Reviewing chronic ailments: predicting diseases with a multi-symptom approach

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Article InfoABSTRACTArticle history:
Received Dec 6, 2023
Revised Feb 15, 2024The integration of machine learning (ML) techniques is now indispensable
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Revised Feb 15, 2024 Accepted Mar 20, 2024

Keywords:

Chronic diseases Ensemble model Hybrid model Machine learning Symptoms The integration of machine learning (ML) techniques is now indispensable in healthcare, especially in addressing the challenges posed by chronic illnesses, which present a significant global health concern due to their unpredictable nature. This study compares ML techniques employed in the diagnosis and treatment of chronic conditions such as diabetes, liver disease, thyroid disease, breast cancer, heart disease, Alzheimer's disease, and others. Two primary criteria guided the selection of diseases under investigation. Firstly, those extensively studied with ML methods, and secondly, those leveraging ML models to resolve issues or yield promising results. The research concludes that in real-time clinical practice, there is no universally proven method for selecting the optimal course of action due to each method's unique advantages and disadvantages. While a hybrid technique may exhibit slightly slower speed growth, it holds the potential to enhance the accuracy and performance of a model.

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1. INTRODUCTION

Machine learning (ML) is an artificial intelligence (AI) method in which a machine learns and improves it is performance based on previous experiences. Healthcare is currently being influenced by ML algorithms. Health data is highly sensitive, and any error might jeopardize a person's life. Humans are unable to process data quickly using traditional methods. In these circumstances, ML techniques are employed to determine illness patterns and causes. The integration of new technologies, such as ML, into healthcare facilitates its development [1]. ML techniques are also employed in a variety of applications, including illness diagnosis, drug detection, and assistive technology. Accuracy, decision-making, rapid and powerful processing, managing complicated data, and cost-effectiveness are all advantages of ML algorithms. Several tasks have shown promise for the use of ML approaches, including the classification of interstitial lung diseases, such as the segmentation of brain tumours, the identification of body parts in medical pictures, and the detection of lung nodules [2]. ML models have already surpassed human performance in disciplines such as clinical dermatology, ophthalmology, radiology, and pathology [2]. Additionally, it will be possible to predict patient outcomes, identify chronic diseases, and reduce death rates brought on by these diseases using ML models.

This study focuses on the prediction of chronic illnesses, one of the primary contributors to decreased quality of life and increased healthcare costs. Through frequent hospitalizations, disabilities, and treatment costs, chronic illnesses impose significant burdens on individuals and healthcare systems. According to [3], the cost of therapies for these diseases equals more than 70% of a patient's income.

The direct costs of chronic illnesses to healthcare systems in the United States are close to US\$214 billion annually. Furthermore, lost productivity at work due to chronic illnesses costs US\$138 billion. According to Delpino *et al.* [4], the costs associated with chronic illnesses are much greater in low- and middle-income nations than in high-income ones, as indicated by [5]'s findings.

AI's potential for use in a variety of industries, including healthcare, has improved in recent years. According to [5], information technology platforms are already in place, along regional medical and public health collaboration, as well as individual electronic health records, to develop the fundamental components for AI-based services for chronic illness management systems. This study examines ML methods employed for diagnosing and treating chronic diseases such as heart disease, Alzheimer's, diabetes, liver disease, thyroid disease, breast cancer, and more. Refer to Table 1 in the appendix for a concise summary of the incorporated studies. The organization of the paper is as follows: section 2 outlines the methods used; section 3 delves into the results; section 4 addresses challenges and potential future work; and the paper wraps up with a concise summary in section 5.

2. METHODS

The goal of this study is to review the prediction of chronic diseases. For that, we have collected various papers from different sources (Science Direct, Google Scholar, Springer Nature, Springer databases, and IEEE Xplore) by using expressions like "Chronic diseases using ML", "Novelty ML and deep learning in disease prediction", or "Chronic diseases categorization using machine learning". There were 443 documents found after the search, as shown in Figure 1. The amount 265 papers were deleted after studying the abstracts. Doctorate dissertations, reports, theses issued in languages other than English, and studies that do not predict the incidence of chronic diseases are excluded from our review, 112 objects were deleted in this examination. After reviewing the complete text, 35 papers were deleted because they used similar methodologies or had already been presented elsewhere, and 66 publications were selected for detailed review. In the end, this study looked at 31 articles.



Figure 1. PRISMA diagram showing the included studies chosen for the review

Table 1 in the APPENDIX provides a summary of the evaluated studies in this publication, outlining details such as illness type, dataset, employed algorithms, and metrics used for evaluation (including accuracy, precision, sensitivity, specificity, area under the curve (AUC), and F1-score) for each study. The reviewed research incorporates various methods like decision tree (DT), Naïve Bayes (NB), k-nearest neighbor (KNN), logistic regression (LR), support vector machine (SVM), and random forest (RF). These algorithms are not only applied to standard datasets across multiple illnesses but are also anticipated to play an increasingly significant role in medical practice in the near future. These algorithms are also valuable for categorizing and diagnosing chronic disorders.

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Based on our current understanding, this research serves as the initial evaluation, examining a broad array of metrics such as accuracy, precision, sensitivity, specificity, AUC, and F1-score relevant to ML algorithms predicting chronic illnesses. Our primary findings confirm that ML algorithms demonstrate a significant ability to predict chronic illnesses with high accuracy. The reviewed articles covered a range of chronic diseases, including heart disease, chronic kidney disease, diabetes, Alzheimer's disease, thyroid disease, liver disease, breast cancer, cerebral infection, and hypertension.

3. DISCUSSION AND RESULTS

Diverse algorithms, encompassing KNN, LR, DT, SVM, NB, and RF, were applied to varied datasets and features in [6]. The study revealed that the DT algorithm outperformed the SVM method, contrasting with [7], which observed the reverse, with the SVM method surpassing the DT algorithm. In the context of liver disease identification, [8] explored six alternative methods, with LR exhibiting the highest accuracy among them. Mishra et al. [9], LR achieved an accuracy of 98.95%, RF reached 99.75%, and the hybridization of LR and RF attained the peak accuracy at 99.83%. Post-feature selection in [10], the KNN algorithm outperformed all other methods; the authors emphasize that feature selection is a pivotal step in every ML model. Conversely, in [11], the SVM technique coupled with the recursive feature elimination (RFE) feature selection technique yielded the highest accuracy. The assertion is that the advantages of feature selection include a reduction in overfitting, improved accuracy, and shorter training time. Bharti et al. [12], the application of the DL approach to the original dataset yielded an accuracy of 76.7%. However, through feature selection and outlier detection, the accuracy significantly improved to 94.2%. Asnaoui [13], combining ResNet50, MobileNet V2, and InceptionResNet V2 achieved an accuracy of 95.09%, surpassing individual accuracies of InceptionResNet V2 (94.50%), MobileNet V2 (93.73%), and ResNet50 (93.73%). This underscores the effectiveness of combining DL algorithms in enhancing overall model accuracy. Reddy et al. [14], the accuracy of individual methods such as RF, DT, Adaboost classifier, KNN, and LR was found to be lower compared to the combined accuracy of all these algorithms, resulting in an 80% accuracy. The study emphasizes that hybridization and the number of approaches in ensemble ML algorithms significantly impact the model's accuracy. The researchers [15]-[18] explored hybrid deep learning approaches, combining the CNN algorithm with another algorithm. The outcomes revealed varying accuracy levels depending on the specific procedures employed. The careful selection of algorithms for merging is crucial, as it directly influences the overall performance of the model. The study concludes that all methods demonstrate effective performance even with small datasets.

Based on this study, we can derive the following conclusions and identify both favorable and unfavorable outcomes. First, the choice of algorithm(s) for disease prediction is contingent upon the specifics of the task and the available data. Optimal strategy selection may require testing various algorithms to assess their effectiveness. Second, predicting the best-performing algorithm without testing is challenging, given that different algorithms may exhibit distinct behaviors on varied datasets and attributes. It is advisable to test a range of algorithms, evaluating performance measures such as accuracy, precision, recall, F1-score, and area under the receiver operating characteristic curve (AUC-ROC), to identify the most suitable algorithm(s) for the given problem. Third, the performance of a predictive model is influenced by multiple factors, including the chosen algorithm(s), data quality and volume, feature engineering and preprocessing methods, selected hyperparameters, and the evaluation methodology. Thoroughly assessing model performance and considering all relevant criteria is crucial before deploying the final model(s). Fourth, the accuracy of a ML algorithm is affected by the dataset size, quantity and quality of features, problem difficulty, chosen methods, and selected hyperparameters. Fifth, in comparative studies, incorporating various datasets is advantageous. However, ensuring meaningful and useful outcomes requires careful evaluation of the quality and relevance of the data. Last, while combining algorithms may enhance results in some cases, success in ensemble learning depends on several parameters, including the quality and diversity of individual algorithms, the combination and weighting techniques employed, and the nature of the problem addressed. An ensemble may not yield substantial benefits if individual algorithms are strongly correlated or exhibit similar biases, and the approach used, such as simple averaging or majority voting, may be inappropriate.

This following study identify positive and negative outcomes. Positive outcomes: i) accuracy: when dealing with huge amounts of data, ML models can produce predictions that are more accurate than those produced by conventional statistical models; ii) scalability: ML models are capable of processing enormous volumes of data and may be trained using data from a variety of sources, including electronic health records and medical imaging; iii) automation: predictions may be made more quickly and with less effort by using ML models, which can automate the process; and iv) better patient outcomes can result from earlier intervention and the accurate and early diagnosis of chronic diseases. Negative outcomes: i) data bias: ML algorithms are only as accurate as the data used to train them, and data bias can lead to erroneous predictions;

ii) overfitting: overfitting can happen when a model has too many parameters and is overly complicated. As a result, performance results on training data may be overly optimistic, while results on unobserved data may be subpar; iii) inability to be interpreted: some ML models, such as deep learning models, can be challenging to grasp how the model arrived at a specific prediction; and iv) cost: creating and deploying ML models can be costly and necessitate specific training and expertise.

4. CHALLENGE AND POTENTIAL FUTURE WORK

Based on the preceding section, various chronic diseases pose distinct challenges, encompassing, i) lack of adequate data: finding adequate data to train ML models is one of the main obstacles to disease prediction. It is challenging to produce precise forecasts because the quantity and quality of data vary substantially among various diseases; ii) disease complexity: many illnesses are complicated and multifactorial, meaning that various genetic, environmental, and lifestyle variables contribute to their development. An accurate illness prediction requires a thorough understanding of the underlying biology and a large dataset with all pertinent variables; iii) data bias: the potential for data bias is another difficulty in disease prediction. This can happen when specific variables are overrepresented or underrepresented in the data, or when the data used to train the model does not represent the researched population; iv) interpreting results: even when a ML model produces accurate predictions, the interpretation of the results can be challenging. A deep understanding of the underlying biology and statistical analysis is necessary to comprehend the elements that go into prediction and how these factors interact with one another; v) generalization to new populations: ML models trained on a single population may not generalize well to different groups. This can be especially difficult for diseases with varying risk factors or prevalence rates in various populations; and vi) ethical and legal issues: utilizing ML to forecast diseases presents several ethical and legal concerns. For instance, there may be issues with data privacy, informed consent, and the use of private medical data.

We will guide our future work according to the conclusions drawn from the preceding analysis, which indicated that: i) the amalgamation of data from diverse sources yields more impactful and practical solutions [19]; ii) the application of feature extraction and selection techniques is crucial in ML [20]; and iii) enhanced accuracy in predictions is achieved through the utilization of hybrid ML algorithms [21]–[23]. We will implement these insights by following the steps outlined below, as illustrated in Figure 2:

- Collect the data sets: we will focus on gathering data related to the disorders examined, encompassing diabetes, cancer, thyroid issues, liver conditions, kidney diseases, Alzheimer's, hypertension, and cardiovascular ailments. Additionally, diseases not covered in the initial study may be included.
- Prepare the data: normalize the data, eliminate lower-ranked values, remove duplicate entries, and address
 missing values.
- Extract and select features: identify common indicators across all diseases, recognize distinctive symptoms for each disease, compile all symptoms, and construct a new dataset encompassing all symptoms and selected features.
- Select ML techniques: drawing from the ML algorithms explored in the study, we will: i) determine the optimal combination strategy, ii) select algorithms that produce the most favorable results; and iii) combine algorithms using the chosen strategies.
- Predict diseases: after assessing the chosen ML algorithms using relevant metrics, the model will predict the likelihood of the existence of a disease and estimate it is severity percentage.



Figure 2. Ensemble model based on the symptoms

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5. CONCLUSION

When cutting-edge technologies like ML are integrated into the medical sector, they empower healthcare professionals with tools to analyze disease-related data. Consequently, ML algorithms play a crucial role in facilitating the early detection of diseases. This research extensively examined various ML algorithms for predicting illnesses, utilizing standard datasets across conditions such as liver diseases, heart ailments, breast cancer, and others. Researchers employed ML algorithms to diagnose illnesses, relying on a set of outcomes. A thorough review of preceding articles focusing on illness prediction models revealed that certain algorithms, including NB, SVM, KNN, RF, and DT, exhibited excellent accuracy. However, it was noted that the accuracy of a given method could vary across datasets. This variability is influenced by significant parameters such as the nature of the datasets, the process of feature selection, and the number of features considered, all of which impact the model's accuracy and overall performance. To address these considerations and enhance accuracy and performance, the forthcoming study will introduce a novel approach: constructing a unified ensemble model based on the signs and symptoms associated with each illness. This innovative paradigm aims to further advance the field of disease prediction.

APPENDIX

		10	ible 1. Summary	of the me	iuucu stut	iies			
Ref	Diseases/	Dataset	Used	Accuracy	Precision	Sensitivity	Specificity	AUC	F1-
	Year		Algorithms	(%)	(%)	(Recall)	(%)	(%)	measu
			U	. ,	× /	(%)	. ,	· /	re (%)
[24]	2023	Heart disease	IP	85	87	84			84.5
[24]	2023	datasat	CVD	83	82	04			04.5
	nean	dataset	SVK	04	03	00.1			04
			KF	98.6	97.8	98.1			98.4
[25]	2023	Kaggle	DT	75					
	Chronic Kidney		LR	80					
			NB	76.6					
[26]	2022	From the gene	K-NN	89					
	Alzheimer's	expression	NB	85					
	disease	omnibus (GEQ)	SVM	96					
[27]	2022	From UCI	ANN	85.8		85.4			
[27]	Heart	1 Ioin OCI	SVM	80.1		80.1			
[20]	2022	Obtained		05.02	04.22	00.70	05 10		
[28]	2022	Obtained		95.05	94.23	90.70	95.10		
	COVID-19	from the	XGBoost	94.25	92.43	90.89	95.01		
		registry of	KNN	89.56	80.11	97.38	82.15		
		Ayatollah	multi-layer	91.25	87.19	90.81	91.07		
		Taleghani	perceptron						
		Hospital,	(MLP)						
		Abadan city,	LR	91.23	83.94	91.45	84.47		
		Iran	J48 decision tree	92.17	89.97	87.77	94.47		
		,	NB	87 47	81.32	90.44	84 31		
[29]	2021	The curated	Extreme	0/11/	64.11	64.09	01101	68 29	64 10
[27]	Breast Cancer	broast	Gradient		04.11	04.09		00.27	04.10
	Dieast Calicel	imaging	Deseting						
		magnig	(VCD t)						
		subset of	(AGBOOST)					~ ~ ~	< 4 0 F
		DDSM	VGG-16		64.05	64.06		68.22	64.05
		(CBISDDSM)							
[30]	2021		LR	84					91.11
	Diabetes		SVM	84					91.3
			RF	79.6					88.75
[31]	2021		LR	88.24					
L- J	Alzheimer		NB	74.65					
			DI	78 32					
			K-NN	13.26					
			DT	74.22					
[20]	2020	W <i>T</i> !		14.22	06.59				
[32]	2020	wisconsin	K-ININ	85.55	90.58				
	Breast Cancer	Breast cancer							
		patient's							
		dataset							
[33]	2020	From the ML	{With Rough K						
	Diabetes	repository	Means}						
			NB	80.55	90	80.14	80.14		84.78
			SVM	77.78	88.19	77.24	78.87		82.35
			RF	77 20	56.9	56.9	69.05		62.06
			K-NN	71.30	77.08	79.29	70.67		78.17

Table 1. Summary of the included studies

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ISSN: 2502-4752

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		Table 1. S	ummary of the	included s	studies (co	ntinued)			
Ref	Diseases/ Year	Dataset	Used Algorithms	Accuracy (%)	Precision (%)	Sensitivity (Recall)	Specificity (%)	AUC (%)	F1- measure
[33]	Breast cancer	Kaggle	NB	94.44	95.92	94.95	93.65		95.43
			SVM	97.53	97.27	99.07	94.44		98.17
			RF	96.30	95	93.09	96.01		93.09
	Vidnov	Vagala	K-NN ND	85.80	84.21	95.05	70.49		89.30
	Kiuliey	Kaggle	SVM	100	100	100	100		100
			RF	100	100	100	100		100
			K-NN	84.91	92.59	80.65	90.91		86.21
[34]	2020	UCI ML	RF	68	70	69			69
	Diabetes	repository	DT	55	58	60 70			59
			Adaboost	67	68	/0			69
			K-NN	65	67	65			66
			LR	77	82	74			78
[35]	2020	University of	Framework	93.44		89.28	96.96	93.12	92.59
	Heart	California	consisting of						
		(UCI) heart	factor Analysis						
		Cleveland	(FAMD) + RF						
		Cleveland	FAMD+LR	91.80		92.85	90.90	91.88	91.22
			FAMD+KNN	9.16		92.85	87.87	90.36	89.65
			FAMD+DT	81.96		71.42	90.90	81.16	78.43
[26]	2020	TT 1 4 4	FAMD+SVM	91.80		100	84.84	92.42	91.80
[36]	2020 Heart	I wo datasets	DBSCAN	98.40					
	ficalt	(Statiog and Cleveland)	XG BOOST	95.90					
[37]	2020	From UCI	SVM	98					
	Breast Cancer	website	Artificial	98					
			Neural						
[29]	2020	Alzhaimark	Network	95					
[36]	Alzheimer	disease		83 83					
	7 inzholiner	Neuroimaging Initiative (ADNI)		05					
[39]	2020		SVM			61	44	54	
	Cardio		RF			68	63	68	
	vascular		Neural network			76	57	75.3	
			LK K-NN			74 76	57 60	74.8 75.2	
			Gradient			76	59	73.7	
			boosting						
			machine						
	Chronic kidney		SVM			86	65	84.8	
			KF Neural network			81 84	80 80	89.5 90.1	
			LR			87	78	90.5	
			K-NN			81	77	86.6	
			Gradient			86	80	90.3	
			boosting						
	Diabetes		SVM			64	48	60.6	
	Diabetes		RF			72	40 64	73.9	
			Neural network			78	62	76.4	
			LR			74	63	76.8	
			K-NN Gradiant			82	58 20	75.8	
			boosting			0/	08	/6	
			machine						
	Hypertension		SVM			85	60	78	
			RF			80	63	76.5	
			Neural network			83	58	77.5	
			LR K NN			80 61	60 81	76 9	
			Gradient			84	01 56	76.7	
			boosting			0.	20		
			machine						

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Table 1. Summary of the included studies (continued)										
Ref	Diseases/	Dataset	Used	Accuracy	Precision	Sensitivity	Specificity	AUC	F1-	
	Year		Algorithms	(%)	(%)	(Recall)	(%)	(%)	measure	
						(%)			(%)	
[40]	2019	Alzheimer's	LR	98.12		90	95			
	Alzheimer	Disease	DT	97.02		83	84			
		Neuro	SVM	97		91	90			
		imaging								
		Initiative								
		(ADNI)								
[41]	2019	Kaggle	Random Over							
	Heart		sampling:							
			SVM							
			Synthetic	99	99.7	100				
			Minority							
			Oversampling:							
			RF							
			Adaptive	91.3	93	89				
			synthetic			07				
			Sampling	90.3	93	87				
[40]	2010	E 1101	approach: RF	07						
[42]	2019	From UCI	NB	8/						
	Heart	ML	DT	91						
	2010	repository								
[43]	2019		(Class=0)	05	70	71			- 4	
	Diabetes		DI	85	/8	/1			/4	
			SVM	11.3	70	100			82	
			NB	11	82	/9			80	
			Artificial	82	70	100			82	
			Neural							
F 4 4 1	2010	F (1	Network	75	01	70	47		0.4	
[44]	2019	From the	LK	/5 74	91	/8	47		84	
	Liver	UCI ML	KF DT	74	85	81	50		83 79	
		Repository	DI	69	// 60	/9	48		/8 77	
				64	69	88	21		77	
			N-ININ NID	52	22	100	33		74 52	
[45]	2010	Enom LICI		33	50	100	40		33	
[45]	2019 Thursid	From UCI		99.40	99	99			99	
	Thyrold	IVIL .	NI [*]	99.30	99	99			99	
		repository	Multilayor	90.23	90	90			90	
			Feed forward	93.17	91	95			91	
			I D	97.50	07	07			07	
[46]	2019	The	k-10 cross	97.50	21	21			21	
[+0]	Breast Cancer	Wisconsin	validation							
	Dieast Calleer	Breast	SVM	96 99	97	97				
		Cancer	57101	<i>J</i> 0. <i>JJ</i>	71	71				
		(Original)	* SMO	95 70	96	95 7				
		(Oliginal)	*LibSVM	25.10	20	20.1				
			Artificial	95 44	95.4	95.4				
			Neural	<i>JJ</i> .++	<i>))</i> .4	<i>)).</i> +				
			Network							
			*MLP							
			*Voted	90.98	91.9	91				
			Perceptron	20.20	,,,,,	71				
[47]	2018	UCI	DT	64	65	64			65	
[.,]	Heart	repository.	51	0.	00	01			00	
		Kaggle in the								
		dataset.								
			RF	65	65	66			65	
			SVM	69	60	69			61	
[47]	Diabetes		DT	76	76	76			75	
L . J			RF	98	70	71			71	
			SVM	82.46	82	82			82	
	Liver		DT	69.81	70	70			70	
			RF	83	84	83			83	
			SVM	75.47	81	75			74	
[48]	2017	From real-	CNN-UDRP	94.2		98.08				
-	cerebral	life hospitals	CNN-MDRP	94.8	99.9					
	infarction	in central								
		China in								
		2013-2015								

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Table 1. Summary of the included studies (continued)									
Ref	Diseases/	Dataset	Used	Accuracy	Precision	Sensitivity	Specificity	AUC	F1-measure
	Year		Algorithms	(%)	(%)	(Recall)	(%)	(%)	(%)
						(%)			
[49]	2017	Routine	RF			65.3		74.5	
	Heart	clinical data	LR			67.1		76	
		of 378,256	Gradient boosting			67.5		76.1	
		patients from	machines						
		UK family	Neural networks			67.5		76.4	
		practices							
[50]	2016	From the	NB	65.07					
	Diabetes	Center for	SVM	87.32					
		ML and	DT	87.46					
		Intelligent	Artificial Neural	76.2					
		Systems at	Networks						
		UCI.							
	Heart	From UCI	NB	93.85					
		(University	SVM	95.2					
		of	DT	92.59					
		California,	Artificial Neural	94.27					
		Irvine C.A).	Networks						

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