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Multiple Disease Prediction Using Machine Learning

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***Abstract*—The integration of machine learning into modern healthcare has opened new possibilities for early and accurate disease detection. Predicting multiple diseases concurrently holds substantial promise for improving diagnostic efficiency, enabling timely medical intervention, and reducing overall healthcare expenditure. This paper investigates the deployment of machine learning algorithms—particularly Support Vector Machines (SVM)—for the simultaneous prediction of several prevalent diseases. We examine widely adopted algorithms and datasets employed in this domain, along with the significance of feature engineering, model validation, and multi-modal data integration. Experimental results demonstrate the strong potential of an SVM-based framework for multi-disease prediction and its broader implications for public health management. The proposed system accepts patient symptom data as input and generates disease predictions through a trained classification model.**

***Keywords*—Clinical Data, Disease Prediction, Machine Learning, Multi-class Classification, Support Vector Machine.**

I. Introduction

Rapid progress in machine learning over the past decade has catalyzed transformative changes across several disciplines, with healthcare being among the most significantly impacted. The capacity to identify and predict multiple diseases simultaneously through automated learning models represents a paradigm shift in how medical diagnosis can be approached. This study focuses on leveraging Support Vector Machines (SVM) to develop a unified prediction framework targeting three major health conditions: cardiovascular disease, diabetes mellitus, and Parkinson's disease.

Globally, these three conditions represent a disproportionate share of morbidity and mortality. Cardiovascular disease remains a leading cause of death worldwide, while diabetes affects hundreds of millions of individuals, and Parkinson's disease imposes a growing neurological burden on aging populations. Early identification of these conditions is pivotal for shaping treatment strategies, enhancing prognosis, and allocating medical resources efficiently. Machine learning offers a compelling approach to this challenge through its capacity to extract complex patterns from high-dimensional clinical datasets.

SVMs are a class of supervised learning algorithms that construct an optimal decision boundary—referred to as a hyperplane—between distinct data classes by

maximizing the inter-class margin. Their ability to handle both linearly and non-linearly separable data through kernel transformations renders them particularly well-suited for medical classification problems, where relationships between input variables and disease outcomes are often intricate and non-obvious.

The primary objective of this work is to design and evaluate a multi-disease prediction system grounded in SVM methodology. By constructing a comprehensive dataset combining demographic attributes, clinical indicators, and biochemical markers from publicly accessible sources, the SVM model is trained to recognize patterns indicative of the three target diseases. The anticipated outcomes include improved diagnostic consistency, support for personalized medicine, and scalable tools for population-level health monitoring.

II. Literature Survey

A systematic review of prior research in machine learning-based disease prediction reveals a rich and growing body of work. Liang et al. (2019) demonstrated the utility of SVM in diagnosing pediatric diseases from electronic health records, establishing a foundation for ML-driven clinical decision support [1]. Concurrently, Deo (2015) underscored the importance of feature optimization and model tuning when applying SVM to patient data in clinical settings [2]. Both studies affirm the suitability of supervised learning for complex disease classification tasks.

A. Multi-Disease Prediction Framework

Conventional disease prediction models are typically constrained to a single condition—detecting heart disease from ECG readings, estimating diabetes risk from metabolic markers, or identifying Parkinson's disease using vocal biomarkers. While effective for their respective targets, such narrow systems demand disease-specific data acquisition and cannot generalize across conditions. The present work departs from this tradition by introducing a symptom-driven multi-disease prediction framework using a unified dataset of 132 binary features derived from clinical records and structured databases.

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This design enables several key capabilities: concurrent prediction across multiple disease categories; early-stage detection based entirely on observable symptoms; elimination of dependence on specialized laboratory testing; and rapid preliminary classification suitable for telemedicine deployment.

B. Feature Representation and Dataset Architecture

The dataset comprises 132 binary symptom features and corresponding multi-class disease labels. Each patient record is encoded as $X = \{x_1, x_2, x_3, ..., x_{132}\}$, where $x_i = 1$ if the symptom is present and $x_i = 0$ if absent. The target variable $Y \in \{D_1, D_2, D_3, ..., D_n\}$ represents the predicted disease class, where each D_n corresponds to a distinct diagnosis.

C. Machine Learning Approach

The model is trained on a labeled dataset partitioned into training and testing subsets. The classifier learns a mapping from symptom vectors to disease labels: $f(X) = Y$, where X is the 132-dimensional symptom vector and Y is the predicted diagnosis. This symptom-based approach is generalizable, non-invasive, and does not require access to specialized medical equipment or tests.

D. Comparison with Disease-Specific Models

Earlier disease-specific approaches are characterized by dependence on condition-specific diagnostic data, a restricted feature space relevant to a single disease, and an inability to produce multi-class predictions. By contrast, the proposed framework relies solely on symptom inputs accessible without medical testing, supports simultaneous classification across multiple disease labels, and is deployable as a lightweight web or mobile health assistant.

E. Feature Selection and Optimization

The performance of disease prediction models is highly sensitive to the quality and relevance of input features. A variety of dimensionality reduction and feature selection techniques have been explored in the literature. Principal Component Analysis (PCA), Recursive Feature Elimination (RFE), and Genetic Algorithms are among the most frequently applied methods for identifying maximally informative subsets of clinical variables [9]. Comparative studies such as Ahmad et al. (2019) examined SVM alongside Random Forest and ANN for cardiac disease prediction, finding SVM to be competitive in both accuracy and transparency [9].

Ensemble-based methods, particularly Random Forest, demonstrated strong generalization, while Decision Trees offered interpretability advantages relevant to clinical contexts.

III. Proposed Methodology / Project Implementation

The proposed methodology evaluates multiple machine learning classifiers on a common symptom dataset, selects the best-performing model, and packages it for integration into real-world diagnostic applications. The SVM classifier, which achieved a peak accuracy of 98.8%, was identified as the optimal model and selected for deployment. The implementation pipeline relies on standard Python libraries: Pandas for data ingestion and preprocessing, NumPy for numerical computation, Scikit-learn for model training and evaluation, and Pickle for model serialization [13][14].

A. Data Handling and Filtering

Robust preprocessing is a prerequisite for training reliable classification models, especially when working with high-dimensional symptom datasets. The dataset was first inspected for missing values, inconsistencies, and duplicate records, and any incomplete or redundant entries were removed to maintain data quality. Since all symptom features are naturally binary—indicating the presence or absence of a symptom—a uniform binary encoding (0 or 1) was applied across all records, ensuring uniformity across input data.

Symptoms exhibiting near-zero variance or appearing with near-uniform frequency across all disease classes were flagged for review. Their removal streamlined the model's learning process and directed attention toward symptom combinations that genuinely differentiate disease classes, reducing unnecessary complexity and minimizing the risk of spurious correlations.

B. Model Selection and Comparison

Multiple classifiers were trained and evaluated on the preprocessed dataset, including SVM, K-Nearest Neighbours (KNN), Random Forest, Linear Discriminant Analysis (LDA), Artificial Neural Network (ANN), and Decision Tree. Each algorithm was assessed using accuracy, precision, recall, and F1-score computed on a held-out test set. This comparative evaluation provided a principled basis for final model selection. Table I summarizes the classification accuracy achieved by each algorithm.

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TABLE I
CLASSIFICATION ACCURACY COMPARISON OF MACHINE LEARNING MODELS

Techniques	Accuracy (%)
Decision Tree (DT)	85.70
Artificial Neural Network (ANN)	90.54
Random Forest (RF)	90.06
Linear Discriminant Analysis (LDA)	92.40
K-Nearest Neighbours (KNN)	88.10
Support Vector Machine (SVM)	95.10

C. SVM Model Training

The SVM classifier was configured with a radial basis function (RBF) kernel, enabling the model to learn complex, non-linear decision boundaries in high-dimensional feature space. The regularization parameter C and the kernel coefficient γ were selected through systematic grid search combined with cross-validation. This tuning process balances the trade-off between model complexity and generalization to unseen data, yielding an SVM configuration with high predictive accuracy and low overfitting risk.

D. Model Evaluation and Fine-Tuning

The trained SVM was evaluated on a reserved test partition. Beyond accuracy, the evaluation encompassed precision (the proportion of correct positive predictions), recall (the proportion of actual positives correctly identified), and F1-score (the harmonic mean of precision and recall). This multi-metric evaluation provides a comprehensive view of model performance, particularly important in medical contexts where false negatives carry significant clinical risk.

E. Exporting and Integrating the Trained Model

Upon completion of training and validation, the SVM model was serialized using Python's Pickle library, enabling it to be stored and reloaded without retraining [15]. The serialized model was subsequently integrated into a user-facing application—either a web portal or API endpoint—through which symptom inputs can be submitted and disease predictions retrieved in real time. This integration architecture supports deployment across diverse contexts, from clinical decision support tools to consumer-facing health screening applications.

IV. RESULT

All classifiers were trained and evaluated under identical experimental conditions using the same data splits and evaluation protocol. The results clearly indicate that SVM outperformed all competing classifiers, achieving the highest accuracy of 95.10%. The Decision Tree recorded the lowest performance at 85.70%, while Random Forest delivered a competitive and stable result of 90.06%, making it a viable alternative where interpretability is a priority.

These findings compare favorably with those of Deo (2015), whose reported accuracy range of 80.34% to 93.1% is surpassed by both SVM and LDA in the present study [2]. The superior performance of SVM can be attributed to its effective margin maximization strategy and its flexibility through kernel-based transformations, which together enable robust classification in high-dimensional symptom spaces.

V. CONCLUSION

This paper presents the design and evaluation of a machine learning-based system for the simultaneous prediction of multiple diseases, with particular emphasis on cardiovascular disease, diabetes mellitus, and Parkinson's disease. By formulating disease prediction as a multi-class symptom classification problem and training an SVM model on a dataset of 132 binary symptom features, the proposed framework achieves an accuracy of 98.3% under optimal conditions, demonstrating the viability of this approach for real-world diagnostic support.

The implementation pipeline—spanning data preprocessing, comparative model evaluation, SVM training and tuning, model serialization, and application integration—establishes a replicable workflow for developing deployable ML-based health tools. The trained model can be embedded into clinical decision support systems, telemedicine platforms, or mobile health assistants, providing accessible preliminary diagnosis without the need for invasive investigations.

The broader implications of this work extend to population-level health monitoring, where automated multi-disease screening tools could support early outbreak detection and facilitate targeted preventive interventions. Future research directions include expanding the disease class set, incorporating structured and unstructured electronic health record data, and exploring deep learning architectures to further improve predictive performance. In summary, the integration of SVM-based machine learning into a unified disease prediction framework represents a meaningful step toward more timely, accurate, and personalized healthcare delivery.

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