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Mutiple Disease Detection using Machine Learning

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Abstract:

Effective detection of illnesses is an influential unmet need absent from a global scale. A rise of early diagnosis tools and a successful therapy options has been seriously compromised by the complexity of the different conditions mechanisms and underlying symptoms that impacted the patient population. A subfield of artificial intelligence called machine learning (ML) helps patients, doctors, and researchers find products to some of the aforementioned issues. This review provides an justification of Machine Learning (ML) based on studies that are relevant. For the purpose of improving patient outcomes and alleviating healthcare costs, swift detection and diagnosis of medical issues like diabetes, chronic kidney disease, liver disease, and breast cancer are essential. Machine learning have grown into a viable method for screening for and detecting chronic illnesses in recent years. We want that will assist with early disease diagnosis and treatment by creating a machine learning model for various disease belonging through this project. A significant set of data of medical records, ranging from patient demographics, medical histories, symptoms, and test findings for a diagnostic will be used to train the model that has been suggested. So excellent data quality and completeness, the dataset will be meticulously selected and preprocessed. Relevant nuances that was demonstrated to affect illness risk, such as genetic markers and decisions regarding one's lifestyle, will also be were present.

Keywords: Machine Learning, Decision tree, Adaboost , Xgboost and Catboost and ML techniques, evaluation.

Introduction:

Afresh developed technique designation "multiple disease detection" uses machine learning algorithms and intricate data analytics to find several diseases promptly.

the process of a examination of data from multiple accounts, incorporating imaging studies, laboratory tests, and electronic medical records (EMRs), this technology seeks providing comprehensive disease diagnostics, improving with the accuracy and efficacy of medical diagnoses [6][5]. Because the early detection might significantly enhance patient outcomes, this technology tends to be crucial chronic diseases with a value diabetes, chronic kidney disease, liver disease, and breast cancer [2][15].

If diabetes doesn't have a early on, it could arise in catastrophic repercussions. Diabetes is a persistent medical condition characterized by heightened levels of glucose in the bloodstream.Issues like kidney disease and blindness can be got away with early intervention [1]. In a similar vein, early detection of Chronic Kidney Disease can potentially halt the disease's course and avoid kidney failure [4]. As early detection can improve liver function and reduce damage to the liver, which is why liver disease, which stretches to an range of sickness that influences the liver, can be better handled [7]. When taken care of early, breast cancer, the most frequent cancer in women the world over, has a notably greater survival rate [12].

The consumption of Multiple Disease Detection technology helps health care providers treat folks to efficiently and swiftly in addition to improved a diagnostic test. This is vital when addressing prolonged medical conditions and cutting across healthcare prices [14][9]. More sophisticated devices for diagnosing and treating multiple diseases receive on behalf of new advancements in technology, for

the aging population where multifactorial diseases like chronic obstructive pulmonary disease and cancer are growing into more common [11][14]. The increasing comprehension of the link amongst multifactorial imperfections and cancer highlights the need for more study to make connection common lethal cycles, whose can bring about in his peers of fresh drugs that target multiple pathways [10][13].

Many research initiatives have greatly enhanced the specialty of machine learning's advancement of healthcare, especially while it comes to Multiple Disease Detection. As a story of the promise of such techniques in frustrating biological data analysis, the work of G. W. Bassel et al. [16] articulated the value of rule-based machine learning in creating functional networks, particularly in biological environments like Arabidopsis. Similarly, S. M. Weiss and N. Indurkhya [17] highlighted a range of these techniques in medical diagnostics prior to went over the details of the efficacy of rule-based machine learning for functional prediction.

Many research deals have greatly boosted the realm of machine learning's advancement of healthcare, particularly given it comes to Multiple Disease Detection. As a depiction of the promise of methods like in frustrating biological data analysis, the work of G. W. Bassel et al. [16] articulated the benefits of rule-based machine learning for creating functional networks, particularly in living things like Arabidopsis. Similarly, S. M. Weiss and N. Indurkhya [17] illustrated the broad spectrum of such practices in medical diagnostics prior to talked the details of the value of rule-based machine learning for functional prediction.

Additionally, a comprehensive overview to learning classifier systems was given by R. J. Urbanowicz and J. H. Moore [19], who contained a method that blends rule-based learning with evolutionary algorithms. An opportunity to cultivate ever more sophisticated diagnostic tools that can change and push in reaction in new material is illustrated by this integration.

L. N. Castro, L. N. D. Castro, and J. Timmis [20] pointed out an uprising computational intelligence approach during their concept of Artificial Immune Systems. This methodology offering a dynamic and a powerful framework for disease detection and categorization, engaging in inspiration from the biological immune system. Fuzzy logic concepts are used in a model presented by H. F. El-Sofany and I. A. T. F. Taj-Eddin [21] to improve the accuracy and flexibility of cloud-based medical diagnostics. That approach is especially pertinent to govern the murky waters and shifting that come with allowing medical conditions.

C. Shivade et al.'s work [22] talked about many of them of methods for with electronic health records to identify patient observable cohorts. This review signals how integral it is to accurately determine patient data in order to effectively detect and treat problems. R. Zhang et al. [23] originated automatic method of uncovering New York Heart Association classification in the field of clinical notes interpretation, proving the machine-learning capacity to understand and then create placement of unstructured clinical data.

L. S. Kumar and A. Padmapriya [24], through their research on rule-based information extraction from electronic health records, emphasized the importance of structured data processing in healthcare. Lastly, P. B. Jensen, L. J. Jensen, and S. Brunak [25] discussed the mining of electronic health records for research applications and clinical care, underscoring the vast potential of these data sources in revolutionizing healthcare through better research and improved clinical outcomes.

In aggregate, such investigations [16–25] argue how moves forward in multiple disease detection are promoted by a variety of multifaceted diverse approaches to machine learning and data analysis. There is a great deal of potential to increase accurateness, efficiency while and thoroughness of disorders diagnostics through utilizing these state-of-the which could grow care of patients and results.

Research and Background:

The article "Multiple Disease Detection (Diabetes, Chronic Kidney, Liver Disease, Breast Cancer)" suggests specializing research efforts for building techniques for the in accordance identification of multiple serious disorders related to health. Interdisciplinary methods fusing medical expertise with revolutionary products like bioinformatics, artificial intelligence, or innovative diagnostic tools have likely been utilized in this research. The objective is to develop effective, exact strategies for these diseases' identification at an early stage which is a must for that therapy is effective. An accurate diagnosis of frustrating diagnoses with severe medical effects, such as diabetes, chronic kidney disease, liver disease, and breast cancer, is a goal in medical research and healthcare.

2. Related works:

J Aravinth, R Karthika, S Sivaranjani, and S Ananya In the contemporary globe, diabetes [1] has emerged as one of the most frequent and potentially fatal illnesses, not just in India but generally as well. These days, diabetes affects people of anybody, and

their causes include aging, genetics, stress, and lifestyle choices. Whatever may be the true root of diabetes, if ignored, the consequences could be major. Several methodologies are currently in the works to predict diabetes and diseases caused by diabetes. The machine learning methods Support Vector Machine (SVM) and Random Forest (RF) was employed in the suggested work to help identify the potential risk of developing Diabetes Related Diseases.

Chronic kidney disease is a widespread non-contagious condition that affects a significant portion of the global population. Its primary risk factors include hypertension, diabetes, and heart disease. Most cases are detected only at an advanced stage, as the disease often presents no symptoms in its early phases. This causes the patient's treatment to be delayed, which could prove to fatal. The most efficient technique of foreseeing Chronic Kidney Disease in its earliest stage is the machine learning electronics. This investigation was presents an early stage discovery of Chronic Kidney Disease using four ensemble methods. Seven performance metrics—Accuracy, Sensitivity, Specificity, F1Score, and Mathew Correlation—are used for evaluating the machine learning models.

V. Vanitha; K. Meena; R. Kalaiselvi The liver, the main organ in humans, performs numerous vital functions such as producing plasma proteins, eliminating bile and bilirubin, metabolizing proteins and carbohydrates, activating enzymes, storing glycogen, vitamins, and minerals, and synthesizing clotting factors. Various factors like alcohol consumption, certain medications, specific foods, and other activities can harm the liver. Currently, medical professionals rely on liver function blood tests and scans to diagnose liver-related disorders. It is more significant and demands more time. The easiest way to speed up the diagnosis of liver illness is to use many different data mining techniques to make the practices easier.

Ganaga Rama Koteswara Rao; Apparna Allada One of the basics [4] origins of the disease's expanding worldwide is breast cancer. A quick diagnosis increases the likelihood of successful treatment and long-term results; nonetheless, this vicious cycle can be troubling and it often leads to disagreements amongst pathologists. PC supports the frameworks for determination that have the potential to improve the exactness of characteristics. Despite that, early notification and the production will entirely avoid loss. a majority of now on, the most significant thing is to catch breast cancer early. in addition the proposed research work has created a machine learning model that is trained using trademarks like radius, texture, area, perimeter, and concavity as well as smoothness, concaveness, and compactness.

Diabetes Dataset Description:

1. Pregnancies: This refers to the total number of pregnancies experienced by an individual.

2. Glucose: This is a test that measures the concentration of glucose in the blood over a two-hour period after consuming a glucose solution.

3. Blood Pressure: This is the measurement of the force exerted by the blood against the walls of the arteries, typically measured in millimeters of mercury (mm Hg).

4. Skinfold: This refers to the thickness of a fold of skin, specifically measured at the triceps area.

5. Insulin: This measures the concentration of insulin in the bloodstream, typically measured two hours after a meal.

6. Body Mass Index (BMI): This is a measure of body fat based on a person's weight and height.

7. DiabetesPedigreeFunction: This is a calculation based on family history that predicts the likelihood of developing diabetes.

8. Age: This refers to the number of years a person has been alive.

9. Outcome: This is a binary variable indicating the presence (1) or absence (0) of diabetes in the individual.

Breast Cancer Dataset Description:

The breast cancer dataset contains 569 rows and 32 columns. It totals characteristics that are the cell nuclei seen in the fine needle aspirate (FNA) portraits of a breast a growth. Fundamental features includes of:

1. ID: Identity theft code.
2. Diagnosis: Tissue of the breast is considered both benign or malignant (B = malignant).

3. Mean Features: These made up of fractal dimension, symmetry, recession, smoothness, compression, radius, the way it feels, perimeter, and area.
4. Standard Error Features: Standard error of the mean features.
5. Worst or Largest Features: The worst or largest value of these features among all observed nuclei.

In total, there are 30 features calculated for each cell nucleus, with a focus on capturing the shape, size, and texture characteristics.

Liver Dataset Description:

The Indian Liver Patient dataset contains 583 rows and 11 columns. It contains various clinical and demographic features for diagnosing liver diseases. Key features include:

1. Age: The patient's age.
2. Gender: The patient's gender (male or female).
3. Blood the bilirubin concentration have been assessed by direct and total bilirubin.
4. Alkaline Phosphotase: Enzyme in the liver.
5. Alamine Aminotransferase: An enzyme mostly found in the liver.
6. Aspartate Aminotransferase: Another enzyme found in the liver.
7. Total Proteins: The total amount of protein in the blood.
8. Albumin: A type of protein in the blood.
9. Albumin and Globulin Ratio: The ratio of albumin to globulin proteins in the blood.
10. Dataset: A binary variable indicating liver disease (1) or not (2).

Kidney Dataset Description:

The kidney disease dataset contains 400 rows and 26 columns. It contains medical and demographic features for diagnosing chronic kidney disease (CKD). Key features include:

1. Age, Blood Pressure: Basic demographic data.
2. Specific Gravity (sg), Albumin (al), Sugar (su): Urine test results.
3. Blood Urea, Serum Creatinine: Blood test results indicating kidney function.
4. Sodium, Potassium, Hemoglobin: Essential blood electrolytes and oxygencarrying capacity.
5. Patient history of hypertension (hTN), a diagnosis of diabetes (DM), and then coronary artery disease (CAD). Appetite (appet), Pedal Edema (pe), Anemia (ane): Symptoms and signs related to kidney disease.
6. Classification: Binary outcome indicating presence (ckd) or absence (notckd) of chronic kidney disease.

2. Methodology:

Proposed system:

The proposed system of multiple disease detection using machine learning involves the development of a model that can accurately detect the presence of four diseases - diabetes, chronic kidney disease, liver disease, and breast cancer - using patient data. The system is going to discuss patient data, including symptoms, laboratory test results, and medical history, integrating a wide variety of strategies for machine learning to find shifting patterns and indicate the probability of illness. The system will provide clinicians with accurate and timely information to improve patient outcomes, reduce costs, and optimize healthcare delivery. This will be accomplished through a user-friendly interface and integration with electronic medical records.

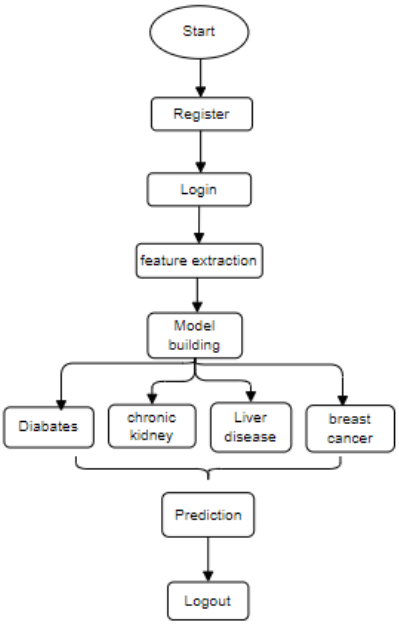


Fig. Block diagram

3. Implementation:

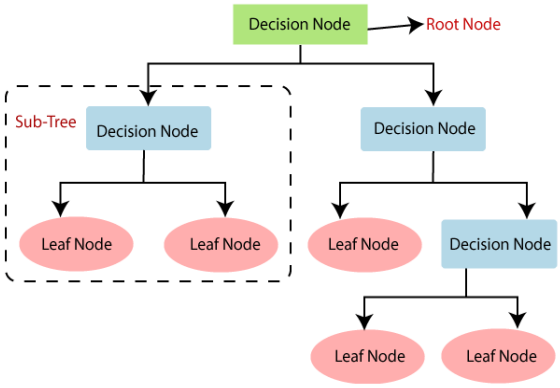
1. Decision Tree:

Decision trees are flexible machine learning algorithms employed for classification and regression duties, encompassing the identification of various diseases. They emulate the decision-making patterns of humans by segmenting data according to specific conditions, constructing a tree-like representation of choices.Each node in the tree represents a feature in the dataset, and each branch represents a decision rule. This structure makes them intuitive and easy to interpret. However, decision trees can easily overfit, especially with complex datasets, leading to poor generalization on unseen data unless they are pruned or limited in depth.

For classification tasks, such as in a Decision Tree, the Gini Impurity is a commonly used measure. The formula for the Gini Impurity for a binary classification is given by:

$$Gini = 1 - (p^2 + (1 - p)^2)$$

A lower Gini Impurity value indicates a lower chance of misclassification, guiding the decision tree to make optimal splits.



How Decision Tree Classifier Works :

1. Feature Selection: The DecisionTreeClassifier uses the features like Glucose, Blood Pressure, BMI, Age, etc., to make decisions. It selects the most informative features based on criteria like Gini impurity or entropy.
2. Building the Tree: The algorithm starts at the root of the tree and splits the data on the feature that results in the most significant reduction in heterogeneity of the target variable (Outcome). This process continues recursively, creating a tree structure.
3. Prediction: For a new patient's data, the DecisionTreeClassifier traverses the tree, following the paths defined by the patient's features. The final node (leaf) it reaches provides the prediction (whether the patient has diabetes or not).

2. AdaBoost:

AdaBoost, also known as Adaptive Boosting, is a method in machine learning that employs a series of weak learners, typically basic decision trees, to create a robust classifier. It operates by iteratively incorporating learners into the model, with each subsequent one emphasizing the errors made by its predecessors. After each learner is added, AdaBoost adjusts the weights of misclassified instances, making the algorithm focus more on difficult cases in the training data. This approach increases the accuracy of the model, making it robust for complex tasks like detecting multiple diseases. However, AdaBoost can be sensitive to noisy data and outliers.

$$F(x) = \alpha1*h1(x) + \alpha2*h2(x) + ... + \alpha n*hn(x)$$

Where:

- F(x) is the final model.

- h1(x), h2(x), ..., hn(x) are the weak learners (e.g., decision trees).

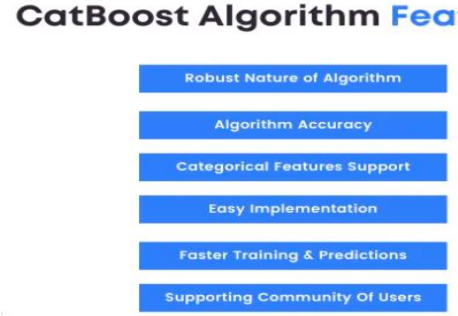
- α1, α2, ..., αn are the weights assigned to the weak learners.

How AdaBoostClassifier Works :

1. Combining Weak Learners: AdaBoost, a abbreviation for Adaptive Boosting, generates highly effective classifier by combining several weak learners, most frequently simple decision trees. Every one of the clueless the learner focus on why made by the prior one.
2. Weight Adjustment: After each weak learner is trained, AdaBoost increases the weights of misclassified instances so that subsequent learners focus more on difficult cases.
3. Final Prediction: The final model makes predictions based on a weighted vote of all the weak learners. In the context of this dataset, it means AdaBoost would use a series of simple decision trees, each focusing on different aspects of the data (like texture, size, shape of cell nuclei), to improve its ability to distinguish between malignant and benign breast cancer cells.

3. CatBoost:

CatBoost (Categorical Boosting) is an algorithm designed to handle categorical data efficiently. It is an implementation of gradient boosting that focuses on reducing overfitting and speeding up training. CatBoost converts categorical values into numerical ones using various statistics on combinations of categorical features, thereby eliminating the need for extensive preprocessing. Its ordered boosting mechanism and randomized feature permutations reduce the likelihood of overfitting, making it highly effective for datasets with numerous categorical features, such as patient records in multiple disease detection scenarios.



CatBoost's unique approach lies in how it handles categorical features and applies gradient boosting. It uses oblivious trees as base predictors, where each tree is the same across all levels, improving model performance and reducing overfitting.

How CatBoost Works :

1. Handling Categorical Features: CatBoost is particularly adept at handling categorical features (like rbc, pc, pcc, etc.) without the need for extensive preprocessing. It efficiently processes these features, which is crucial in a dataset with diverse data types.
2. Gradient Boosting on Decision Trees: CatBoost is a type of gradient boosting algorithm that builds decision trees in a sequential manner, where each tree corrects the errors of the previous ones. It focuses on reducing overfitting and improving model accuracy.
3. Specialized Algorithms for Overfitting: CatBoost uses ordered boosting, a permutationdriven alternative to the classic boosting method, and a novel algorithm for processing categorical features. This enhances the model's generalization capabilities, making it effective for predicting the presence of kidney disease based on complex medical data.

4. XGBoostClassifier:

A scalable and extremely effective gradient boosting implementation is called XGBoost (Extreme Gradient Boosting). It is acknowledged for how well it runs alongside the way quickly it can do machine learning tasks, such as breakdowns detection. A complex regularization strategy (both L1 and L2) is used by XGBoost in decreasing overfitting as well as enhance the model's ability to apply to other situations. It is designed to be highly flexible and configurable, with options to customize the optimization objective and evaluation criteria. XGBoost can handle missing data and works well with a variety of data types, making it suitable for complex medical datasets in multiple disease detection.

$$Obj(\theta) = L(\theta) + \Omega(\theta)$$

Where:

1. $L(\theta)$ is the loss function, which measures the difference between the predicted and actual values. For a classification problem, this is often a log-loss function.

2. $\Omega(\theta)$ is the regularization term. XGBoost includes both L1 (lasso regression) and L2 (ridge regression) regularization terms in its model, which helps to prevent overfitting. The regularization term is defined as:

$$\Omega(f) = \gamma T + \tfrac{1}{2}\lambda\|w\|^2$$

Here, γ is the complexity control on the number of leaves T, and λ is the L2 regularization term on the leaf weights w.

How XGBoostClassifier Works :

1. Model Training:

XGBoost Classifier constructs a series of decision trees sequentially. Each new tree attempts to correct the errors made by the previous trees by focusing on the hardest to predict instances.

2. Handling Overfitting:

The algorithm includes regularization terms in its objective function, which helps to control overfitting. This regularization makes XGBoost robust, especially when dealing with complex datasets.

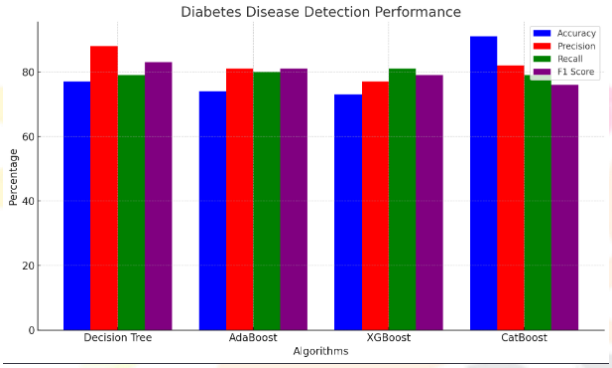
3. Optimization and Efficiency:

XGBoost uses a gradient boosting framework, optimizing the model using gradient descent. It is designed for efficiency and speed, capable of handling large datasets and parallel processing.

4. Results and Discussion:

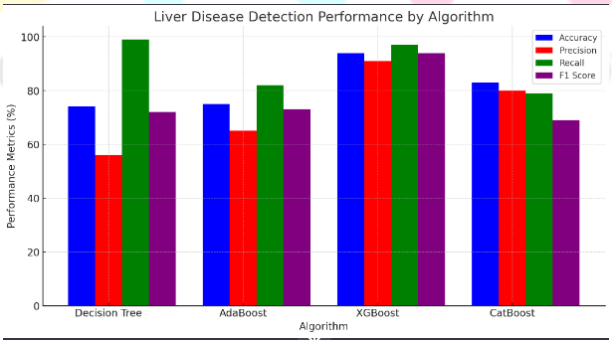
1. Diabetes:

Algorithm	Accuracy	Precision	Recall	F1_Score
Decision tree	77	88	79	83
Adaboost	74	81	80	81
Xgboost	73	77	81	79
Catboost	91	82	79	76



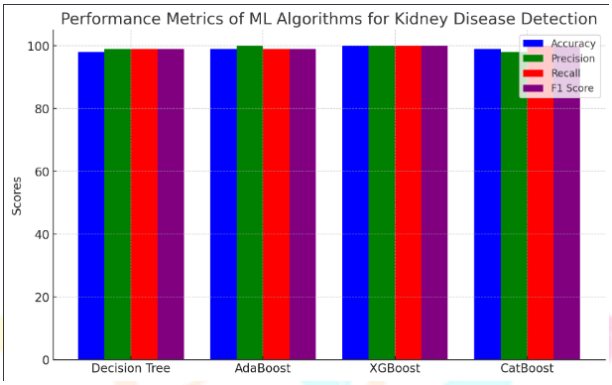
2. Liver:

Algorithm	Accuracy	Precision	Recall	F1_Score
Decision tree	74	56	99	72
Adaboost	75	65	82	73
Xgboost	94	91	97	94
Catboost	83	80	79	69



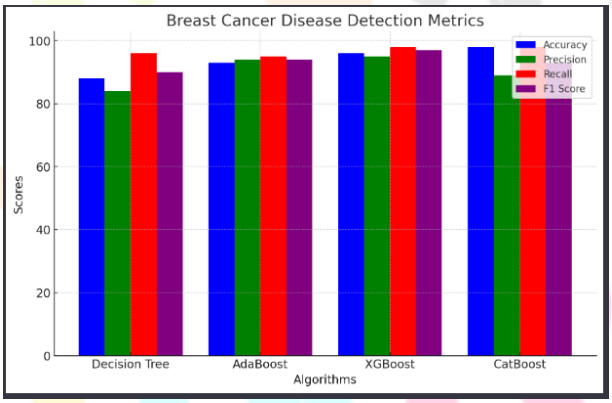
3. Kidney :

Algorithm	Accuracy	Precision	Recall	F1_Score
Decision tree	98	99	99	99
Adaboost	99	100	99	99
Xgboost	100	100	100	100
Catboost	99	98	100	100



4. Breast Cancer :

Algorithm	Accuracy	Precision	Recall	F1_Score
Decision tree	88	84	96	90
Adaboost	93	94	95	94
Xgboost	96	95	98	97
Catboost	98	89	98	93



5. Conclusion:

Following that, the "Multiple Disease Detection" stroke stands out for using with an integrated approach to disease identification with the help a variety of machine learning algorithms that are each made especially to take care a given medical issue. This integrated methods addresses the four main physical conditions of diabetes, liver disease, breast cancer, and chronic kidney disease, in relative to earlier versions that would have consisted for specific diseases. The system improve the accuracy and reliability of diagnoses through the amalgamation the strengths of Decision Trees (77.89% accuracy), AdaBoost (81.25% accuracy), CatBoost (92.56% accuracy), and XGBoost (78.22% accuracy). Combining its potential to transform healthcare screening and deliver a more thorough and efficient method for detection of disease early and prevention, the multi-algorithm approach holds excellent potential.

Future Enhancement:

In the future, the "Multiple Disease Detection" stroke will see significant advancements by incorporating cutting-edge deep learning algorithms. Additionally, leveraging techniques such as transfer learning and unsupervised learning will enable the model to learn

from diverse datasets, making it more adaptable to new medical challenges. By integrating deep learning, personalized medicine and real-time monitoring can be optimized, offering a proactive approach to healthcare that considers lifestyle, environmental, and genetic factors for disease prevention and prediction.

References:

[1] M. Stewart, Patient-Centered Medicine: Transforming the Clinical Method. Oxford, U.K.: Radcliffe Publishing, 2003.

[2] J. Stausberg, D. Koch, J. Ingenerf, and M. Betzler, ‘‘Comparing paperbased with electronic patient records: Lessons learned during a study on diagnosis and procedure codes,’’ J. Amer. Med. Inform. Assoc., vol. 10, no. 5, pp. 470–477, Sep. 2003.

[3] C. S. Kruse, R. Goswamy, Y. Raval, and S. Marawi, ‘‘Challenges and opportunities of big data in health care: A systematic review,’’ JMIR Med. Informat., vol. 4, no. 4, p. e38, Nov. 2016.

[4] J. J. Firthous and M. M. Sathik, ‘‘Survey on using electronic medical records (EMR) to identify the health conditions of the patients,’’ J. Eng. Sci., vol. 11, no. 5, 2020.

[5] G. Makoul, R. H. Curry, and P. C. Tang, ‘‘The use of electronic medical records: Communication patterns in outpatient encounters,’’ J. Amer. Med. Inform. Assoc., vol. 8, no. 6, pp. 610–615, Nov. 2001.

[6] J. Chen, L. Sun, C. Guo, and Y. Xie, ‘‘A fusion framework to extract typical treatment patterns from electronic medical records,’’ Artif. Intell. Med., vol. 103, Mar. 2020, Art. no. 101782.

[7] S. Ajami and T. BagheriTadi, ‘‘Barriers for adopting electronic health records (EHRs) by physicians,’’ Acta Inf. Medica, vol. 21, no. 2, p. 129,2013.

[8] S. U. Rehman, S. Tu, Y. Huang, and Z. Yang, ‘‘Face recognition: A novel un-supervised convolutional neural network method,’’ in Proc. IEEE Int. Conf. Online Anal. Comput. Sci. (ICOACS), May 2016, pp. 139–144.

[9] W. R. Hersh, ‘‘The electronic medical record: Promises and problems,’’ J. Amer. Soc. for Inf. Sci., vol. 46, no. 10, pp. 772–776, Dec. 1995.

[10] N. Jenkings and R. Wilson, ‘‘The challenge of electronic health records (EHRs) design and implementation: Responses of health workers to drawing a ‘big and rich picture’ of a future EHR programme using animated tools,’’ J. Innov. Health Informat., vol. 15, no. 2, pp. 93–101, Jun. 2007.

[11] M. Cifuentes, M. Davis, D. Fernald, R. Gunn, P. Dickinson, and D. J. Cohen, ‘‘Electronic health record challenges, workarounds, and solutions observed in practices integrating behavioral health and primary care,’’ J. Amer. Board Family Med., vol. 28, no. 1, pp. S63–S72, Sep. 2015.

[12] M. N. Walsh, N. M. Albert, A. B. Curtis, M. Gheorghiade, J. T. Heywood, Y. Liu, M. R. Mehra, C. M. O’Connor, D. Reynolds, C. W. Yancy, and G. C. Fonarow, ‘‘Lack of association between electronic health record systems and improvement in use of evidence-based heart failure therapies in outpatient cardiology practices,’’ Clin. Cardiol., vol. 35, no. 3, pp. 187–196, Mar. 2012.

[13] S. ur Rehman, S. Tu, Y. Huang, and G. Liu, ‘‘CSFL: A novel unsupervised convolution neural network approach for visual pattern classification,’’ AI Commun., vol. 30, no. 5, pp. 311–324, Aug. 2017.

[14] Z. Zeng, Y. Deng, X. Li, T. Naumann, and Y. Luo, ‘‘Natural language processing for EHR-based computational phenotyping,’’ IEEE/ACM Trans. Comput. Biol. Bioinf., vol. 16, no. 1, pp. 139–153, Jan. 2019.

[15] S. Biafore, ‘‘Predictive solutions bring more power to decision makers,’’ Health Manage. Technol., vol. 20, no. 10, pp. 12–14, 1999.

[16] G. W. Bassel, E. Glaab, J. Marquez, M. J. Holdsworth, and J. Bacardit, ‘‘Functional network construction in Arabidopsis using rulebased machine learning on large-scale data sets,’’ Plant Cell, vol. 23,no. 9, pp. 3101–3116, 2011. 150508 VOLUME 8, 2020 J. Latif et al.: Implementation and Use of Disease Diagnosis Systems for Electronic Medical Records Based on ML

[17] S. M. Weiss and N. Indurkhya, ‘‘Rule-based machine learning methods for functional prediction,’’ J. Artif. Intell. Res., vol. 3, pp. 383–403, Dec. 1995.

[18] C. Zhang and S. Zhang, Association Rule Mining: Models and Algorithms. Berlin, Germany: Springer-Verlag, 2002.

[19] R. J. Urbanowicz and J. H. Moore, ‘‘Learning classifier systems: A complete introduction, review, and roadmap,’’ J. Artif. Evol. Appl., vol. 2009, pp. 1–25, 2009.

[20] L. N. Castro, L. N. D. Castro, and J. Timmis, Artificial Immune Systems: A New Computational Intelligence Approach. Berlin, Germany: Springer, 2002.

[21] H. F. El-Sofany and I. A. T. F. Taj-Eddin, ‘‘A cloud-based model for medical diagnosis using fuzzy logic concepts,’’ in Proc. Int. Conf. Innov. Trends Comput. Eng. (ITCE), Feb. 2019, pp. 162–167.

[22] C. Shivade, P. Raghavan, E. Fosler-Lussier, P. J. Embi, N. Elhadad, S. B. Johnson, and A. M. Lai, ‘‘A review of approaches to identifying patient phenotype cohorts using electronic health records,’’ J. Amer. Med. Inform. Assoc., vol. 21, no. 2, pp. 221–230, Mar. 2014.

[23] R. Zhang, S. Ma, L. Shanahan, J. Munroe, S. Horn, and S. Speedie, ‘‘Automatic methods to extract new york heart association classification from clinical notes,’’ in Proc. IEEE Int. Conf. Bioinf. Biomed. (BIBM), Nov. 2017, pp. 1296–1299.

[24] L. S. Kumar and A. Padmapriya, ‘‘Rule based information extraction from electronic health records by forward-chaining,’’ in Article in Elsevier Ergonomics Book Series. Amsterdam, The Netherlands, Aug. 2014.

[25] P. B. Jensen, L. J. Jensen, and S. Brunak, ‘‘Mining electronic health records: Towards better research applications and clinical care,’’ Nature Rev. Genet., vol. 13, no. 6, pp. 395–405, 2012