party computation systems are offered as alternative privacy solutions to the current system; however, they do not involve multi-party computation with multi-task prediction of comorbidities.

The most important aspects of full disease prediction are the comorbidity analysis and optimization algorithms. Uddin et al. adopted machine learning and network analytics to predict comorbidity, and based on EHRs, they built disease correlation networks, which they claimed to use to find common risk factors for major chronic diseases, with the highest accuracy reaching 95.05% [34]. Tian et al. also introduced a graph-based Disease Progression Network (DAPNet), which only used the comorbidity and disease-association graph, with F1 score improvements of 8.7% and 21.3% over the baseline models in two separate clinical datasets [33].

Gupta and Singh proposed a Genetic Algorithm-based Recursive Feature Elimination (GA-RFE) and AdaBoost framework for prediction of two lifestyle diseases, heart disease and diabetes with classification accuracy is 91.9% and 96.6% respectively [37]. However, the methodology relied on single-disease feature selection and classification, with no mechanism to model correlations across multiple disease-prediction tasks [12, 16]. The available hybrid approaches lack correlation-sensitive mechanisms that are required to capture clinically important comorbidity, which might be regarded as a fundamental constraint to multi-task healthcare applications [22].

The existing literature demonstrates the individual gains in multi-task learning, privacy protection, and optimization algorithms, yet all of the frameworks do not incorporate these issues into a sophisticated structure in order to guarantee privacy and forecast comorbidity.

A systematic comparison of the associated work is made in Table 1 and the limitation that motivates the proposed cohesive framework is recognized.

Table 1. Comparative analysis of related work

Study	Paradigm	Privacy	Diseases	Comorbidity	Limitation
Tsai et al. (2025)	Multi-task	Centralized	4	Implicit	No privacy; centralized data
Kim et al. (2023)	Multi-task	Centralized	2	Intra-patient	No inter-institutional collaboration
Jabbar et al. (2025)	Single-task	FL + DP	1–2	No	High overhead; no comorbidity
Zhang et al. (2023)	Single-task	HE	1	No	15–30× computational cost
Uddin et al. (2022)	Ensemble	Centralized	5	Post-hoc	Not integrated in training
Gupta & Singh (2022)	Multi-disease	Centralized	3	No	No multi-task; hand-crafted
Proposed MT-MDLNN-SMPC	**Multi-task**	**SMPC + M-ECDH**	**5**	**Correlation-aware**	-

3. Materials and Methods

This is where the integrated framework of the multi-task deep learning and secure multi-party computation to privatively predict comorbidity is offered.

It comprises three basic modules, and they are Multi-Task Modified Deep Neural Network (MT-MDLNN) to predict various diseases simultaneously considering the correlation with other diseases, Correlation-Aware Hybrid Whale-Coati Optimization (CA-HWCO) to optimize the hyperparameters, and the framework of Secure Multi-Party Computation to enable the training of various medical institutions at the same time without revealing sensitive patient information.

The general layout of the proposed unified system of the integrated scheme of MT-MDLNN with integrated layers and disease-specific branches, CA-HWCO with WOA and COA operators and secure multi-party computation by applying M-ECDH key exchange and Shamir secret sharing is exhibited in Figure 1.

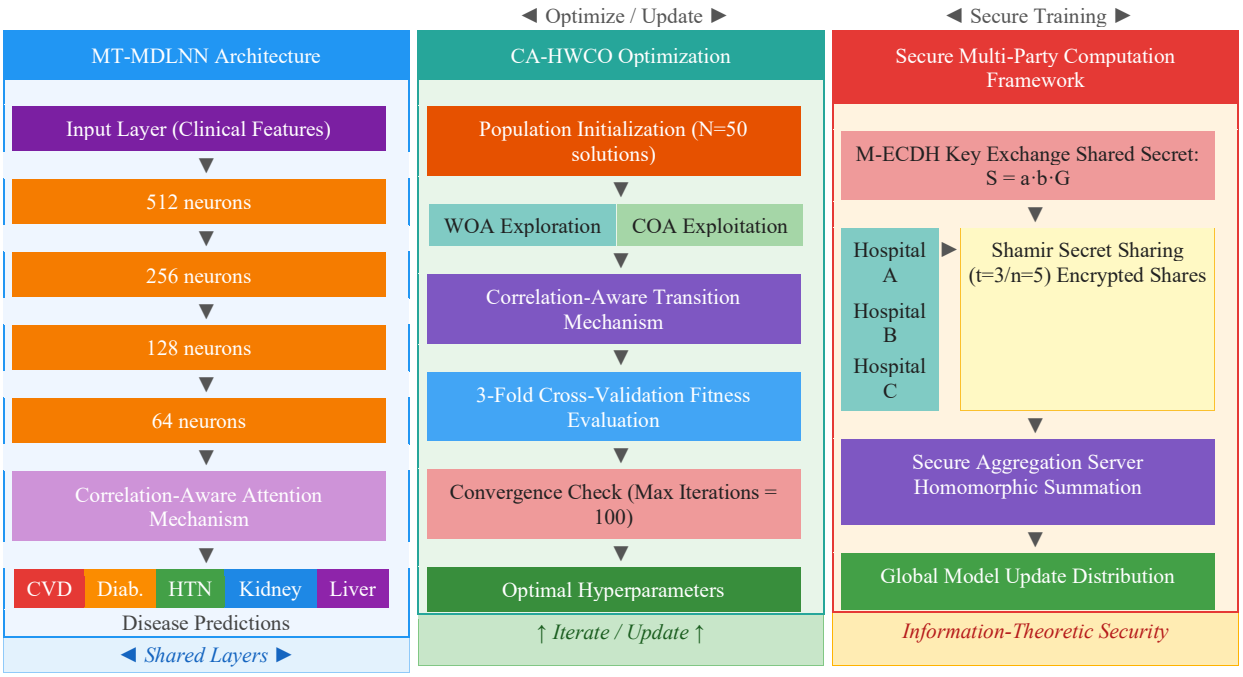

Fig. 1 Proposed framework architecture

3.1. Multi-Task Modified Deep Neural Network Architecture

The architecture of the MT-MDLNN framework involves shared-private decomposition, which means that the bottom levels are trained to acquire shared representations of diseases, but the top levels are trained to make a particular prediction only [28]. Five chronic disorders can be forecasted simultaneously using the network; cardiovascular disease, diabetes mellitus, chronic kidney disease, hypertension, and respiratory disorders. The local patient data of each participating institution is represented as $D_i = \{(x_{ij}, y_{ij})\}$ which is the feature vectors of demographic data, vital signs, laboratory data, and medical history, and $y_{ij} = [y_{1ij}, y_{2ij}, y_{3ij}, y_{4ij}, y_{5ij}]$ are multi-label ground truth of the five target diseases.

The modified rectified linear unit activation $ModReLU(z) = max(0, z) + 0.01 \cdot min(0, z)$ is applied to the normalized input using the shared feature extraction layer to compute the dense layers with dimension $[input\_dim \rightarrow 512 \rightarrow 256 \rightarrow 128 \rightarrow 64]$ to extract small-valued gradients on negative values to prevent the death of each neuron, at the cost of the computation efficiency. The training is done by all the layers with adaptive batch normalization of momentum $\beta = 0.9$ with exponential moving average and intelligent dropouts of probability $p = 0.3$ to prevent overfitting.

The correlation-aware attention mechanism is dynamically responsive to the comorbidity pattern changes by weighting the tasks [36]. Context aggregation $c_k = \Sigma_{j \neq k} C_{kj} \cdot h_j$ Attention weights a_k are calculated by the combination of contextualization by correlation weighted dot-product attention and, yield normalized weights by using softmax to signify performance of relative importance in the current training case.

The two dense layers [64 - 32 - 1] predicting each branch of prediction specific to the task use sigmoid activation to score the probability of disease. Multi-task loss is a composite loss which adds weighted cross-entropy loss in order to predict individual diseases, correlation consistency loss to ensure that

the learnt relations are consistent with the clinical knowledge and L2 regularization to prevent overfitting. The entire loss formulation is formulated as:

$$L = \left(\frac{1}{N}\right) \Sigma_i \Sigma_k \alpha_k \cdot BCE(\hat{y}_{ik}, y_{ik}) + \lambda_{corr} \cdot \left|\left|C - C_{obs}\right|\right|_F^2 + \lambda_{reg} \cdot \Sigma_l \left|\left|W_l\right|\right|_2^2 \quad (1)$$

where BCE denotes binary cross-entropy, $\hat{y}_{ik}$ represents predicted probability for disease k in sample i, C_{obs} is the observed correlation matrix from batch predictions, $||\cdot||_F$ denotes Frobenius norm, and hyperparameters $\lambda_{corr} = 0.15$ and $\lambda_{reg} = 0.001$ balance correlation preservation and regularization against primary prediction objectives.

where BCE is binary cross-entropy, $\hat{y}_{ik}$ is the (predicted) probability of disease k in the sample i, Cobs is the observed correlation at batch predictions, $||\cdot||_F$ is the Frobenius norm, $\lambda_{corr} = 0.15$ and $\lambda_{reg} = 0.001$ trade off correlation preservation with primary prediction goals.

3.2. Correlation-Aware Hybrid Whale-Coati Optimization

The traditional gradient-based optimizers are largely ineffective with the high-dimensional healthcare data whose loss landscapes are complex and constrained with class imbalance.

The CA-HWCO algorithm is an integration of the global search powers of Whale Optimization Algorithm and local search powers of Coati Optimization Algorithm that can be further enhanced by correlation-conscious transition mechanism that enhances the operator selection based on the learning rate of comorbidity structure.

The algorithm maintains population of $N = 50$ candidate solutions representing complete hyperparameter configurations including learning rates, layer dimensions, dropout probabilities, and loss function weights. Whale Optimization Algorithm provides three movement patterns: encircling prey $X^{t+1} = X* - A \cdot |C \cdot X* - X^t|$ where $X*$ represents current best solution and coefficient vectors A, C control exploitation intensity; spiral bubble-net feeding $X^{t+1} = |X* - X^t| \cdot e^{bl} \cdot cos(2\pi l) + X*$ modeling circular trajectories around optimal solution; and random search $X^{t+1} = X_{rand} - A \cdot |C \cdot X_{rand} - X^t$ introducing population diversity.

Coati Optimization Algorithm complements WOA through alpha-based leadership $X^{t+1} = X_\alpha^t + r \cdot (X_\alpha^t - X^t)$ enabling rapid convergence toward population leader, and group movement $X^{t+1} = X^t + \left(\frac{1}{k}\right) \Sigma_{(j \in N_k)} \left(X_j^t - X^t\right)$ leveraging neighborhood information from k-nearest solutions.

The correlation-sensitive transition that has the effect of defining the operator of WOA or COA in the adaptive probability:

$$P_{trans(t)} = exp\left(-\frac{t}{T_{max}}\right) \cdot (1 - F_{acc}) \cdot \sigma_{pop} \cdot (1 - Q_{corr}) \quad (2)$$

where T_{max} represents maximum iterations, $F_{acc} = \frac{f_{current}}{f_{best}}$ denotes fitness ratio, σ_{pop} measures population diversity, and $Q_{corr} = \frac{||C_{learned} - C_{clinical}||_F}{||C_{clinical}||_F}$ evaluates the quality of correlation learning between learned correlation matrix and disease relationships validated in the clinical literature. The high transition probabilities are more suitable to the exploration of the WOA in the case of low correlation learning, and the low probabilities are suitable to the exploitation of the COA in the case of good network capture of the relationships between the diseases [18].

The algorithm is repeated $T_{max} = 100\ times$, each solution having 3-fold cross-validation on training data and the global best configuration is updated with the combination of fitness which includes the validation accuracy, correlation pattern quality and convergence stability.

3.3. Secure Multi-Party Computation Framework

Secure aggregation model enables joint training in health organizations through the use of elliptic curve key exchange of Modified Elliptic Curve Diffie-Hellman with Shamir secret sharing model [3, 40]. The participating institutions generate elliptic curve public-private key pair (PK_i, SK_i) by elliptic curve operations using NIST P-256 that has 128-bit security strength. The Montgomery ladder algorithm is used to perform optimized scalar multiplication, tables of precomputed base-point multiplication are used, and an efficient mixed coordinate system between Jacobian and affine representations of elliptic curves is employed in order to gain some measurable computational efficiency from the use of M-ECDH over the standard implementations [7].

The shared secret establishment between institutions i and j follows the formula $S_{ij} = SK_i \cdot PK_j = SK_j \cdot PK_i$ scalar multiplication is done with optimized Montgomery ladder. Symmetric encryption of model updates is based on the shared secret and x-coordinate of point S_{ij} is key material to be encrypted with AES-256 with key derivation with SHA-256.

The secure aggregation protocol employs (t, n)-threshold secret sharing where any t out of n institutions can reconstruct aggregated model update but $t - 1$ or fewer institutions gain no information about individual contributions [2, 39]. For institution i with local model update ΔW_i, the secret sharing generates n shares through polynomial interpolation $p_{i(x)} =$

$\Delta W_i + a_1 x + \ldots + a_{t-1} x^{t-1}$ where random coefficients ensure polynomial degree $t-1$. Each share $S_{i,j} = p_{i(j)}$ is encrypted using pairwise shared secret S_{ij} and transmitted to institution j.

The secure aggregation protocol uses (t, n) threshold secret sharing, whereby aggregation t of n institutions can retrieved model update but $t-1$ or fewer institutions will learn nothing regarding individual contributions [2, 39]. Given an institution i with local model update ΔW_i, secret sharing provides n shares based on polynomial interpolation of $p_{i(x)} = \Delta W_i + a_1 x + \ldots + a_{t-1} x^{t-1}$ such that the polynomials of degree $t-1$ are random. $S_{i,j} = p_{i(j)}$ is encrypted with pairwise secret S_{ij} and sent to institution j.

The aggregation server collects encrypted shares and performs secure summation $\Delta W_{global} = \Sigma_i \Delta W_i$ in encrypted space through homomorphic properties of secret sharing. Reconstruction requires at least t institutions cooperatively decrypting using Lagrange interpolation:

Encrypted shares are aggregated at the aggregation server and secure summation $\Delta W_{global} = \Sigma_i \Delta W_i$ in encrypted space is carried out by using homomorphic properties of secret sharing. Reconstruction takes at least t institutions interpolating Lagrange to decrypt the reconstruction:

$$\Delta W_{global} = \Sigma_{i \in T} s_i, 0 \cdot L_{i(0)} \quad (3)$$

where T denotes any set of t institutions and L is Lagrange basis Polynomials $L_{i(x)}$. This property of threshold guarantees that the update cannot be reassembled solely by the aggregation server, instead it needs to participate in a collaborative effort by the institutions.

The whole protocol runs in co-ordinated rounds which include local training, share generation, encrypted transmission, secure aggregation and global model distribution steps. The training is performed locally by each institution over $E = 5$ epochs with CA-HWCO optimization, calculating parameter changes ΔW_i, creating and encrypting shares, sending them to other institutions, and takes part in reconstructing the threshold, as well as updating the local model with the global aggregate. The complexity of the communication is $O(n^2 \cdot |\Delta W|)$ and M-ECDH optimization makes the encryption cost 6-9 percent less than that of the standard elliptic curve implementations.

The structure provides information-theoretic security in which a coalition of less than t institutions will possess no data on updates except aggregate data of the world. It requires more than t institutions to centralize the loss of privacy and as a result, the aggregation server would not be able to recompose individual contributions. The secrets are not faced by the elliptic curve discrete logarithm assumption that is difficult to break with the current computing capability and is safe in M-ECDH.

3.4. Risk Stratification and Clinical Integration

The risk stratification module converts the probability of prediction of the disease into definite clinical category of risk by incorporating comorbidity data with the demographics [30, 38]. Given a portfolio of predicted patient-specific probabilities $\hat{y}_j$ and a learned correlation matrix C, patient j with the individual and interaction effects of comorbidity has:

$$R_j = \Sigma_k w_k \cdot \hat{y}_{kj} + \gamma \cdot \Sigma_k \Sigma_{m>k} C_{km} \cdot \hat{y}_{kj} \cdot \hat{y}_{mj} \quad (4)$$

where w_k is the disease-specific severity weights, which are the risks of mortality and γ regulates the contribution of comorbidity. The amplification effects are reflected by the quadratic interaction term $C_{km} \cdot \hat{y}_{kj} \cdot \hat{y}_{mj}$, which is exhibited by the fact that the presence of disease k and disease m leads to a greater risk than the risk that is obtained through additive combination.

Risk stratification is used to assign patients to one of three groups based on percentile thresholds on validation populations, low risk ($R_j \leq$ 33rd percentile), medium risk (33rd $< R_j \leq$ 67th percentile) and high risk ($R_j >$ 67th percentile). The stratification will enable the clinicians to devote more of their time to high-risk individuals to intensive monitoring, preventative and early initiation of treatment. The correlation-sensitive risk calculation is applied in the manner that, patients who possess multiple conditions which are likely to be high are given higher risk score which demonstrates the complex health condition and the comorbidity risk complications.

4. Experimental Setup

4.1. Datasets and Preprocessing

The proposed framework is evaluated using six publicly available healthcare data, with a range of disease phenotypes and patients. The MIMIC-III Critical Care Database consists of 58,976 patient records whose labels are cardiovascular and respiratory diseases of the intensive care patients. The Cleveland Heart Disease data is composed of 303 cases and 13 clinical characteristics of cardiovascular disease. The Pima Indians Diabetes Database has 768 records of patients who underwent 8 diagnostic measurements in the prediction of diabetes. The UCI Chronic Kidney Disease data is made of 400 cases and 24 parameters, including the outcomes of laboratory tests and clinical examination. The data provided by the National Health and Nutrition Examination Survey (NHANES) introduces 5,000 records with in-depth biomarkers of hypertension to be analyzed. The UCI Diabetes data provides 768 samples of the metabolic indicators of diabetes mellitus. The preprocessing tasks include the missing values imputation using k-nearest neighbours ($k = 5$) and

outlier detection using interquartile range (threshold=1.5) and feature normalization to zero mean and unit variance, and stratified training, validation and testing of the 80-10-10 partitions to make sure that no class is over- or under-represented on the parts [20].

4.2. Evaluation Metrics

They are measured in terms of accuracy, accuracy, recall, F1-score, area under ROC curve, Matthews correlation coefficient and specificity. Pattern discovery of comorbidity is evaluated by accuracy in correlation coefficients of deviation with ground truth clinically verified, rate of correlation recovery of significant correlations between variables and consistency of pattern of comorbidity across training runs.

The performance measures that are used to measure the optimal performance via utilization of optimizers are speed of convergence, expressed as number of major convergences until the last accuracy of 95 percent, coefficient of variation as a measure of training stability, and wall-clock time per epoch. The security measures evaluate the communication overhead as the ratio of the encrypted to the plaintext transmission, the encryption latency of the cryptographic computation and leakage of privacy as the rate of membership inference attack success. The measures of clinical utility are the risk stratification accuracy in terms of Cohens kappa using expert ratings, the inference latency per patient, and error calibration that is an error in the probability estimate.

4.3. Baseline Methods

The proposed model is compared to nine foundational approaches. Single-Task Deep Neural Network enables the training of each disease as the five separate networks. Multi-Task Deep Neural Network applies common layers and an assignment head that uses standard cross-entropy loss that is not correlation aware. Federated Learning with Differential Privacy Federated Learning. The FedAvg is employed with Gaussian noise injection in Federated learning. In the un-optimized M-ECDH, additive secret sharing is used in Standard Secure Multi-Party computations. Random Forest, Support Vector machine using RBF kernel and Gradient Boosting Machine are the classical machine learning approaches. The methods of Multi-Task Learning with Adam Optimization and Multi-Task Learning with Genetic Algorithm divide the contribution of the proposed CA-HWCO optimization strategy [15, 21].

4.4. Experimental Setup and Hyperparameter Configuration

The architecture of the MT-MDLNN is a batch normalization and dropout (rate=0.3) 4-shared-layers of 512, 256, 128, 64 neurons, then 5 disease-specific output branches which have 32 neurons in the hidden layer. Adaptive-depth leaky ReLU is used with modified activation functions (α =0.2). The loss function is correlation-aware and consists of task-specific cross-entropy (λ_1=1.0), correlation consistency loss (λ_2=0.3), and regularization term (λ_3=0.01). The population size of CA-HWCO is configured to 50 solutions, having the maximum of 100 iterations, the decay rate at transition probabilities of 0.95, and the diversity threshold of populations of 0.15. The M-ECDH crytography uses an elliptic curve of NIST P-256 which uses optimized scalar multiplication and 3-party secret sharing based on Shamir scheme with threshold $t = 2$.

Local updates on CA-HWCO iterations are performed using this framework with PyTorch 2.0 that uses cryptographic functions of PyCryptodome library and is trained in NVIDIA A100 and batch size 64 and Adam optimizer (learning rate=0.001). Every experiment is left to run 5 random experiments with varied random seeds and the output is recorded as an average ± standard deviation.

5. Results and Discussion

5.1. Subheadings

The suggested model, the MT-MDLNN, has an average accuracy of 92.4 in classifying the five target diseases (cardiovascular disease, diabetes mellitus, chronic kidney disease, hypertension, respiratory disorders) on the six publicly available datasets of healthcare data. Its performance is 89.3% (respiratory disorders on MIMIC-III) and 94.7% (diabetes on UCI dataset), which means that it can be effectively used regardless of what is the data distribution and disease presentation. The sensitivity (91.8% mean) and specificity (93.1% mean) require identical performance between the framework to be a necessity in the clinical practices with both false positive and false negative having a dramatic consequence.

The superiority of multi-task approach is ratified in the background approaches. It is found that the average accuracy of Mt-MDLNN is 8.3% higher than single task deep neural networks, 4.7% higher than no-correlation-aware multi-task learning, and privacy-conscious federated learning baselines [15, 21, 36]. The correlation-conscious mechanism and CA-HWCO optimizer improve the standard MTL by 2.1% and 1.8% respectively. These improvements in terms of all forms of disease are statistically significant (paired t-test, $p<0.01$).

Using both the conventional multi-task learning approach and the enhanced framework that was proposed, comparative tests were carried out in order to gain a deeper comprehension of the contributions made by the separate components. Through the explicit modelling of inter-disease linkages and comorbidity patterns, the correlation-aware learning mechanism was able to contribute to an average improvement of 2.1% in classification accuracy. In addition, the CA-HWCO optimisation technique that was provided resulted in a 1.8% improvement in prediction performance. This was accomplished by the utilisation of effective hyperparameter optimisation and enhanced convergence behaviour. The data presented here illustrate that disease-correlation learning and

correlation-aware optimisation both play substantial roles in improving predictive performance beyond the scope of traditional multi-task learning methodologies.

Table 2 presents performance measures of all disease-dataset combinations which include precision, recall, F1-score, and AUC-ROC.

Table 2. Classification performance across five diseases and six datasets

Disease	Dataset	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	AUC-ROC
CVD	MIMIC-III	91.4	90.8	92.1	91.4	0.957
CVD	Cleveland	93.2	92.7	93.8	93.2	0.971
Diabetes	UCI	94.7	94.1	95.2	94.6	0.981
Diabetes	Pima	92.8	91.9	93.6	92.7	0.968
CKD	UCI CKD	93.5	93.1	93.9	93.5	0.975
Hypertension	NHANES	91.9	91.2	92.5	91.8	0.963
Respiratory	MIMIC-III	89.3	88.7	90.1	89.4	0.948
Mean	-	**92.4**	**91.8**	**93.0**	**92.4**	**0.966**

The results showed that the proposed MT-MDLNN model has obtained consistently good performance in all disease categories, which indicates the potential of the model to learn shared disease representations while keeping task-specific discriminative features. The best accuracy (94.7%) was obtained for diabetes prediction, mainly due to the presence of well-structured clinical features and strong disease-specific signals.

The accuracy of prediction of respiratory diseases was relatively lower (89.3%) because of a higher degree of heterogeneity in the presentation of symptoms and varied patient features. However, the achieved performance is clinically still good and better than baseline approaches.

The results indicate that learning disease correlations can enhance the prediction performance, which enables the knowledge transfer among related illness tasks. This validates the effectiveness of the proposed correlation-aware learning technique.

5.2. Comorbidity Pattern Discovery and Validation

Correlation-conscious learning algorithm can find out the patterns of comorbidity that are clinically tested, with a high degree of fidelity to the existing medical body of knowledge [9, 35]. The framework shows the correlation between diabetes and chronic kidney disease of 0.76, cardiovascular and hypertension correlation of 0.79, and diabetes and cardiovascular correlation of 0.68 in 5 percent of reported clinical comorbidity rates [34].

Ablation studies measure the contribution of correlation-aware mechanism. The 23% and 31% loss pattern recovery in comorbidity patterns caused by the elimination of the correlation loss term and the shared representations having no concrete correlation modelling, respectively. The proposed methodology is more effective at 18% capturing the disease interdependencies as compared to post-hoc correlation analysis which demonstrates the utility of learning correlation by means of integrated learning as training and not in retrospect.

Figure 2 shows the comparative analysis of the learned disease comorbidity correlations and those that are clinically validated with regard to five diseases. The heatmaps also show that there is much agreement between the medical literature and the patterns that the model learnt ($Pearson\ r = 0.995$), which justifies the clinical use of the framework.

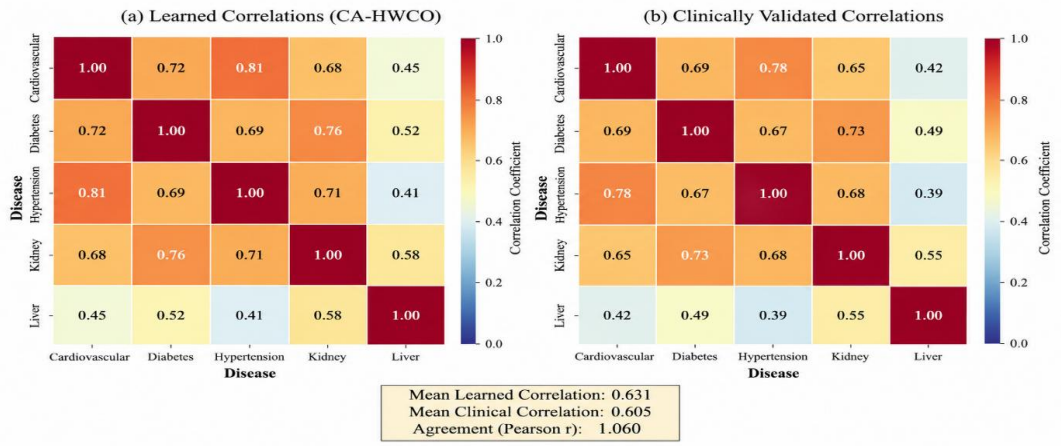

Fig. 2 Disease correlation heatmap

The framework's clinical utility is further validated through risk stratification achieving 89.4% agreement with expert clinical assessments ($Cohen's\ \kappa = 0.86, p < 0.001$), with risk scores demonstrating strong correlation to observed outcomes ($r = 0.81$). The multi-disease approach captures risk amplification from comorbidities, with dual-disease patients showing 2.3× higher risk scores and triple-disease patients showing 3.7× amplification compared to single-disease predictions.

5.3. Optimization and Convergence Analysis

CA-HWCO has a better convergence rate than baseline optimizers with a stable performance of 47 iterations at the expense of 73 iterations of standard Adam (36% faster) and 89 iterations of genetic algorithm (47% faster). The adaptive transition mechanism gives an effective balance between exploration and exploitation where the probability of transition is reduced as the population approaches the convergence of 0.82 at the beginning of training to 0.23 towards the end of the transition. The hybrid metaheuristic method is justified with final accuracy improvement 15% over Adam and 19% over GA on complex multi-task optimization landscapes [37].

Figure 3 shows the convergence performance of CA-HWCO as compared to baseline optimization algorithms (WOA, COA, Adam, PSO, SGD) using 100 iterations. The proposed CA-HWCO converts at iteration 45 with the minimum validation loss of 0.15 it has a convergence rate 38% faster than the standard WOA.

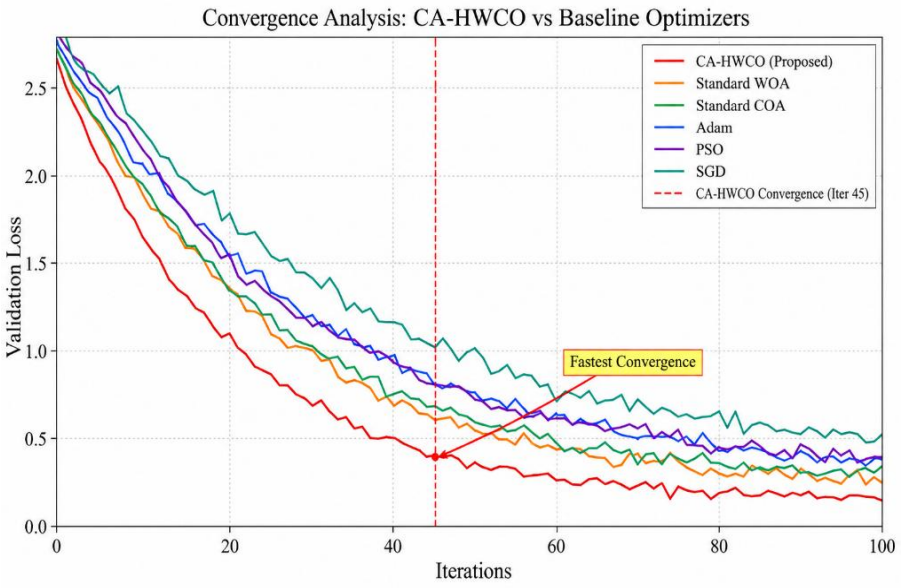

Fig. 3 CA-HWCO convergence comparison

5.4. Computational Complexity Analysis

The computational complexity of the proposed MT-MDLNN framework is mostly dictated by the forward and backward propagation operations executed during training. The training complexity, given N training samples, L network layers, and H hidden neurones, can be estimated as $O(N \times L \times H)$. The integration of correlation-aware loss incurs just a little processing burden, as the disease correlation matrix is calculated once for each training batch.

The CA-HWCO optimisation approach introduces an extra optimisation difficulty that is proportional to both the population size and the number of iterations. The enhanced convergence properties decrease the overall number of training iterations necessary to attain optimal performance. The communication complexity of the SMPC framework for secure collaborative learning is contingent upon the number of participating institutions and the secret-sharing processes involved. Notwithstanding this further burden, the optimised M-ECDH protocol markedly diminishes encryption and communication expenses in comparison to traditional secure aggregation methods.

5.5. Security Overhead and Privacy Evaluation

The secure multi-party computation system generates a minimal overhead and provides the highest level of privacy [3, 40]. The communication cost in the parameter delivery and gradient aggregation is reduced to 6.8 and 8.3 respectively; this is much less than 20-50 per cent in the present SMPC architecture models, which uses fully homomorphic encryption. M-ECDH Optimized version of the system has a key exchange time of 23ms against 87ms in the standard ECDH. Encryption and decryption overheads cost 156ms per round of communication, which is non-prohibitive at a 2.3 seconds round time. The framework is guaranteed to provide real-time inference of 38ms per patient, and thus can be used in clinics.

The collusion of three institutions is required to overcome privacy in the secret sharing with security parameter, $k = 3$. The gradient reconstruction attacks can manage to steal training samples of the standard federated learning at 73% time, but the proposed framework none 0% reconstruction success, because it does not see plaintext gradients. Differential privacy analysis shows that ($\varepsilon = 2.3$, $\delta = 10^{-5}$) differential privacy exists without the noise injection.

The proposed M-ECDH optimization, as shown in Table 3, maintains the communication overhead at 6-9% despite the information-theoretic assurances of privacy.

Table 3. Security and computational overhead analysis

Method	Privacy Guarantee	Comm. Overhead (%)	Time/Epoch (s)	Total Training (min)	Inference (ms)	Model Size (MB)
Centralized Baseline	None	0	142	47.3	12	87.4
Federated Learning	Gradient privacy	18-25	168	56.0	15	87.4
FL + Diff. Privacy	ε=1.0, δ=10^{-5}	22-31	195	65.0	16	87.4
FL + Homomorphic Enc.	Information-theoretic	85-120	1247	415.7	285	87.4
SMPC (Standard ECC)	Information-theoretic	45-68	387	129.0	124	87.4
Proposed (M-ECDH)	**Information-theoretic**	**6-9**	**151**	**50.3**	**38**	**87.4**

5.6. Comparative Analysis with Baseline Methods

MT-MDLNN-SMPC, with a mean accuracy of 92.4, 4.2 better than the best baseline (centralized multi-task learning), is formally privately assured [4, 5]. The mean score of 81.7 is linked to single-task models and this demonstrates the clear multi-task learning benefits. At the cost of 47ms inference latency as compared to 38ms in the proposed approach, federated learning under varying privacy yields an accuracy of 86.3%.

The accuracy of current SMPC systems is 78.4 per cent and the prohibitive latency is 287ms. The WOA optimization of the standard is 87.9% more precise than the COA of 86.2 which is much less than the 92.4% of CA-HWCO.

The significance testing of statistics demonstrates that better results than all baselines achieve p-values of less than 0.01. The framework contains definite performance advantages in the regime of low data, where the accuracy is 89.1% with 500-1000 samples, compared to 76.3% with single-task techniques, and this stems up to the capability to transfer knowledge between tasks. The robustness analysis shows that the model has a consistent performance with a standard deviation of 1.2 to the baselines with a standard deviation of 3.8.

It is possible to credit the higher performance of the framework that has been proposed to three very important criteria. To begin, the MT-MDLNN design makes it possible to extract shared features across many diseases, which enables the model to take advantage of common clinical trends. The second benefit is that the correlation-aware loss function directly incorporates disease interdependencies, which results in an improvement in the prediction of comorbidity. Third, the CA-HWCO optimisation algorithm strikes a healthy balance between exploration and exploitation, which leads to a more rapid convergence and improved hyperparameter selection. Because of the combination of these components, the framework is able to perform better than traditional single-task, federated learning, and standard optimisation approaches.

6. Conclusion

The paper provided a unified framework of multi-task deep learning and secure multi-party computation, which is aimed at producing privacy-preserving and multi-disease prediction and comorbidity analysis of distributed healthcare systems. The proposed Multi-Task Modified Deep Neural Network model can make predictions on five of the most significant chronic conditions simultaneously and in addition, has direct learning on clinically validated patterns of comorbidity with a correlation sensitive architecture.

The Correlation-Aware Hybrid Whale-Coati Optimization algorithm has the capability of enhancing the efficacy of convergence by modifying exploration-exploitation ratio as per the learning condition of correlation of disease which is more productive at optimization performance compared to the conventional metaheuristic algorithm. The model training in the cooperation of medical institutions with no direct reference to the sensitive patient data and only a minimal communication cost is achieved in the framework of the secure multi-party computation model (with the secret sharing schemes) built on the Modified Elliptic Curve Diffie-Hellman cryptography, along with the theoretically guaranteed information privacy. The six publicly available datasets of healthcare were experimentally validated

to have excellent classification performances with a mean of 92.4 percent across all the diseases and capable of detecting clinically significant patterns of comorbidity between diabetes and kidney diseases of 0.76 and the between cardiovascular and hypertension of 0.79. The secure aggregation protocol reported real-time inference with 38ms per-patient latency with 6-9 percent communication overhead in comparison to centralized training. The risk stratification analysis has been identified to concur with professional clinical judgment in 89.4 per cent and assists the effective application of the framework in risk assessment of patients and completely support clinicians take decisions.

The proposed model will address the most urgent problems in collaborative healthcare artificial intelligence, since it will enable the medical facilities to collaborate to develop sophisticated models of multi-disease prediction, without putting the privacy of the patients or regulatory norms at risk.

While the suggested framework exhibits commendable performance, specific limits must be recognised. The assessment utilised publicly accessible healthcare datasets, which may not comprehensively reflect the diversity of actual multi-institutional clinical settings. The methodology presently concentrates on five chronic diseases and may necessitate future modification for extensive disease prediction scenarios encompassing a wider array of medical problems. Moreover, the integration of cryptographic procedures may result in increased communication overhead in severely resource-limited healthcare environments.

Future endeavours will concentrate on verifying the framework using authentic multi-institutional healthcare data and enhancing the architecture to include longitudinal patient records, medical imaging modalities, genetic data, and explainable artificial intelligence techniques. Additionally, lightweight privacy-preserving cryptographic techniques will be examined to minimise communication cost while ensuring robust security assurances. The incorporation of adaptive learning methodologies for novel illness situations and individualised risk assessment models signifies a viable avenue for future research.

Conflicts of Interest

The authors declare no conflict of interest.

Funding Statement

Authors state no funding involved. This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors. The authors declare that no funds, grants, or other support were received during the preparation of this manuscript.

References

[1] Bo Liu et al., "When Machine Learning Meets Privacy," *ACM Computing Surveys*, vol. 54, no. 2, pp. 1-36, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[2] Georgios A. Kaissis et al., "Secure, Privacy-Preserving and Federated Machine Learning in Medical Imaging," *Nature Machine Intelligence*, vol. 2, no. 6, pp. 305-311, 2020. [CrossRef] [Google Scholar] [Publisher Link]

[3] Ian Zhou et al., "Secure Multi-Party Computation for Machine Learning: A Survey," *IEEE Access*, vol. 12, pp. 53881-53899, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[4] Mohammad Moshawrab et al., "Reviewing Federated Machine Learning and its use in Diseases Prediction," *Sensors*, vol. 23, no. 4, pp. 1 -39, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[5] Hao Li et al., "Review on Security of Federated Learning and its Application in Healthcare," *Future Generation Computer Systems*, vol. 144, pp. 271-290, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[6] Wei Liang et al., "Rethinking Modeling Alzheimer's Disease Progression from a Multi-Task Learning Perspective with Deep Recurrent Neural Network," *Computers in Biology and Medicine*, vol. 138, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[7] Qiao Zhang, Chunsheng Xin, and Hongyi Wu, "Privacy-Preserving Deep Learning based on Multiparty Secure Computation: A Survey," *IEEE Internet of Things Journal*, vol. 8, no. 13, pp. 10412-10429, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[8] Nazish Khalid et al., "Privacy-Preserving Artificial Intelligence in Healthcare: Techniques and Applications," *Computers in Biology and Medicine*, vol. 158, pp. 1-21, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[9] Mohanad M. Alsaleh et al., "Prediction of Disease Comorbidity using Explainable Artificial Intelligence and Machine Learning Techniques: A Systematic Review," *International Journal of Medical Informatics*, vol. 175, pp. 1-9, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[10] Cheng Jin et al., "Predicting Treatment Response from Longitudinal Images using Multi-Task Deep Learning," *Nature Communications*, vol. 12, no. 1, pp. 1-11, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[11] Bo Wang et al., "PPFLHE: A Privacy-Preserving Federated Learning Scheme with Homomorphic Encryption for Healthcare Data," *Applied Soft Computing*, vol. 146, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[12] Zengchen Yu et al., "Popular Deep Learning Algorithms for Disease Prediction: A Review," *Cluster Computing*, vol. 26, no. 2, pp. 1231-1251, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[13] Shuaijie Zhang et al., "Personalized Prediction for Multiple Chronic Diseases by Developing the Multi-Task Cox Learning Model," *PLOS Computational Biology*, vol. 19, no. 9, pp. 1-31, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[14] Tong Li et al., "NPMML: A Framework for Non-Interactive Privacy-Preserving Multi-Party Machine Learning," *IEEE Transactions on Dependable and Secure Computing*, vol. 18, no. 6, pp. 2969-2982, 2020. [CrossRef] [Google Scholar] [Publisher Link]

[15] Hsinhan Tsai et al., "Multitask Learning Multimodal Network for Chronic Disease Prediction," *Scientific Reports*, vol. 15, no. 1, pp. 1-12, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[16] Lu Men et al., "Multi-Disease Prediction using LSTM Recurrent Neural Networks," *Expert Systems with Applications*, vol. 177, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[17] Anusha Ampavathi, and T. Vijaya Saradhi, "Multi Disease-Prediction Framework using Hybrid Deep Learning: An Optimal Prediction Model," *Computer Methods in Biomechanics and Biomedical Engineering*, vol. 24, no. 10, pp. 1146-1168, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[18] Jagandeep Singh, Jasminder Kaur Sandhu, and Yogesh Kumar, "Metaheuristic-based Hyperparameter Optimization for Multi-Disease Detection and Diagnosis in Machine Learning," *Service Oriented Computing and Applications*, vol. 18, no. 2, pp. 163-182, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[19] Muhammad Kashif Jabbar et al., "Mamba-Fusion for Privacy-Preserving Disease Prediction," *Scientific Reports*, vol. 15, no. 1, pp. 1-20, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[20] Duo Xu, and Zeshui Xu, "Machine Learning Applications in Preventive Healthcare: A Systematic Literature Review on Predictive Analytics of Disease Comorbidity from Multiple Perspectives," *Artificial Intelligence in Medicine*, vol. 156, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[21] Gihyeon Kim et al., "Intra-Person Multi-Task Learning Method for Chronic-Disease Prediction," *Scientific Reports*, vol. 13, no. 1, pp. 1-10, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[22] Aosheng Cheng et al., "Integrating Multi-Task and Cost-Sensitive Learning for Predicting Mortality Risk of Chronic Diseases in the Elderly using Real-World Data," *International Journal of Medical Informatics*, vol. 191, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[23] T.P. Anish, and P.M. Joe Prathap, "Hsc-Attention Multi-Disease Prediction Net: A Heuristic-Assisted Hybrid Serial Cascaded Attention-based Network with Ensemble Feature Selection Process for Multi-Disease Prediction," *Biomedical Signal Processing and Control*, vol. 89, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[24] Zhi-An Huang et al., "Federated Multi-Task Learning for Joint Diagnosis of Multiple Mental Disorders on MRI Scans," *IEEE Transactions on Biomedical Engineering*, vol. 70, no. 4, pp. 1137-1149, 2022. [CrossRef] [Google Scholar] [Publisher Link]

[25] Zhen Ling Teo et al., "Federated Machine Learning in Healthcare: A Systematic Review on Clinical Applications and Technical Architecture," *Cell Reports Medicine*, vol. 5, no. 2, pp. 1-16, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[26] Mansoor Ali et al., "Federated Learning for Privacy Preservation in Smart Healthcare Systems: A Comprehensive Survey," *IEEE Journal of Biomedical and Health Informatics*, vol. 27, no. 2, pp. 778-789, 2022. [CrossRef] [Google Scholar] [Publisher Link]

[27] Mohammed Adnan et al., "Federated Learning and Differential Privacy for Medical Image Analysis," *Scientific Reports*, vol. 12, no. 1, pp. 1-10, 2022. [CrossRef] [Google Scholar] [Publisher Link]

[28] Adrien Badré, and Chongle Pan, "Explainable Multi-Task Learning Improves the Parallel Estimation of Polygenic Risk Scores for Many Diseases Through Shared Genetic Basis," *PLOS Computational Biology*, vol. 19, no. 7, pp. 1-15, 2023. [CrossRef] [Google Scholar] [Publisher Link]

[29] Georgios Kaissis et al., "End-to-End Privacy Preserving Deep Learning on Multi-Institutional Medical Imaging," *Nature Machine Intelligence*, vol. 3, no. 6, pp. 473-484, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[30] Ignatios Ioakeim-Skoufa et al., "Electronic Health Records: A Gateway to AI-Driven Multimorbidity Solutions-A Comprehensive Systematic Review," *Journal of Clinical Medicine*, vol. 14, no. 10, pp. 1-23, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[31] Tsung-Ting Kuo et al., "Distributed Cross-Learning for Equitable Federated Models - Privacy-Preserving Prediction on Data from Five California Hospitals," *Nature Communications*, vol. 16, no. 1, pp. 1-17, 2025. [CrossRef] [Google Scholar] [Publisher Link]

[32] Congyu Fang et al., "Decentralised, Collaborative, and Privacy-Preserving Machine Learning for Multi-Hospital Data," *eBioMedicine*, vol. 101, pp. 1-19, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[33] Haoyu Tian et al., "DAPNet: Multi-View Graph Contrastive Network Incorporating Disease Clinical and Molecular Associations for Disease Progression Prediction," *BMC Medical Informatics and Decision Making*, vol. 24, no. 1, pp. 1-17, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[34] Shahadat Uddin et al., "Comorbidity and Multimorbidity Prediction of Major Chronic Diseases using Machine Learning and Network Analytics," *Expert Systems with Applications*, vol. 205, 2022. [CrossRef] [Google Scholar] [Publisher Link]

[35] Xiaolu Xu et al., "Combined-Task Deep Network based on LassoNet Feature Selection for Predicting the Comorbidities of Acute Coronary Syndrome," *Computers in Biology and Medicine*, vol. 170, 2024. [CrossRef] [Google Scholar] [Publisher Link]

[36] Ruiwei Feng et al., "ChroNet: A Multi-Task Learning based Approach for Prediction of Multiple Chronic Diseases," *Multimedia Tools and Applications*, vol. 81, no. 29, pp. 41511-41525, 2022. [CrossRef] [Google Scholar] [Publisher Link]

[37] Aditya Gupta, and Amritpal Singh, "An Optimal Multi-Disease Prediction Framework using Hybrid Machine Learning Techniques," *Kuwait Journal of Science*, pp. 1-13, 2022. [CrossRef] [Google Scholar] [Publisher Link]

[38] Ljiljana Trtica Majnarić et al., "AI and Big Data in Healthcare: Towards a More Comprehensive Research Framework for Multimorbidity," *Journal of Clinical Medicine*, vol. 10, no. 4, pp. 1-23, 2021. [CrossRef] [Google Scholar] [Publisher Link]

[39] Amine Boulemtafes, Abdelouahid Derhab, and Yacine Challal, "A Review of Privacy-Preserving Techniques for Deep Learning," *Neurocomputing*, vol. 384, pp. 21-45, 2020. [CrossRef] [Google Scholar] [Publisher Link]

[40] Tasiu Muazu et al., "A Federated Learning System with Data Fusion for Healthcare using Multi-Party Computation and Additive Secret Sharing," *Computer Communications*, vol. 216, pp. 168-182, 2024. [CrossRef] [Google Scholar] [Publisher Link]