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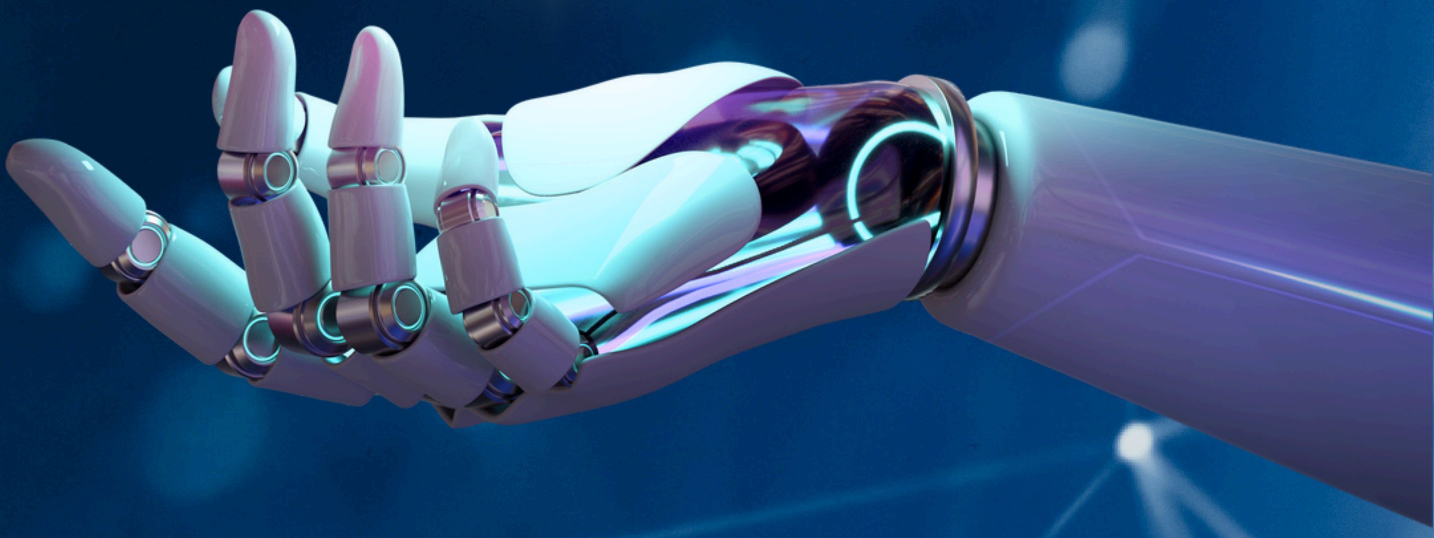

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Juxtaposition across Mathematical Modeling, Stochastic Processes along with the Lenses of Philosophy of Science and AI integration in Medicine and Biology: An Overview

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ABSTRACT The ultimate reason for the ubiquity of mathematics in modern science entails the essence of mathematical thinking and processes so that complex phenomena including those emerging in medical and biological systems can be understood, and thus, scientific models at their crux can be generated. The consequent complexities and uncertainties require the applications of stochastic processes in mathematical modeling with Artificial Intelligence (AI) techniques used in realms of medicine and biology. Within these conditions, clinical evaluation evidence and model explainability are considered to ensure accountable, effective and safe uses of AI in clinical settings, along with robust, reliable as well as accurate understanding of various complex processes that manifest huge numbers of heterogeneous temporospatial scales. The role of philosophy within science can be expounded by its juxtaposition with models and empirical data explicated by philosophy whose pillars are driven into semantic, pragmatic and syntactic structures of scientific theory that also make up the foundational tenets of algorithmic thinking and patterns. While philosophy of science examines and reflects on the concepts, theories, arguments and methods of science, it should also be borne in mind that scientific theory, by its definition, relates to applications validated by its predictions as units of analyses. Concerning mathematical models, their structure and behavior in target systems are also to be addressed so that explicit common patterns that are implicit in scientific practice can be included in this complex influx. On the other hand, critical functions of mathematical modeling from the pragmatic aspect include the unification of models and data, model fitting to the data, identification of mechanisms depending on observations as well as predictions of future observations. Given these, philosophy of science in medical and biological fields is stated to prompt a comprehensive understanding to construct holistic mathematical models particularly in complex sciences including different attributes of complexity, evolution and adaptation. Regarding the position of AI, its algorithms and mathematical modeling, the methods of neural networks, statistics, operations research, fractional calculus, fractals, and so forth can be employed with AI being capable of uncovering hidden insights embedded in big data concerning medical and biological issues in view of contemporary scientific thinking and processes. In addition, the treatment and handling of uncertainty in clinical medicine and biological problems over their processes may disclose compelling challenges due the fact that uncertainties are one of the intrinsic features of nearly all mathematical models which are formed based on three basic types of uncertainty: interval, Bayesian and stochastic. Accordingly, the current overview aims at providing answers built on sophisticated models considering the explanation and interpretation of design and formulation considering that the extant research literature could have some fragmented points in terms of original and application-oriented works. To these ends, the opportunities, challenges, limitations and conjunctures with respect to mathematical modeling in medicine and biology are addressed while role of philosophy of science is discussed within the context of mathematical modeling and applications in medicine and biology. In addition to these points, the delineation of forecasting, prediction, estimation and approximation concerning different mathematical modeling with the integration of AI in medicine and biology is explained. Thereby, an overview is inclusively presented by comprising the principles underpinning the medical and biological systems within a framework in relation to the diagnostic and disease-related treatment processes and follow-up, which can provide new directions in novel formulations, designs and interpretations based on mathematical modeling processes to be constructed and solved through practicality as well as to-the-point specific means.

KEYWORDS
Mathematical modeling
AI-based mathematical modeling
Differential equations
Philosophy of science
Fractional calculus
Fractals
Applied Mathematics
Computational fractal-based methodologies in medicine and biology
Engineering applications in medicine and biology
Biomedical decision-making
Probabilistic clinical reasoning
Stochastic processes
Brownian motion
Data analytics-based models
Data distribution
Dynamic precision medicine
Public health challenges
Predictive bias
Complexity
Computational complexity
Complex systems
Algorithmic thinking and processes

INTRODUCTION

Mathematical modeling in medicine and biology is not only the implication of the development of advanced computer capabilities but also the increasing access to the simulations of complex systems. The sampling of clinical data leading to the experiments generated has paved the way for novel and profound outlooks regarding the dynamics and complex patterns of medical and biological systems which do not always manifest steady attributes. Another input of mathematical modeling employed in medicine and biology is its emphasis placed on accurate and precise definitions of medical notions so that misunderstanding and overlooking instances and / or observations can be prevented, which can also preclude the waste of time and efforts. Against this backdrop, mathematics is stated to provide the means for the structuring of thoughts, models, computations, simulations, schemes and ultimately applications.

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The adoption of systemic properties and addressing them by unveiling the spontaneous processes in a dynamical system further from the equilibria without any existence of an external force acting on the system are among the pivotal tenets of modern scientific thinking which reveals a challenge posed against the dichotomy between the natural world and social world by considering the notions revolving around evolution, order and complexity. Even though simplicity may be thought as the direct dichotomy of complexity, as Leonardo da Vinci put: "Simplicity is the ultimate sophistication.", simplicity embodies certainty, coherence and intelligibility. To illustrate, clarity of water reveals transparency and purity, and simplicity on these surfaces is retained thoroughly unpretentious and effortless, which implies the fundamental ground of consolidation of inherent peace.

The ultimate reason for the ubiquity of mathematics in modern science is the necessity of mathematical thinking to understand complex phenomena. The mathematical approach includes quantification of observations, modelling, classification, optimization, data processing, analysis, prediction and validation. Correspondingly, computational technologies in different complex systems depending on mathematical-driven informed frameworks are able to allow for the generation of more realistic and applicable adaptive models under transient, dynamic and ever-evolving circumstances of different complex systems (Karaca 2022b).

AI and applications thereof as well as related digital technologies and their tools can enable the mimicking of human intelligence, generating ample ideas based on personalized needs and functions with better precision and less time consumption in medicine and biology. The employment of different machine learning methods can provide significant affordances in healthcare systems through the extraction of the relevant patterns and determination of correlations as well as associations among the multiple features concerning big datasets. Regarding mathematics, a value to convert empirical data into applicable models can be found based on mathematical operations, which may reduce the human toll in processes such as disease identification to a large extent.

Machine learning's predictive models, on the other hand, can demonstrate enhanced rules in medical and clinical practices for critical decision-making concerning individuals' care. Among the related studies, the work (Chen *et al.* 2023) uses custom machine learning algorithm for large-scale disease screening handling heart disease as an example. For this aim, the authors introduce a novel algorithm to train a patient-specific machine learning model with customization attained on neural network architecture, data processing as well as loss function. The results show the powerfulness of the algorithm proposed for the screening of disease to save lives and lessen the economic burdens of heart diseases. The adoption of AI by a stream of machine learning with extraordinary performance is handled in (Ge *et al.* 2023) where the impact of inflationary effects on healthcare tasks concerning medical datasets are investigated. The study's experiments show that removal of each inflationary impact can correspond with a decrease in classification accuracy, yet removal of all the inflationary effects produce a reduction of the evaluated performance by 30 %. Another study (Wang *et al.* 2023) provides a novel model named MLFL-NET with high accuracy for the fine-grained classification of bone marrow cells using multi-level features.

The study shows the significance of AI-assisted diagnosis support system of morphological examination depending on bone marrow smears, ie. classification, prediction and cells detection of leukemia types. Last but not least, clinical evaluation evidence and model explainability are considered for ensuring accountable, effective and safe uses of AI in clinical settings. A related study (Jin *et al.* 2024) conducts a clinical user-centered evaluation to make the assessment of AI assistance utility. The evaluation obtained by the study shows the clinical utility of AI in terms of providing assistance to physicians on the glioma grading task while identifying clinical usage gaps as well as the limitations related to existing explainable AI techniques for future improvement.

Fractals, as intriguing forms of infinitely complicated shapes in mathematics, display peculiar patterns of their own with their inherent properties, repeating in continuum. Fractals provide a unified perspective concerning varied trajectories of complexities in the natural world as well as medicine and biology by opening up novel dimensions with multiple layers. Fractals, fractal theory and analysis are directed toward the assessment of data's fractal characteristics with multiple methods assigning fractal dimensions to the datasets. Moreover, it is possible to model dynamical processes and systems of fractional order with respect to both natural and artificial phenomena by ordinary or partial differential equations with integer order, which can be described fittingly by ordinary and partial differential equations. Furthermore, fractional, or non-integer order, calculus can provide a concise model to describe the dynamic events occurring in medical and biological elements.

Concerning non-integer (or fractional) power model, it can be noted that a unit with a non-integer exponent is stated to represent a fractional power, whereas a unit with an integer exponent is said to represent a whole number power, which suggests that a unit with a non-integer exponent is a more precise measurement compared to a unit with an integer exponent. To illustrate, analytical results of linear integer-order differential equations are signified by the exponential functions' combination. The Mittag-Leffler function displays a power-law asymptotic behavior, representing the analytical results pertaining to linear fractional-order differential equations. Owing to this inherent quality, the results of linear fractional-order differential equations often manifest the properties related to power-law (Karaca and Baleanu 2022).

Expanding on these aspects, the use of artificial intelligence and machine learning ensure the maximization of model accuracy and minimization of functions such as computational burden, which can provide one with mathematical-informed frameworks that can allow for robust, reliable and accurate understanding of various complex processes manifesting huge numbers of heterogeneous temporal and spatial scales. Such a degree of complexity entails a holistic understanding of different processes through multi-stage integrative models able to capture significant attributes to explain complex systems' confounding behavior in terms of prediction and control. Accordingly, a study (Havlin *et al.* 1995) provides a review of biological systems which are marked by fractal geometry focusing on long range power law correlations in DNA sequences. The study also provides the discussion of applying fractal scaling analysis to different medical aspects like the dynamics of heartbeat regulation.

Another paper (Grizzi *et al.* 2019) aims at reviewing complexity and fractal geometry concerning the nuclear medicine images in biomedical imaging, addressing the identification of pathognomonic patterns of shape in anatomical entities as well as their changes from natural states to pathological states. The use of fractional calculus models related to complex dynamics in biological tissues is handled in (Magin 2010) where several bioengineering research-related areas with the application of fractional calculus to build new mathematical models are explained. The contribution of fractional calculus is provided in the study (Vosika *et al.* 2013) which shows that fractional calculus gives a new dimension for understanding and describing complex systems' behaviors and basic nature. Using fractional calculus to model biological systems' electrical properties, the authors derive a new class of generalized models for electrical impedance and apply those to human skin based on experimental data fitting.

Mathematical modeling in medicine and biology demonstrates the significance of mathematical models as a result of the development and spread of efficient and time-saving computers, which can facilitate the access to simulations of complex systems characterized by uncertainty, nonlinearity, irregularity, randomness, and so forth. Another important point in this emergence and spread is due to the precise continuous samplings of new clinical data generating experiments which can provide insights into biological and medical systems' dynamics, behaviors and patterns.

In addition, mathematics provides a tool to structure thoughts which can help with the answering of new important questions brought about by the application of mathematical models. Consequently, used as a part of mathematical models, differential equations lend a vast diversity of their applications to describe various phenomena, patterns and processes, and yet, the need to develop more universal and efficient methods to solve differential equations has been satisfied with the emergence of computer science and also scientific computing, namely ANNs, as being one of those methods (Evans 2022). This attribute becomes more critical particularly in complex dynamic problems including disease identification, classification, diagnosis, prognosis, treatment, control and management as well as other issues emerging in biological and medical systems. The study (Yang *et al.* 2023) is concerned with the development of a neural ordinary differential equation (ODE) model to visualize deep neural network behaviors when multiparametric MRI-based glioma segmentation is done, which is a method to improve the capability of deep learning explainability.

The results of the study show that all neural ODE models illustrated image dynamics successfully. By addressing equation-based modeling and showing its complementary quality, the study (Daun *et al.* 2008) states the importance of differential equations as a simulation tool in biological and clinical sciences. Another work (Ning *et al.* 2023) shows the power of differential equations in epidemic models as well as deep neural networks with AI models as reliable tools to analyze and treat COVID-19 transmission, demonstrating that the inferred parameters from the proposed epidemiological deep neural networks (Epi-DNNs) method can provide a predictive compartmental model, which can serve to forecast future dynamics. Subsequently, the paper concerned with a fractional recurrent neural network (RNN) proposes a novel approach for the aim of achieving the synchronization of a cancer cell model based on observer scheme.

Considering the importance of recurrent neural networks, the framework proposed by the study is stated to serve as a method for prediction into the fractional-order chaotic cancer systems with uncertain orders' behavior (Behinfaraz *et al.* 2023). All these findings and points point to the significance of mathematical medicine and biology along with the tools they offer in cases of diagnosis, model building, classification, differentiation, uncertainty management and complexity quantification, among many others.

The juxtaposition of mathematical modeling with stochastic processes can be handled within the framework of AI integration in medical and biological systems while keeping philosophy of science in mind. Correspondingly, mathematical models are formulated and solved systematically based on the particular type of the problem at hand arising in medicine and biology. Inter- and multidisciplinary-driven research includes mathematical modeling being exposed to evolving in diverse areas. In view of the fact that the extant research literature may have some incomplete and fragmented points in terms of original and application-based works, the current overview aims to address the following relevant questions:

What could make up the opportunities, challenges, limitations and conjunctures with respect to mathematical modeling in medicine and biology?

How can the role of philosophy of science be interpreted within the context of mathematical modeling and applications in medicine and biology?

What demarcates the distinctions of forecasting, prediction, estimation and approximation concerning different mathematical modeling with the integration of AI in medicine and biology?

How could an overview be presented encompassing principles which underpin medical and biological systems that consider a framework to be provided with regard to the diagnostic and disease-related as well as follow-up processes?

In line with the responses to the questions set above, the remainder of the present review is as follows. Section 2 provides an overview of mathematical modeling in medicine and biology in relation to the questions forwarded herein. Section 3 provides Conclusion, Contemporary Mathematical Medicine and Biology Thoughts, and Future Directions.

OVERVIEW OF MATHEMATICAL MODELING IN MEDICINE AND BIOLOGY

Mathematical Modeling in Medicine and Biology: Opportunities, Challenges, Limitations and Conjunctures

Mathematical modeling is to establish a mathematical model according to the actual- veritas problems, while generating new ways of solving and calculating the model so that the actual problems in real life can be solved in line with the results calculated. Henceforth, the essence of a mathematical model is noted to be a dynamic simulation, rather than being directed by a fixed way of thinking. More precisely, mathematical modeling involves the converting of problems from application realm into manageable mathematical formulations bearing arithmetical and hypothetical analyses to ensure answers, solutions, perception and guidance that will benefit for the relevant configuration of peculiar application. Along these lines, the value of mathematical modeling lies in precision and strategy geared towards problem solution, which could be the schemes allowing a systematic understanding of the system modeled besides more optimal designs as well as efficient employment of modern computing capabilities from the lenses of novel perspectives.

Having a robust grasp of inputs and outputs concerning mathematical modeling can be considered to be a noteworthy stage from theoretical mathematical domain to application-oriented mathematical expertise, which can pave the way for tackling challenges in current modern technological landscape so that mastering and excelling can be realized by making most of the opportunities and mitigating the risks.

The essence of mathematical modeling as a process is derived from understanding, analyzing and forecasting behavior concerning real-world phenomena through the creation of mathematical representations of them. Regarding the relevance of machine learning and AI, mathematical modeling can allow for the description and analysis of big datasets through the use of mathematical equations and algorithms, which can make one gain profound insights into the latent and underlying correlations as well as patterns within the data. Machine learning, as a technique of data analytics, can teach computers to do what comes naturally to humans and animals, which is to say, learning based on experience. Accordingly, machine learning algorithms make use of computational methods to directly learn from the data with no reliance on a predetermined equation as a model. It is possible to represent mathematical models as systems of differential equations which describe the way different variables in the model may change over time or as depending on other independent variables. Partial differential equations involve an unknown function with several variables or one or several of its partial derivatives. If one is solved, it means one may determine the unknown function satisfying the partial differential equation (Karlsson Faronius 2023; Pinchover and Rubinstein 2005). Ordinary differential equations (ODEs) and partial differential equations (PDEs) are ubiquitous in applied mathematics due to their description of time-depending phenomena. In specific cases, the supplementing of differential equations is conducted to tackle memory effects (integro-differential equations or time-delay differential equations) as well as noise (stochastic differential equations) (Amigó and Small 2017).

Differential equations are generally employed in medicine, biology, physics, engineering, and so forth for expressing a relation between the function and its derivatives. In exact sciences, they are used as a technique for the determination of the functions over their domain if the functions and some of the derivatives are known. A differential equation includes one or more functions along with its derivatives. The rate of change of a function at a point is defined by the derivatives of the function. Overall, the aim of a differential equation is the examination of the solutions which satisfy the equations and the solutions' properties. Some types of differential equations are ODEs, PDEs, linear differential equations, nonlinear differential equations, homogeneous differential equations, nonhomogeneous differential equations, among others. Accordingly, a first-order differential equation is defined by an equation: $dy/(dx=f(x,y))$ of two variables x and y with its function $f(x,y)$ which are defined on a region in the xy-plane. Having only the first derivative dy/dx, the equation is of the first order, and higher-order derivatives do not exist. The differential equation in first-order can also be denoted according to Equation 1 as follows (Daun *et al.* 2008):

$$y' = f(x,y) \text{ or } (d/dx)y = f(x,y) \tag{1}$$

The five basic types of differential equations in the first order are linear differential equations, homogeneous equations, exact equations, separable equations and integrating factor. The second order differential equation is a specific type of differential equation involving a derivative of a function of order 2 without other higher-order derivative of the function which may appear in the equation. The equation with the second-order derivative is the second-order differential equation denoted according to Equation 2 as follows:

$$d/dx(dy/dx) = d^2y/dx^2 = f''(x) = y'' \tag{2}$$

The five basic types of differential equations in the second order are linear second ODE, homogeneous second ODE, nonhomogeneous second ODE, Second ODE with constant coefficients, and so forth. A second order differential equation is defined as a differential equation that includes a function and its second-order derivative and no other higher-order derivative of the function can appear in the equation. It can be of different types depending upon the power of the derivative and the functions involved. Fractional order differential equations are generalized and noninteger order differential equations that can obtained in space and time through a power law memory kernel of nonlocal relationships by taking into account the properties of fractional-order calculus and he use of non-local information of the image for reconstruction (Li and Zhao 2024). Since they are robust in terms of describing memory-related aspects of different substances, theoretical analyses and numerical methods are significant with viable applications in various fields of research. One relevant study aims to understand tumor growth in human liver, and thus, the authors used a temporal fractional-order parabolic partial differential equation, carrying out the analysis by numerical methods. They employed the Caputo derivative to explore the impact of medication therapy on tumor growth (Takale *et al.* 2024). A fractional order total variation model for additive noise removal employing a different fractional order of the regularization term of the objective function is the content of another study which deals with the denoising model for medical images based on space and time fractional derivatives on a finite domain as discretized with effective applications of Grünwald-Letnikov and Caputo derivatives. The study shows the benefits of the model in terms of smoothing the homogeneous regions, which in turn improved edge information by showing further details of the image (Abirami *et al.* 2023).

Treatment and handling of uncertainty in clinical medicine and biological problems over their due processes pose compelling challenges due the fact that uncertainties are known to be one of the intrinsic features of nearly all mathematical models which are constructed based on three basic types of uncertainty involving interval, Bayesian and stochastic (Karaca and Cattani 2018; Karaca and Moonis 2022). The application of these models is for the description of measurements in unmonitored fluctuations that may bring about ambiguities in the results. There are also other reasons why uncertainties appear. The most significant reasons include the factors that impact the behavior of the system that is modeled being unknown to the modeler, some factors being overlooked during the modeling process as they may have little effect on the model behavior and relationships among the impactful factors being simplified because of the complexity concerning the mathematical description.

Besides these reasons, model uncertainty has two main sources, which are the model's mathematical structure and the parameter values (Koen-Alonso and Yodzis 2005). While modeling a predictive model, the major aim would be to replicate a certain phenomenon as closely as possible, so uncertainty may be deemed to be undesirable at this level which needs to be eliminated or reduced as much as possible (Brugnach *et al.* 2008). In that regard, uncertainty is considered to be an attribute which must be understood and associated with the quality of the information employed for building or running a model (Zimmermann 2000). Regarding uncertainty in data, numerical computations can be conducted to deliver an output which has uncertainty formulated in terms. Furthermore, uncertainty models need their corresponding rules themselves within well-defined semantics (Oberguggenberger 2005).

Uncertainties can be divided into three broad categories: complete uncertainty (obscurity), inauthenticity and ambiguity. Some methods are typically used to account for the uncertainty in mathematical models. Regarding the types of uncertainty, Aleatoric uncertainty signifies inherent uncertainty in a given system, which is more difficulty to tackle by more data collection or experimentation. It is known to be a stochastic type of variation which his possible to be represented via a probability distribution. On the other hand, epistemic uncertainty is due to the actual model, which can be followed up towards a lack of knowledge about the latter one in terms of shortcoming. It is stated that this specific uncertainty can be managed if more information can be obtained regarding the system as a whole (Heid *et al.* 2023). Accordingly, the term stochastic derived is from the word originally meaning random or chance, which is the opposite of sure, certain or deterministic (Arthur 1985). While a deterministic model makes the prediction of a single outcome based on a particular set of circumstances, a stochastic model makes the prediction of a set of possible results that are weighted by their probabilities. In fact, stochastic models are mathematical models for random phenomena that evolve in space or indexed by time in a random way. A stochastic model's specification with the techniques may change in four likely combinations of discrete or continuous time and discrete or continuous state space. A stochastic process involves the representation of a family of random variables which are denoted by a function on a variable $f(x)$, which approximates a number with the result of the related experiments (Fortier and Michel 2003).

Some advanced topics handled in stochastic processes include but are not limited to stopping theorems, filtration, theoretic probability Brownian motion, Itô calculus, functional limit theorems and stochastic integration. Stochastic processes, as mathematical approaches, are beneficial for understanding and analyzing dynamical systems which random components evolving over time. A stochastic model or process signifies an equation with a random variable. Stochastic models are known to be complex in terms of analyzing in computational and analytical ways, so in-depth probability and statistical theories are required along with the advance techniques (Mubayi *et al.* 2019).

Fractal method, namely box-counting dimension with the least square regression, besides multifractal method (Wavelet transform modulus maxima with Gaussian wavelet analysis) were applied to the stroke subtypes' dataset for identifying efficient and significant attributes in the stroke subtypes which were classified with the Feedforward Backpropagation (FFBP) algorithm (Karaca *et al.* 2020b). The values of the Hurst exponent may range from 0 to 1, which is considered to be an important feature with its range being considerably appropriate for serving as the domain of images. When the sub-images of an original image are converted into estimates of Hurst exponent, the estimates of 0-1 can be saved as a characteristic image or feature belonging to another input source image.

With the application of ML and DL models on certain images, it becomes possible to supply the characteristic image for another input so that the general classification rate can be enhanced through the two inputs. Consequently, the effectiveness is concerned with the accuracy of the estimation as based on the Hurst exponent, which indicates that the higher the accuracy of estimation is the better the classification rate will be (Chang 2024). Regarding Brownian motion, it can be noted that its mathematical theory and related stochastic processes have indications of the way this theory is connected with other branches of mathematics (Karaca 2022a). Multifractional Brownian Motion (mBm), one of the stochastic multifractal models, is used for analyzing and extracting dissimilar images, signals or patterns. In addition, fractal Brownian Motion (fBm) provides important models for a broad range of phenomena that emerge in the natural world.

Multifractal analysis is known to handle the singularity structure of functions or signals both locally and globally. Hölder exponent at each point, on the other hand, provides the local information with the global information achieved by a characterization of the statistical or geometrical distribution of the Hölder exponents, referred to as multifractal spectrum (Karaca *et al.* 2020a). With respect to nonlinear phenomena which requires the intricate systems' representation on space and time variables, Itô calculus, as the stochastic calculus version of the change belonging to the variables formula and chain rules, involves the second derivative of f, resulting from the property that Brownian motion has non-zero quadratic variation (Karaca *et al.* 2023b).

As a mathematical model of time-dependent random phenomena, stochastic processes being broad and interdisciplinary combine mathematics, computer intensive methods, applied probability and statistical inference. Therefore, they have diverse fields of application and conjunctures such as medicine, biology, neurophysiology, physics, chemistry, computer science, finance, and so forth by addressing Markov chains, random walks as well as branching processes to name some. Derived from these, a related challenge could be put forth as such: mathematical models in medicine are a reality in all the applications whose impact is for the betterment of patient care provided that the medical community in general undertakes a foundational understanding, directing the application of findings based on reasonable confidence following critical reviews. In that regard, it will be possible for modeling to respond to otherwise unanswerable questions and significantly expand our knowledge base from actual study data. Furthermore, reasonable and mathematical components of a model need to be based on valid research concerning actual patients (Chambers 2000).

In view of the diverse related domains of application and conjunctures, mathematical models are instrumental in providing insights into the complex processes also concerning biological systems by retrieving the essential meaning of hypotheses, which allows the true understanding of the system (Torres and Santos 2015). The study of complex systems has experienced an exponential increase since it focuses on large systems which are constituted by different living entities, which makes them difficult to be understood and modeled depending only on the interactions and dynamics of some individual entities localized in time and space. What is needed would be the accurate and precise mathematical description of collectively emerging behaviors (Coscia 2011; Karaca *et al.* 2019; Wang *et al.* 2022). Comprehension of the role of nonlinear interactions happens to be one of the compelling challenges and limitations in some cases while studying complex systems due to the emergence of qualitatively different states, which is to say new collective states, which cannot be regarded as mere combinations of the individual units' states within the system. This complexity suggests one cannot determine the dynamics of each entity by the dynamics of all other entities. Such determination can rather be possible by their action as a whole.

It is widely acknowledged that AI-based mathematical modeling and its means have had transformative robustness in several domains, including medicine and biology owing to high dimensionality and complexity. Along with the opportunities brought, a substantial number of unique attributes, signals and features contained within the data has, on the other hand, led to some challenges in the development and validation of solutions that can be applied to diverse populations, as well as to medical and biological systems. Figure 1 depicts the intricate reciprocal relations and interactions in a network configuration of inherent opportunities and data complexities.

Philosophy of Science within Comprehensive Mathematical Modeling and Related Applications in Medical and Biological Environments

Philosophy can elucidate mathematical modeling and its juxtaposition along with models and empirical data can be explicated, and

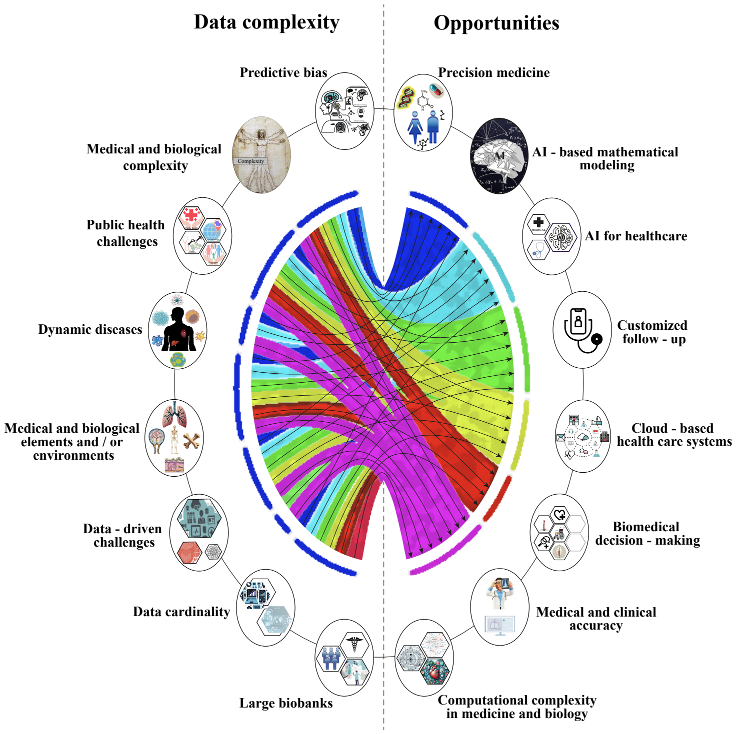

Figure 1 Opportunities and data complexities within the intricate medical and biological systems through their reciprocal interactions

within this context, the main philosophical pillars, namely semantic, pragmatic and syntactic structures of scientific theory, which also constitute core patterns of algorithmic thinking and patterns. Critical functions of mathematical modeling from the pragmatic aspect include the unification of models and data, model fitting to the data, identification of mechanisms relying on observation as well as prediction of future observations (Winther 2012).

The philosophy of science, on the other hand, addresses particular issues that emerge in particular sciences as well as the general issues related to the nature and validity of science. With respect to medicine and biology, one question is posed, which is: if medicine is distinctive, in what ways can one see this distinctiveness? Since a broad array of health and health care practitioners including physicians is involved, it becomes important to analyze the mathematical statements concerning the medical and biological problems. The reason why medicine needs philosophy within new models based on mathematics-informed schemes can be clarified as such: a broad definition of philosophy of medicine is the systematic set of ways to articulate, clarify and address the philosophical issues arising in medicine (Chin-Yee 2017). To give one example, the phenomenological approach focusing on an individual's experiences and the impact of the disease can make one think about a more person-centered approach versus disease-centered approach.

In broad terms, philosophy of science examines and reflects on the concepts, theories, arguments, assumptions, aims and methods of science. In this respect, scientific theory, its definition, applications and those validated by its predictions are units of analyses. With relation to mathematical models, their structure and behavior in target systems are at stake so that explicit common patterns which are implicit in scientific practice are put under scope and analyzed. With target system, it is meant an effectively isolated part of the universe, whether they are physical, biological or empirical, made to function by internal or external causes with their interactions in the universe delineated through a fixed, namely input and output, interface. In virtue of these, mathematical modeling has the constituents of behavior, mechanism and structure. Changes which are generated in the target system are supposed to be detectable in an external way by means of measurements of the system's characterizing quantitative properties.

The application of mathematics to medicine is a research area within the scope of applied mathematics, aiming to create mathematical models of various disease processes which consider the interactions between the complex biological system's various complex components. When integrated with philosophy of thought, this kind of approach can increase understanding into the onset of the diseases and the way they progress. Another benefit of this mode of thinking based on mathematical analysis has to do with the examination of available treatment strategies that can allow the identification of the most optimal one for each medical and / or clinical case. Some of the extensive application areas include but are not limited to cancer treatments and mathematical modeling of them, sequencing of surgical operations, implications of different modes of therapies and their effects on tumors. On neuron level, theoretical neuroscience with the use of mathematical equations aims to understand the way neurons process information which means the way brain coordinates the entire activity of a particular organism, which is related to the behaviors and functions of neurons.

The mathematical description of medicine-related phenomena can be approached in two ways. The first is related to finding the regularities in quantitative analysis of medical data. The mathematical models recommended through this approach is said to have a descriptive design to be implemented for deducing the mechanisms of phenomena under consideration of research. The second approach is related to predicting the system behavior by using the data on mechanisms which lie under the described processes. This sort of mathematical models could have a generalized character describing biological processes on any levels of complexity. In that regard, mathematical models provide a compromise between the two experiments to describe the problem adequately (Karpov 2009). Notwithstanding, the examination of evolutionary many-body and multi-level self-organized complex systems, including medical and biological systems, require the analysis of the following aspects: they own an entangled hierarchy concerning components which may change in time, having the likelihood of their process and components' loss along with their emergence of ever-increasing complexity. To cope with such challenges, it is essential to develop robust and flexible memory which can ensure better adaptation through learning. To sum up, philosophy of science in the medical and biological fields prompt a comprehensive understanding to form holistic mathematical models including simulation, optimization, operationalization, and so forth as experimental and empirical systems with important implications in medicine and biology, particularly complex sciences with the inclusion of complexity, evolution and adaptation so that reassessments in modeling and applications can be conceived and put into practice.

Delineation of Mathematical modeling with Artificial Intelligence in Medicine and Biology: Forecasting, Prediction, Estimation and Approximation

The generation and extensive utilization of modern technologies have prompted the reliance of forecasting and prediction as the principal means for the guiding of critical decision-making processes. Forecasting and prediction are used interchangeable, yet they have certain differences. Forecasting refers to the process of estimating future events or trends based on statistical methods and historical data, involving the analyses of patterns and trends in past or historical data so that informed guesses can be made about the outcomes. As for time frame, forecasting, as a time-based prediction, focuses typically on the prediction of such outcomes over a longer time frame, like months, years or decades, and the aim of forecasting is to provide more accurate estimates of future outcomes. For these reasons, forecasting would be more appropriate to be used while dealing with time series data.

On the other hand, prediction refers to the making of an educated projection or guess regarding a specific outcome without reliance on statistical methods and historical data, which is one difference between forecasting. Another difference is related to the aspect of time frames with prediction not having the need to be time based merely, as it can also be based on multiple causal factors that have impact on the target variable. With this aspect, it is stated that predictions can be short-term and immediate, so they can be employed for the estimation of outcomes for near future up until one year, for example. In addition, predictions are said to be less accurate for their reliance on assumptions and judgement. To sum up, forecasting and prediction are used as methods for the future outcomes' estimation with certain differences. The reliance on historical data and statistical methods characterizes forecasting, whereas prediction is marked by the making of educated projections or guesses with no dependence on the factors mentioned above. Another element is estimation which suggests the finding of the optimal parameter with the use of historical data. Prediction, on the other hand, makes use of the data for the computation of the unseen data's random value. Historical data are what is needed for learning the dependencies for machine learning and modeling.

Multiple observations may be the case with the data with each observation having multiple variables, with this aspect, estimation is known to be the process of optimizing the true state of nature. This aspect of estimation makes it relevant to model building so that it becomes possible to find the most appropriate parameter to best describe the historical data's multivariate distribution. While prediction makes the leveraging of the model that is already built. Mathematical models include equations that have variables and constants, and while estimating with models four steps can be followed for the related process: a priori bounds (limit to the number of solutions regarding the problem), existence and uniqueness (the proving that there is one solution exactly), convergence (an iterative method rather than a closed form) and approximations (the level of goodness an approximation has to the ideal solution for the converged solution to be provided) (Saaty and Alexander 1981).

Estimation is following the event's occurrence, namely posterior probability, while prediction is a type of estimation prior to the event's occurrence, which is to say apriori probability. In summary, forecasting is oriented towards process by following a particular methodology and assuming the past behavior deemed to be an adequate indicator of what will happen in the future. Forecasting encompasses the projection of future developments with a certain level of uncertainty as a result of external factors which may influence the outcome. Prediction, by considering all the historical processes, influences variables and interactions so that future can be revealed. Although all forecasts are predictions, all predictions are not estimations.

Mathematics can provide the language and means for modeling and analyzing structures, including networks, and for profound understanding of the inner workings of Artificial Neural Networks (ANNs), it is of utmost importance to capture the underlying mathematical principles. Artificial neural networks (ANNs), which are known to be intricate networks of interconnected nodes namely neurons are capable of learning from data, recognizing patterns and thus making predictions (Baleanu *et al.* 2023; Karaca *et al.* 2022b). Owing to these aspects, ANNs which adopt the basic model of neuron analogues have had a groundbreaking impact in AI through the emulation of the way human brain operates. In these regards, mathematical principles enable one to gain insights and generate informed decisions, and hence, the crucial role of mathematics becomes evident from the very beginning of initial design until the optimization processes. The connection of mathematical and ANNs is also worthy of mentioning since mathematical modeling constructs the foundation of ANNS by the representation of the relationships between input data and output predictions. Therefore, it becomes possible to create a framework for learning and inference through mathematical models and to formulate the ANNs' behaviors and structures through mathematical techniques so that algorithms and predictions can be rendered efficient and accurate. It should also be noted that mathematical models should be continuously refined, and new mathematical techniques should be generated so that advancements in computational power can be achieved exceeding the boundaries of what neural networks can realize, which can be possible by understanding and optimizing these networks.

At the core of AI, algorithms are placed, and mathematical modeling is regarded to be placed as the core thinking of algorithms. By making use of the methods of neural networks, statistics, operations research, AI is capable of uncovering hidden insights embedded in big data concerning medical and biological issues owing to its judgment abilities and automatic perception properties. The expression of practical problems mathematically is done through ODEs, PDEs, calculus of variations, stochastic processes, nonlinear analyses, and so forth. The contributions of mathematics to the development of AI have been groundbreaking owing to mathematics' laying the theoretical foundations of the AI systems so that the algorithms could be created, modeled and methodologies to enable machines to learn, do reasoning and make informed decisions could be provided. To give one example, linear algebra can enable the data representation and manipulation, which has paved the way for facilitating high dimensional data handling, natural language processing, recommendation systems and signal / image processing and/or recognition. Optimization theory has also witnessed advancements to form the foundation of training and fine-training of the AI-related models. The use of AI has provided numerous opportunities in different areas including the healthcare domain since the integration of mathematical principles with AI can solve the problems related to the enabling of innovative applications. As for the challenges, it is possible that AI may encounter difficulties in the mathematical modeling of problems in medical and biological systems because of the challenge arising in modeling representations of complex cases, incidents and representations whose highly dynamic and heterogenous characteristics cause the exacerbation of the reciprocal interactions and interrelated phenomena.

Nevertheless, AI enables a collaborative environment encompassing the skills, expertise, knowledge and abilities of different individuals from different areas while making it possible that mathematical theories are translated into practical and feasible solutions that can have tangible real-world impacts. In healthcare particularly, mathematics has contributed to the medical imaging techniques which are powered by AI while providing advancements in the disease diagnosis models. The integration of mathematics and AI has also provided contributions to the personalized treatment optimization algorithms, which has had substantial impact on the development of precision medicine which is a form of medicine using information regarding an individual's genes or proteins so that a disease can be prevented and / or diagnosed. Mathematical modeling, AI and datasets for the prediction and management of COVID-19 are reviewed in a study (Mohamadou *et al.* 2020) in regards to the dynamics and early detection of COVID-19 through mathematical modeling and AI so that a comprehensive overview of the methods used the relevant literature and COVID-19 open source datasets could be provided. Another study proposes an integrated approach with multi-source complex spatial data concerning the accurate prediction, diagnosis and prognosis of Multiple Sclerosis (MS) subgroups for their accurate prediction, diagnosis and prognosis by Hidden Markov Model, Viterbi algorithm and Forward-Backward algorithm, being among the dynamic and efficient products of AI-based and knowledge-based systems under the principles of precision medicine (Karaca *et al.* 2022a).

The use of specific information about a person's particular problem can help more precise and accurate diagnosis, plan effective working treatments and make prognosis accordingly. All these pave the way for improved patient outcomes as well as more efficient delivery of healthcare services. Fractional calculus is demonstrated to be a powerful tool for system identification including the ability of approximating nonlinear functions as a result of nonlinear activation functions and diverse inputs as well as outputs' employment. This enhances the processing and control of complex, chaotic and heterogeneous elements in complex and dynamic systems (Karaca 2023a). To put differently, the idea of fractional-order integration and differentiation besides the inverse relationship between them allows fractional calculus applications span across different domains including science, medicine and engineering, to name some. Within the mathematics-informed framework, the approach of fractional calculus can ensure reliable insights into complex processes that comprise a range of temporal-spatial gauges, which can pave the way for developing and implementing novel applicable models through fractional-order calculus.

In these regards, computational science and modeling are geared toward simulating and investigating complex systems via computers by employing different dimensions of mathematics such as entropy, wavelets, differential equations, fractional calculus, fractals, multifractals, fractional methods, quantum means, machine learning techniques, deep learning, AI applications, and so on. A well-constructed computational model, therefore, would consist of numerous variables that characterize the medical and biological system, which can make the performing of many simulated experiments via computerized means possible. Consequently, AI techniques with their combination of fractal, fractional analysis besides mathematical models have provided various applications which may also constitute the prediction of mechanisms that extensively range from living organisms to their intricate reciprocal interactions across spectra. Besides providing solutions to real-world complex problems both on local and global scale.

Across these lines, a neural network is regarded as a black box which approximates a function based on some exemplary computations, so when the complexity of the neural network increases, the functions it can approximate also become further complicated (Karaca *et al.* 2023a). To cite relevant works in these overlapping scopes, one paper (Joshi *et al.* 2023) reviews the use of fractional calculus in different ANN architectures known as fractional-order artificial neural networks (FANNs), which are important. Another paper is related to the review in fractional calculus in image processing (Yang *et al.* 2016) which shows the possibility that fractional-order, as fundamental mathematical tool, can be used to accurately model many systems in science and engineering.

The methods developed are used to solve the fractional systems' problem. Some of the techniques handled in the review are image segmentation, image denoising, image recognition, and so forth. The application of fractional calculus is handled by putting emphasis on signal processing, electromagnetics, continuum mechanics and physics as well. Accordingly, the study (Magin 2010) addresses the fractional derivative's accurate description of natural phenomena that are encountered in common engineering problems. It is further suggested that if the range of mathematical operations is expanded, it will be possible to develop novel and potentially beneficial functional relationships to model complex biological systems rigorously and directly. Last but not least, the study (Karaca 2023b) uses fractional calculus operators and Bloch-Torrey PDE for signal processing and neuronal multi-components to enable to the estimation and prediction of brain microstructure with Diffusion Magnetic Resonance Imaging (DMRI) and SpinDoctor. The study provides contributions to show the way how to tackle the complex structures inherent in the brain composition through sophisticated, integrative and multi-staged mathematical models to be employed effectively as part of healthcare services to maintain the life quality of the patients while providing facilitation in the clinical, medical and other related processes.

CONCLUSION, CONTEMPORARY MATHEMATICAL MEDICINE AND BIOLOGY THOUGHTS, AND FUTURE DIRECTIONS

Mathematical modeling in medicine and biology does not only comprise the implication of the development of advanced computer capabilities but also the ever-increasing access to the processes of complex systems. Mathematics being at the core of AI is capable of providing the means to structure thoughts, models, computations, simulations, schemes and eventually applications. Medical and biological applications of mathematical models situated at each relevant model considered should be profoundly measured, with each model brimming with biology. The ultimate reason for the ubiquity of mathematics in modern scientific and processes is the requirement of mathematical thinking embracing emerging frontiers of scientific inquiry so that complex phenomena can be understood and interpreted. In that regard, mathematical approaches include quantification of observations, modelling, classification, optimization, data processing, analysis, prediction and validation.

Upon the building of higher-level modeling tools and construction of larger modeling knowledge bases, critical processes like integration, cooperative developments and customization have become indispensable. Furthermore, the integration of mathematical modeling including stochastic processes and uncertainty quantization in machine learning and AI has transfigured the capabilities of these technologies, which allow for empowering thereof towards the aim of extracting useful insights and making accurate predictions, estimations and forecasting from the voluminous datasets. The leveraging of powerful computing resources and their integration with advanced image analysis techniques have also enabled the predictions to be manageable by demonstrating how complex systems will be behaving under particular conditions.

It is oft-cited that multiple paths should be directed at and linked with a common end stated towards the overarching aim of unifying sciences. In computational medicine and biology, this point becomes even more critical as it lies at the interface of individualization and personalization of medical decision-making processes so that short-term, medium-term and long-term health outcomes can be enhanced. This opportunity reduces the burden on healthcare and enables timesaving, which shows the aim of precision medicine that includes the tailoring of treatment to suit each patient's specific needs and characteristics. These processes also indicate the significance of prediction and estimation along with anticipation, control and management of the complexity of unexpected events which can be achieved depending on the detailed information retrieved from different biological elements, genetic cues, biomarkers, phenotypic factors, and so forth.

The consideration of these points is pivotal in terms of unraveling the complexities of the related models built, which can offer impactful insights into equilibria, adaptive systems and qualitative transformations underpinning disease dynamics. Aside from these intricate opportunities including the mathematical principles with AI capable of solving the problems related to the enabling of innovative applications, challenges are also at stake. In some instances, it is possible to encounter some difficulties concerning AI, deep learning or machine learning methods in the mathematical modeling of problems in medical and biological systems due to the hardships emerging in the modeling representations of complex cases, incidents and representations which manifest highly dynamic and heterogenous characteristics leading to the exacerbation of the reciprocal interactions and interrelated phenomena. Yet, these challenges can be overcome with the collaborative environment that includes the expertise, knowledge and abilities of individuals from different areas so that mathematical theories can be translated into practical and feasible solutions with tangible real-world impacts.

Based on these opportunities and ways of tackling complexities as well as challenges, some of the following future directions can be succinctly considered:

- Novel and adaptive techniques can be developed to be utilized for the diagnosis of molecular level diseases,
- The subtleties of disorders including genetic, epidemiological, infectious and biological ones,
- Advanced clinical and medical applications with regard to dynamic diseases can be constructed and implemented to deal with a variety of disorders and diseases,
- Mathematical models including stochastic and statistical models, population-dynamics models and complex-network models can be conceived and applied,
- New directions with novel formulations, designs and interpretations based on mathematical modeling processes can be constructed and solved through practicality as well as to-the-point specific means in fields of medicine and biology, among the other related ones,
- The description of major threads concerning mathematical modeling in medicine and biology in science dynamics can be expanded so that the impact of mathematical modeling can be enhanced with improved performance, increased problem-solving capabilities and augmented real-time decision-making processes.

Based on these considerations at the pillars of scientific perspective and holistic vision, the handling of uncertainty and complexity in clinical medicine and biological problems over their processes need the analysis of intrinsic features of almost all mathematical models which are formed based on three basic types of uncertainty: interval, Bayesian and stochastic. Consequently, the present overview has aimed at providing answers built on sophisticated models that encompass the explanation and interpretation of design and formulation. Within this framework, mathematical modeling in medicine and biology has been addressed while elaborating on the important role of philosophy of science as discussed under the context of mathematical modeling, theories as well as applications in medicine and biology.

Availability of data and material

Not applicable.

Conflicts of interest

The author declares that there is no conflict of interest regarding the publication of this paper.

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Examination and Evaluation of Obesity Risk Factors with Explainable Artificial Intelligence

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ABSTRACT There is an increasing need for effective methods for the detection and management of obesity, which is an important public health problem worldwide and is critical for the sustainability of health systems. This study examines the effectiveness of data preprocessing and machine learning techniques in detecting obesity. Data preprocessing steps, including the removal of unnecessary data, handling missing values, and addressing data imbalance, are necessary to enhance the accuracy of machine learning algorithms. In this study, data preprocessing steps were applied to an obesity dataset to make it suitable for machine learning. Using a dataset of 2111 patients, this study evaluates the effectiveness of machine learning techniques in detecting obesity. Following the completion of data preprocessing, obesity was identified using various machine learning algorithms, including Decision Tree Classification, Random Forest Classification, Naive Bayes Classification, KNN, and XGBoosting, and their performances were compared. According to the results, the XGBoosting algorithm exhibited the highest accuracy (0.92), precision, recall, and F1-score values. Explainable Artificial Intelligence (XAI) techniques, such as SHAP and InterpretML, were employed to understand the effects of obesity parameters and determine which parameters have a greater impact on obesity. By visualizing and analyzing the effects of obesity parameters, these techniques facilitated the identification of significant parameters in obesity detection. The findings demonstrate that the XGBoosting algorithm outperforms other algorithms in detecting obesity. Furthermore, XAI techniques play a crucial role in comprehending obesity parameters. Specifically, a family history of obesity and factors like FCVC and CAEC appear to have more significant effects compared to others.

KEYWORDS
Explainable AI
Obesity detection
Machine learning
XGBoost
InterpretML

INTRODUCTION

Obesity has become a significant global health issue, emphasizing the importance of understanding factors associated with obesity (Bray 2003). Fundamental physical attributes such as weight, height, and age have been studied for their effects on obesity (Tariq Aziz 2024). Traditional and artificial intelligence-based methods are employed for obesity detection, with this section focusing on the methods identified by experts and the role of artificial intelligence in obesity detection. The accurate processing and organization of obesity-related data significantly impact the success of machine learning models. Hence, this section will delve into data preprocessing steps and techniques as a crucial aspect. Machine learning models serve as effective tools for predicting obesity, with different models tested on the obesity dataset to analyze the obtained results. XGBoost, a widely used machine learning algorithm, plays a crucial role in obesity prediction. This section will focus on its application in the obesity dataset. Evaluating the results of the XGBoost model and applying explainable artificial intelligence techniques (SHAP, InterpretML) are essential for assessing the accuracy and reliability of the obtained results.

Sejong Oh (2021) conducted a study on explainable machine learning models for glaucoma diagnosis and interpretation. The aim was to develop a machine learning prediction model for diagnosing glaucoma and an explanation system for specific predictions. The study tested support vector machine, C5.0, random

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forest, and XGBoost algorithms for the prediction model. The proposed framework combines global and local interpretable methods, enhancing the transparency of complex models. This framework provides insight into judgments from complex models, guiding treatment strategies, and improving the prognosis of hepatitis patients (Sejong Oh 2021).

Junfeng Peng (2021) explored black-box models such as eXtreme Gradient Boosting (XGBoost), support vector machine (SVM), and random forests (RF). The proposed framework combining global and local interpretable methods improves the transparency of complex models and provides insight into judgments from the complex models, thereby guiding treatment strategies and improving the prognosis of hepatitis patients (Junfeng Peng 2021). Jungsu Park (2022) explored the interpretation of ensemble learning to predict water quality using explainable artificial intelligence. They developed an XGBoost ensemble machine learning model from eighteen input variables to predict Chl-a concentration. Their study showed that the model exhibited the most stable performance when the priority of input variables was determined by SHAP (Jungsu Park 2022).

A. Moore (2022) compared two machine learning methods, XGBoost and logistic regression, in predicting the risk of myocardial infarction (MI). Their findings suggest a future where Explainable AI may bridge the gap between medicine and data science (A. Moore 2022). Jaishree Meena (2022) aimed to find potential diagnostic biomarkers for SCC by applying eXplainable Artificial Intelligence (XAI) on XGBoost machine learning models trained on binary classification datasets. After successfully incorporating SHAP values into the ML models, they identified 23 significant genes associated with the progression of SCC (Jaishree Meena 2022).

B. Kui (2022) identified the most critical factors and their contribution to prediction using SHapley Additive exPlanations (SHAP). They developed a free and easy-to-use web application in the Streamlit Python-based framework for explanation and confidence estimation (B. Kui 2022). Chang Hu (2022) studied the application of interpretable machine learning for early prediction of prognosis in acute kidney injury. Their findings highlight Glasgow Coma Scale (GCS), blood urea nitrogen, cumulative urine output on Day 1, and age as the top 4 most important variables contributing to the XGBoost model (Chang Hu 2022).

Hafsa Binte Kibria (2022) proposed an ensemble approach for predicting diabetes mellitus using a soft voting classifier with explainable AI. They provided global and local explanations using Shapley additive explanations (SHAP) to aid physicians in understanding model predictions (Hafsa Binte Kibria 2022). Artificial intelligence (AI) has diversified into various healthcare applications, such as health services management, predictive medicine, clinical decision-making, and patient data and diagnostics. Hui Wen Loh (2022) aimed to draw attention from the XAI research community to areas of healthcare requiring more focus (Hui Wen Loh 2022). Isfafuzzaman Tasin (2022) developed an automatic diabetes prediction system using various machine learning techniques. They implemented an explainable AI approach with LIME and SHAP frameworks to understand how the model predicts final results (Isfafuzzaman Tasin 2022).

The introduction provides a comprehensive overview of the significance and challenges of utilizing machine learning models, particularly in healthcare. The literature review section delves into various studies that have explored the application of explainable artificial intelligence (XAI) techniques to enhance the interpretability of machine learning models in medical diagnosis and prognosis. However, this study aims to contribute to the existing body of knowledge by offering a unique perspective on the interpretability of machine learning models. Specifically, we focus on the importance of moving away from black-box models and instead emphasize the utilization of techniques that enable us to understand the contributions of input parameters to output parameters. By employing methods such as SHapley Additive exPlanations (SHAP), we can gain insights into the extent to which each input parameter influences the output parameter. This approach not only enhances the transparency of the model but also facilitates the development of more robust and reliable predictive models in healthcare. In the Materials and Methods section, a comprehensive description of the dataset was provided, along with elucidation on the operational principles of the employed machine learning algorithms and the functioning of the utilized explainable artificial intelligence algorithms. The Results section will present the obtained outcomes, while in the Discussion section, an overall overview of the study will be provided. The coherence and scope of the obtained results will be discussed, along with an examination of how the study may inspire further research endeavors.

MATERIALS AND METHODS

Dataset

The dataset used in this study contains a range of demographic and physiological features related to obesity. The features of the dataset include: The dataset initially contained missing or conflicting data. Therefore, preprocessing steps were applied to prepare the dataset. The structure and characteristics of the dataset were examined to identify missing or abnormal values. The ”NObeyesdad” feature, which was unnecessary for analysis, was removed from the dataset. Categorical values in some features were converted to numerical values. Body Mass Index (BMI) was calculated, and participants were assigned to six different obesity categories based on their BMI. Data types of some features were appropriately converted. Obesity categories were converted to numerical values to prepare for analysis. With these preprocessing steps, the dataset was made suitable for analysis and obtaining results.

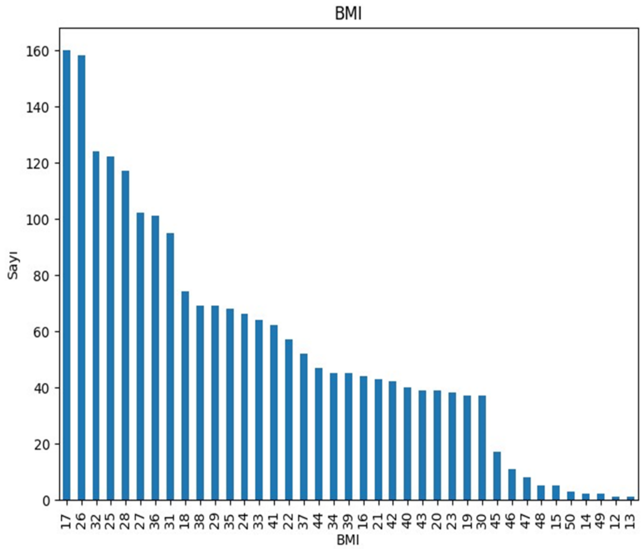

Figure 1 Generated BMI column values

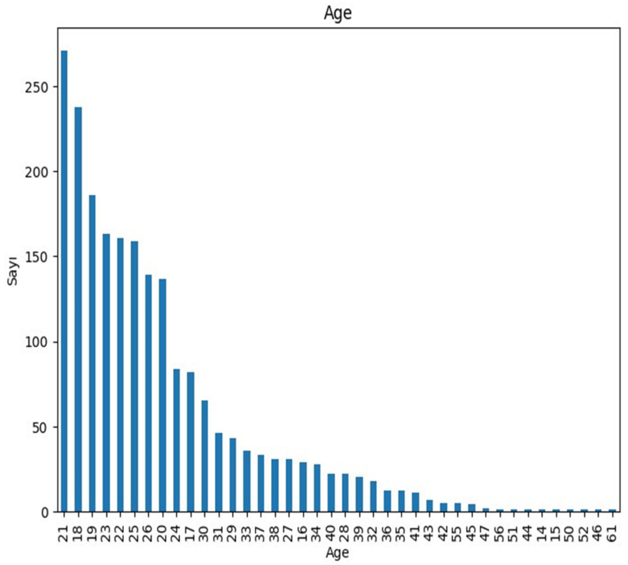

Figure 2 Age values

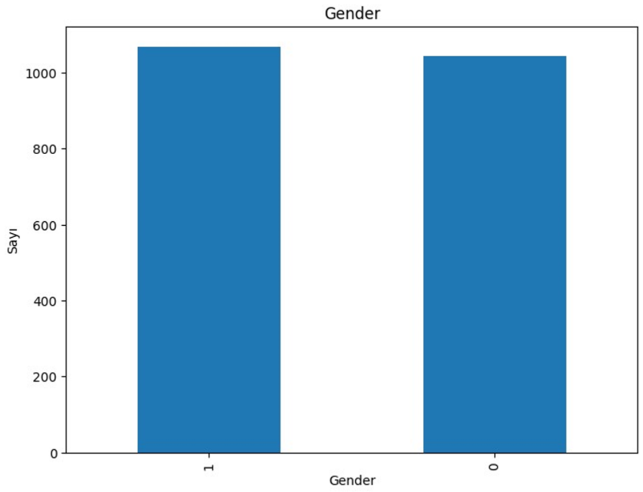

Figure 3 Gender values

Machine Learning

Decision Tree Classification Decision Tree Classification is a machine learning method commonly used for classification problems. A decision tree is widely used for understanding complex relationships in a dataset and making predictions (Charbuty 2021). There are multiple algorithms available for implementing decision trees. C4.5 can handle both categorical and numerical features. It utilizes an advanced algorithm to optimize information gain. Entropy is a concept that measures uncertainty in a system. In decision trees, entropy is used to measure the homogeneity or heterogeneity of the distribution of data points at a node. A lower entropy value indicates a more homogeneous data distribution. Entropy of P is given by (Hssina 2014).

$$\text{Entropy}(X) = -\sum_{x} p(x) \cdot \log_2(p(x)) \tag{1}$$

In the formula, $p(x)$ represents the probability of randomly selecting an element from class x.

Random Forest Classification Random Forest classification is a machine learning technique where multiple decision trees are assembled. Each decision tree is trained on randomly sampled subsets of the data, and then these trees are aggregated to form a forest. Each tree is split using randomly selected features, ensuring diversity. Compared to a single decision tree, Random Forests offer better generalization and higher accuracy. This method is commonly used for classification problems and tends to perform well on high-dimensional and complex datasets (Boateng 2020).

Naive Bayes Classification Naive Bayes classifiers are a family of models based on Bayes' Theorem (Berrar 2019). Bayes' Theorem is given by:

$$P(A|B) = \frac{P(B|A) \cdot P(A)}{P(B)} \tag{2}$$

The expression $P(A|B)$ represents the probability of event A occurring given that event B has occurred. $P(B|A)$, on the other hand, represents the probability of event B occurring given that event A has occurred. $P(A)$ denotes the marginal probability of event A, i.e., the probability of event A occurring when event B is ignored. Similarly, $P(B)$ denotes the marginal probability of event B, i.e., the probability of event B occurring when event A is ignored.

Naive Bayes classification is a machine learning algorithm used to predict the probability of an instance belonging to a certain class. It assumes independence among features to determine the class of an instance, hence the term 'naive.' The Naive Bayes classifier utilizes the relationships between features based on training data to compute the probability of an instance belonging to a given class. As a result, this algorithm is often preferred as a simple yet effective classification solution and yields successful results, particularly in areas such as text classification. Naive Bayes classification can work swiftly and efficiently in high-dimensional datasets and real-time applications (Jadhav 2016).

K-Nearest Neighbors K-Nearest Neighbors (KNN) is a simple and effective classification algorithm that utilizes the labels of neighboring observations to determine the class of an observation. Its fundamental principle is to use the labels of the k nearest neighbors of a new observation to determine its class. The KNN algorithm employs similarity measures between examples in a pre-labeled training dataset. The similarity between observations is typically calculated using Euclidean, Manhattan, or Minkowski distance measures. While the algorithm is commonly used for classifying data points, it can also be applied to regression problems. However, the computational intensity and memory requirements of KNN can be a disadvantage for large datasets.

$$\sqrt{\sum_{i=1}^{k} (x_i - y_i)^2} \tag{3}$$

$$\sum_{i=1}^{k} |x_i - y_i| \tag{4}$$

$$\left(\sum_{i=1}^{k} (|x_i - y_i|)^q \right)^{1/q} \tag{5}$$

$$d(x,y) = \sqrt{\frac{1}{2} \sum_{i=1}^{n} (x_i - y_i)^2} \tag{6}$$

XGBoosting XGBoost is a leading library built upon a machine learning technique called gradient tree boosting. Gradient tree boosting is a powerful technique that captures complex data dependencies, resulting in successful outcomes across various datasets. XGBoost stands out with the following features (Chen 2016):

- **High Prediction Power:** XGBoost has the ability to generate accurate and precise predictions, ensuring high accuracy in its forecasts.
- **Preventing Overfitting:** XGBoost employs various techniques to prevent overfitting, making it a model with high generalization ability.
- **Handling Missing Data:** XGBoost excels in handling missing data, extracting meaningful insights even from incomplete datasets.
- **Fast Processing:** XGBoost operates swiftly due to its optimized algorithms, making it suitable for processing large datasets efficiently.

XGBoost leverages software and hardware optimization techniques to achieve superior results with fewer resources. This capability has positioned XGBoost as one of the top decision tree algorithms.

Explainable Artificial Intelligence

SHAP SHAP represents an Explainable AI (XAI) methodology, employing Shapley values derived from game theory to offer intelligible insights into the pivotal and influential factors influencing the model's forecasts (Zhang 2023). Shapley values originate from cooperative game theory and serve as a concept that impartially gauges a player's contribution. SHAP furnishes a structure for comprehending the mechanism by which a model generates its predictions leveraging these values (Feng 2021).

InterpretML InterpretML (Machine Learning Interpretation) encompasses a range of techniques and methodologies aimed at enhancing the comprehensibility of machine learning model decision processes. It is particularly imperative to elucidate the factors underpinning a specific prediction or classification and to elucidate the rationale behind a model's attainment of a particular outcome. Among the pivotal techniques within InterpretML is the analysis of "Feature Importance". This method is employed to discern the most impactful features in a model's predictions, thereby facilitating an understanding of which features exert a greater influence on the model's outputs. Additionally, methodologies such as "Partial Dependence Plots" and "SHAP Values" are utilized to visually represent and expound upon the influence of specific features on prediction outcomes. These approaches serve as essential tools for fostering a deeper comprehension of model behavior (Nori 2019).

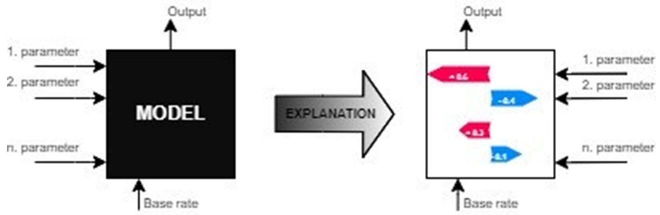

Figure 4 SHAP Structure

RESULTS AND DISCUSSION

The dataset used for the machine learning updates first went through a few pre-processing steps. First, the "NObeyesdad" column was removed from the dataset because it could not be used in model training. Then, some features in the categories were coded as "yes" and "no" in the data set. These features had to be converted into digital values in order to train the model correctly. This conversion is used to introduce properties such as family history with overweight, FAVC, SMOKE, and SCC. Additionally, categorical features such as "Gender", "CAEC", "CALC" and "MTRANS" were converted into digital values through the processing of the categories. Body mass index (BMI) was calculated based on the "weight" and "height" features in the dataset. The people were then divided into obesity categories (underweight, normal, overweight, obesity I, obesity II, obesity III) based on the recorded BMI values. These categories were used to determine tolerance to specific BMI ranges and levels of obesity.

Obesity categories were converted into social digital values during model training. This transformation assigns a value of 0 to the categories "Underweight," "Normal," and "Overweight," while assigning a value of 1 to the categories "Obesity I," "Obesity II," and "Obesity III." This transformation was performed to increase the pores of the model.

Various machine learning models have been applied in machine learning, such as Decision Tree Classification, Random Forest Classification, Naive Bayes Classification, KNN, and XGBoosting. The performance of each model was evaluated using Precision, Recall, F1-Score, and Accuracy metrics. Precision, Recall, F1-Score, and Accuracy are commonly used metrics to evaluate the performance of machine learning models. Precision measures how many of the examples the model classifies as positive are actually positive, while Recall measures how much of the true positive examples are correctly classified. F1-Score is the harmonic average of Precision and Recall and provides a balanced measure of performance. Accuracy shows the proportion of correctly classified samples. The results obtained are presented in the table below:

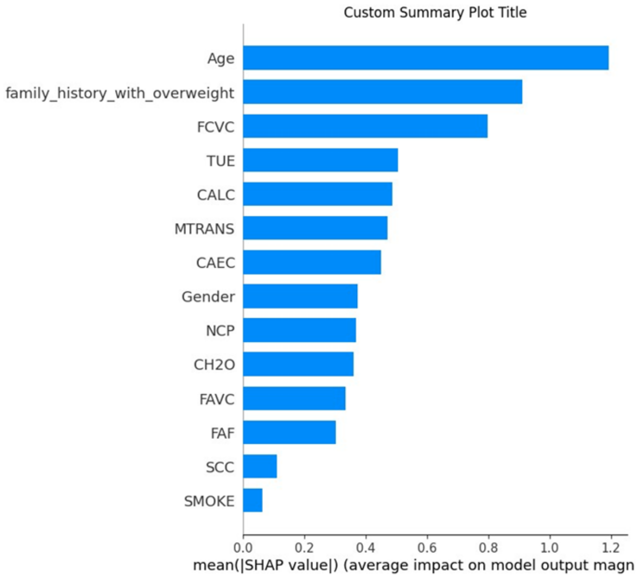

Figure 5 Extracting features with SHAP

Table 1 Classification Metrics

Model	Precision	Recall	F1-Score	Accuracy
XGBoosting	0.92	0.92	0.92	0.92
Random Forest Classification	0.91	0.91	0.91	0.91
Decision Tree Classification	0.89	0.89	0.89	0.89
KNN	0.87	0.87	0.87	0.87
Naive Bayes Classification	0.82	0.78	0.78	0.78

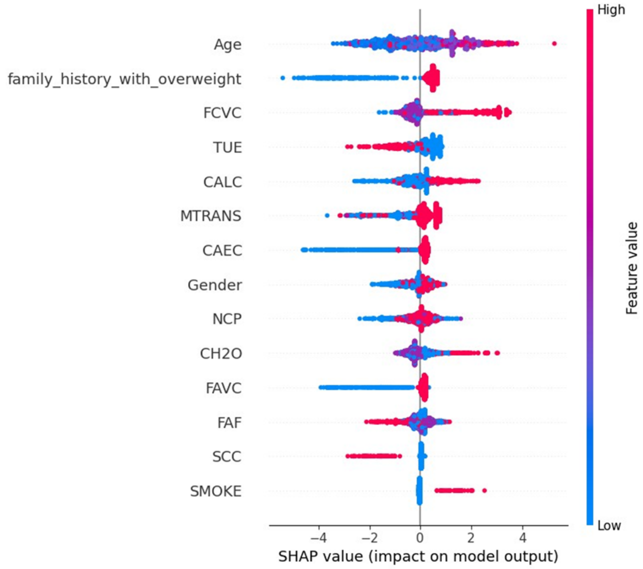

Figure 6 SHAP Summary Plot

According to the results, the XGBoosting model achieved the highest Precision, Recall, F1-Score, and Accuracy values. Therefore, it has been determined as the most effective model for classifying data.

After the machine learning phase, factors influencing obesity risk were examined using SHAP analysis. According to the analysis results, the effect of age on obesity was found to be significant, with obesity risk increasing as age increases. Additionally, it was observed that individuals with a family history of obesity increase their own obesity risk, emphasizing the role of genetic factors. Low consumption of vegetables was found to be associated with obesity risk, highlighting the critical role of regular vegetable consumption in preventing obesity. The widespread use of technological devices was found to increase obesity risk, underscoring the importance of physical activity in obesity prevention. Furthermore, monitoring daily caloric intake and utilizing active transportation modes were identified as factors that reduce obesity risk. Snacking habits were found to be associated with obesity risk, emphasizing the importance of regular and balanced meal planning in obesity prevention. Lastly, the effect of gender on obesity was found to be related to hormonal differences and lifestyle factors, with the female gender increasing obesity risk. These findings contribute significantly to understanding the complex etiology of obesity and developing effective preventive strategies.

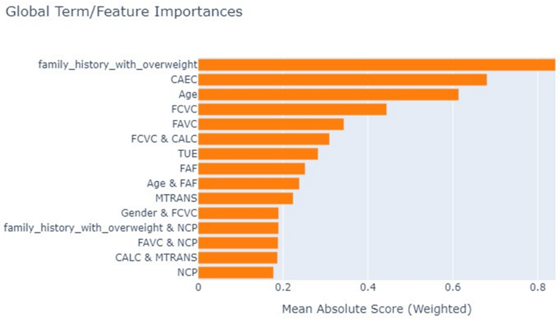

Figure 7 The overall impact of features on the model's predictions

InterpretML In the graph interpretation, the prominent features of the model were family history and overweight, CAEC, and age. These findings emphasize that health status plays an important role in explaining obesity risk. Furthermore, the impact of age on obesity needs to be considered. Other important characteristics indicated in the graph were also observed to contribute to the model's predictions. However, it was noted that the increase of NCP was low. These results allow health professionals to develop more effective solutions for the assessment and prevention of obesity risk. In conclusion, these findings presented in the graph provide an important resource for evaluating the presentation of the model and guiding health policies.

CONCLUSION

In this study, it was aimed to determine the parameters effective in determining obesity and to measure these weights. Various parameters including lifestyle factors such as gender, age, height, weight, and family history of obesity were analyzed using a dataset of 2111 patients. Machine learning techniques, specifically XGBoost and Explainable Intelligence Machine algorithms, were employed to train the dataset. Demonstrated a successful detection of obesity with an accuracy of 0.917 using XGBoost. Additionally, effective parameters and their weights in classification were determined using explainable artificial intelligence (XAI) and InterpretML methods. In conclusion, this study contributes to the understanding of factors related to obesity and the development of effective treatment strategies. The results highlight the importance of further integrating these findings into clinical practice and obesity management. Future research should focus on exploring how these findings can be effectively applied in clinical settings.

Availability of data and material

Not applicable.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The author has no relevant financial or non-financial interests to disclose.

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ANN Algorithms for Parkinson's, ALS, Huntington, and Healthy Walking Detection

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ABSTRACT In this study, the utilization of artificial neural networks (ANN) algorithms, in the diagnosis of neurodegenerative diseases were examined. Data obtained from the measurement of walking parameters were evaluated for disease diagnosis using the ANN model among individuals with ALS, Parkinson's, Huntington's, and healthy individuals. Comparative analyses conducted using Levenberg-Marquardt, Bayesian Regularization, and Scaled Conjugate Gradient algorithms demonstrate that the Levenberg-Marquardt algorithm provides the most effective diagnosis with a success rate of 99%. This study highlights the potential of artificial neural networks in the early diagnosis of neurodegenerative diseases and lays a foundation for future research. In conclusion, artificial neural networks may play a significant role in the diagnosis of neurodegenerative diseases, but further research and method development in this area are warranted.

KEYWORDS
Machine learning
Neurodegenerative diseases
Disease diagnosis
Parkinson's
ALS
Huntington

INTRODUCTION

The control mechanism responsible for the movement of muscles and joints is provided by our nervous system (Bart 2018). Among the fundamental structures that make up our brain are nerve cells, or neurons, and the points where these neurons connect with other neurons, called synapses. All the processes in our nervous system and our memory are associated with electrical currents in neurons. The exchange of information between neurons occurs through these electrical currents. Signals from our brain or other parts of the central nervous system are transmitted to the muscles and joints responsible for movement via motor neurons; the point where muscle and nerve meet is called the motor unit (Yuldashev 2022). Damage or wear and tear that may occur in neurons and motor units can lead to disruptions in nerve transmission, causing problems in our movement system and senses. Additionally, improper functioning of the connections between nerve cells in the brain, known as synapses, can also cause disruptions in many systems, especially the movement system. Such disorders are generally referred to as neurological diseases (Aslan *et al.* 2021).

Amyotrophic lateral sclerosis (ALS) is the most common among acquired motor neuron diseases. Although not certain in our country, it is estimated that the prevalence is 3-8/100,000 and the annual incidence is in the range of 1-2/100,000 globally. The symptoms of the disease vary individually, but commonly include muscle atrophy and weakness, communication difficulties due to speech, pain, difficulty swallowing (dysphagia), deep vein thrombosis, respiratory failure, fatigue, sleep problems, anxiety, and depression (Kaya and Özcan 2017). In the advanced stages of ALS, patients lose their motor functions. As muscle weakness progresses, there are losses in basic physical abilities such as speech, swallowing, hand use, and walking, making communication with patients increasingly difficult (Turner and Benatar 2015).

Huntington's disease is a genetic disorder characterized by progressive neurodegenerative processes. It is more common, especially in Northern European countries, with a prevalence reported to be approximately 10-13 cases per 100,000 people (McColgan and Tabrizi 2018). This disease is accompanied by uncontrolled movements, progressively worsening cognitive functions, and psychiatric disorders. Motor symptoms typically appear at the onset of the disease; clumsiness, difficulty in eye movements, uncontrolled movements, slowing of movements, and speech disorders become apparent in the early stages (Gültekin and Ekinci 2017). In the later stages of the disease, symptoms such as uncontrolled movements, slowing of movements, spasticity, and rigidity develop in addition to motor signs. At the cognitive level, slow progressive cognitive impairment, forgetfulness, attention deficits, and in later stages, speech difficulties and dementia may be observed. The diagnosis of Huntington's disease is based on clinical examination, the pres-

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ence of similar histories in the family, and genetic analyses (Bates *et al.* 2015).

Parkinson's disease is the second most common neurodegenerative disorder after Alzheimer's disease, and its frequency increases with age (Marsden 1994). Although primarily considered a movement disorder, psychotic and cognitive impairments are also frequently associated with this disease. Parkinson's disease is understood to be characterized by approximately an 80% reduction in dopaminergic neurons in the substantia nigra pars compacta region of the brain. Damage to neurons in this region disrupts the regulation of movements and leads to the onset of Parkinson's disease. A decrease in dopamine levels results in the loss of movement fluidity, slowing, and tremors (Fahn 2003). The four main descriptive features of Parkinson's disease are resting tremor, rigidity, bradykinesia, and impaired postural reflexes. These symptoms typically begin subtly and progress asymmetrically. Despite clinical tests used in the diagnosis of Parkinson's disease, there is no biological marker to clarify the diagnosis (Pallone 2007).

Walking on all fours is extremely balanced and comfortable, while walking on two feet becomes difficult and requires flawless neuronal control (Güler 2011). Superior brain control is necessary for a person to be able to progress in the designated direction and speed and to cope with external influences. Without superior brain control, only basic balance and stepping responses can be generated at the spinal cord level (Burke *et al.* 2001). In order to walk for long periods without fatigue, the brain, spinal cord, nerves, muscles, bones, and joints must work together in harmony, and the timing and strength of joint and muscle movements must be appropriate. Additionally, receiving accurate and timely feedback about body position and speed is important for walking. Any problem that disrupts this balance increases energy requirements and affects walking (Yavuzer 2014). Gait analysis presents this information in numerical values by examining the muscles and skeletal system, normal walking characteristics should be known for accurate diagnosis and treatment, pathological conditions should be distinguished, and the causes affecting walking should be understood (Cimolin and Galli 2014). Gait analysis is widely used, especially in fields such as orthopedics, neurology, and sports medicine, to assess health conditions (Akalan and Temelli 2014).

Artificial neural networks (ANN), inspired by the biological nervous system of humans, are sophisticated mathematical models capable of learning and decision-making based on acquired knowledge. This advanced computational method learns complex relationships between events and data by analyzing the data samples provided to the system. The learning process enables the system to make logical and accurate decisions when faced with new situations or examples that it has not encountered before, by utilizing the knowledge and experiences gained in the past. The ability of artificial neural networks to perform these tasks makes them valuable tools in various fields such as data classification, prediction, and pattern recognition. These systems can identify complex relationships and patterns through provided examples, thereby making informed predictions in new scenarios they encounter (Öztürk and Şahin 2018).

There are many studies in the literature that utilize artificial neural networks for the classification of neurodegenerative diseases. One such study conducted by Kaczmarczyk *et al.* (2009) investigates the accuracy of three different models in classifying the gait patterns of post-stroke patients. These methods include qualitative analysis of gait kinematics, as well as two different quantitative research types: minimum and maximum joint angle values, and the progression of all joint angle changes. The study concludes that ANN analysis is superior to the other two methods (qualitative variable analysis and min/max joint angle analysis) in classifying the gait patterns of post-stroke patients, dividing them into three types.

Erdaş et al. Berke Erdaş *et al.* (2022) conduct a study to test the accuracy of deep learning-based classification of ALS, Huntington's, and Parkinson's patients using walking parameters. In the study, one-dimensional walking data and the conversion of one-dimensional data into rapid response codes result in two-dimensional data. It is stated that the obtained data performs well in classification with convolutional neural networks. Shi *et al.* (2022) use IMU sensors to detect freezing of gait in Parkinson's patients during walking. In the study, convolutional neural networks are used to detect freezing of gait with the obtained data. The study concludes that it achieves high accuracy in detecting freezing movements. Prabhu et al. Prabhu *et al.* (2020), aiming to overcome the limitations of traditional Fourier analysis, investigate the dynamics of human walking by adopting Recurrence Quantification Analysis (RQA). It is found that RQA is an effective analysis tool for non-linear and non-stationary data.

In the study, Support Vector Machine (SVM) and Probabilistic Neural Network (PNN) are used to classify walking signals of individuals with neurodegenerative diseases such as ALS, Huntington's, and Parkinson's, including 13 patients and 13 healthy control individuals, with two different classification models. Binary classification results using SVM and PNN show accuracy rates ranging from 96% to 100%. Setiavan et al. Setiawan *et al.* (2022) design a convolutional neural network (CNN) to classify neurodegenerative diseases (NDD) using time-frequency spectrograms of walking force signals, aiming to support physiotherapists in the early diagnosis, effective treatment planning, and monitoring of disease progression. The proposed NDD detection algorithm effectively distinguishes gait patterns between HC and NDD patients, achieving 94.34% sensitivity, 96.98% specificity, 96.37% accuracy, and 0.97 AUC value using 5-fold cross-validation.

Yücelbas C. and Yucelbas S. Yücelbaş and Yücelbaş (2019) mention in their study that using the ANN algorithm for the statistical classification of walking analysis data in Parkinson's disease proves successful. Balaji et al. Balaji *et al.* (2020) demonstrate in their study, where they diagnose and stage 93 Parkinson's patients and 73 healthy individuals using machine learning with walking parameters, that they achieve accuracy rates ranging from 76% to 100%. Shetty and Rao Shetty and Rao (2016) show in their study, where they perform machine learning on Parkinson's, ALS, and Huntington's patients, that they achieve an accuracy rate of 83% and can differentiate between different diseases. In the study conducted by Akgün et al., where ALS patients' walking signs are trained using the ANN model for disease diagnosis, 13 normal and 13 ALS patient individuals are included. The study explains that a success rate of 87.5% is achieved in distinguishing ALS patients.

Neurodegenerative diseases such as ALS, Huntington's disease, and Parkinson's disease pose significant challenges in diagnosis and management due to their complex and progressive nature. Gait analysis has emerged as a valuable method for assessing motor function and detecting subtle changes indicative of these conditions. The aim of this study is to innovate disease diagnosis by leveraging the power of artificial neural networks, specifically the ANN algorithm, to analyze walking parameters associated with ALS, Huntington's, and Parkinson's diseases. Our approach seeks to diagnostic processes by providing a quick and easy-to-use tool for clinicians to differentiate between pathological and healthy gait patterns.

METHOD

Data

In this study, data was obtained from the PhysioNet website (Hausdorff *et al.* 2000). The obtained data from ALS patients were collected from the Neurology Clinic at Massachusetts General Hospital. Records from patients with Parkinson's disease (n = 15), Huntington's disease (n = 20), or ALS (n = 13) were obtained from this database. Records from 16 healthy control subjects were also included. Subjects were instructed to walk at their normal speed in a 77 m corridor for 5 minutes. A force-sensitive insole was placed in the subject's shoe to measure the walking rhythm and timing of the walking cycle. With this information, the step duration or the duration of the walking cycle (the time from the first contact of one foot to the subsequent contact of the same foot) was determined for each step. The average walking speed of each subject was also determined by dividing the total distance walked by the walking time.

The collected data consists of walking speed, walking duration, and turn durations for the right and left legs. The obtained data form a dataset with 16 healthy data, 15 Parkinson's patient data, 20 Huntington's patient data, and 13 ALS patient data. For input data, the last 4 data of each dataset were defined as a separate matrix for testing. Accordingly, a single-column matrix consisting of 14 data for healthy subjects, 11 data for Parkinson's patients, 16 data for Huntington's patients, and 9 data for ALS patients was created. This matrix will be provided to the ANN as a 6-input input data.

For output data, a single column was created where the number 1 corresponds to healthy data, 2 to Huntington's data, 3 to Parkinson's data, and 4 to ALS data. Test data was separated as described above and arranged in a single column matrix, with four data groups arranged vertically. Test output data was created in the same manner as the input data, arranged in groups of four in a single column matrix.

ANN Model

The purpose of the modeling stage in this application is to diagnose whether the input data obtained from walking parameters belong to the healthy group, Huntington's patients, Parkinson's patients, or ALS patients. In this study, ANN algorithms including the Levenberg-Marquardt Algorithm, Bayesian Regularization Algorithm, and Scaled Conjugate Gradient Algorithm were compared and used in the diagnosis differentiation. At the end of the training, the relationship between success rate and algorithm in disease determination is established. An ANN model was created using Neural Network Training Tool in MATLAB. The ANN model was designed with 6 inputs, 10 hidden layers, and 1 output (Figure 1).

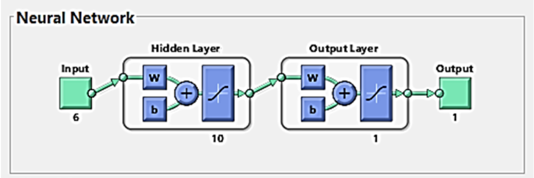

Figure 1 ANN structure of the model.

The performance function has been determined as Mean Square Error (MSE). A neural network with 2 layers has been constructed, with 100 hidden layers and 10000 epochs. Below, the training results for the Levenberg-Marquardt, Bayesian Regularization, and Scaled Conjugate Gradient algorithms are shown in Figures 2-10.

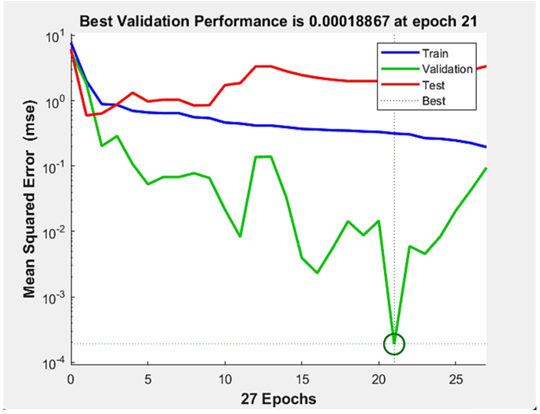

Figure 2 The performance graph for the Scaled Conjugate Gradient Algorithm.

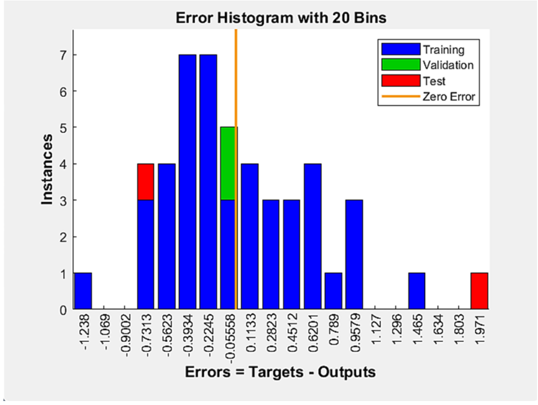

Figure 3 The distribution of error rates for the Scaled Conjugate Gradient Algorithm.

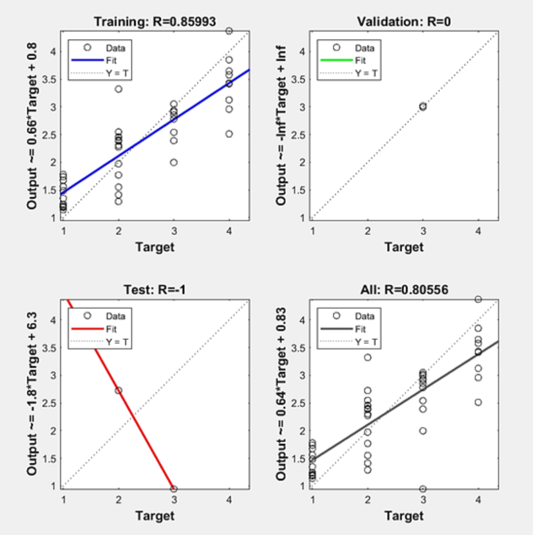

Figure 4 The regression graph for the Scaled Conjugate Gradient Algorithm.

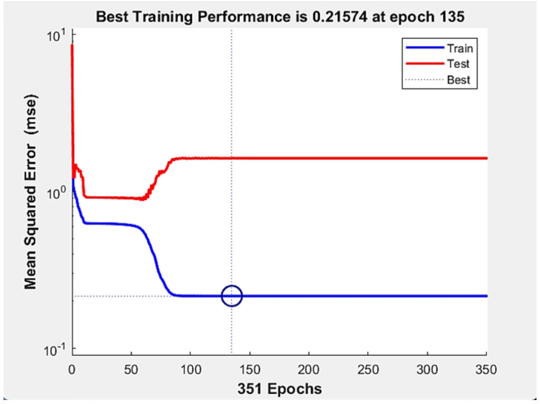

Figure 5 The performance graph for the Bayesian Regularization Algorithm.

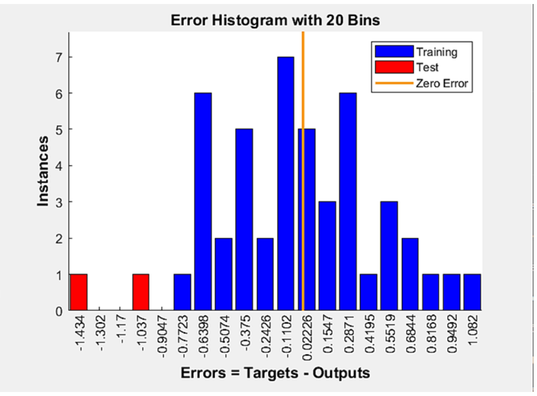

Figure 6 The error distribution graph for the Bayesian Regularization Algorithm.

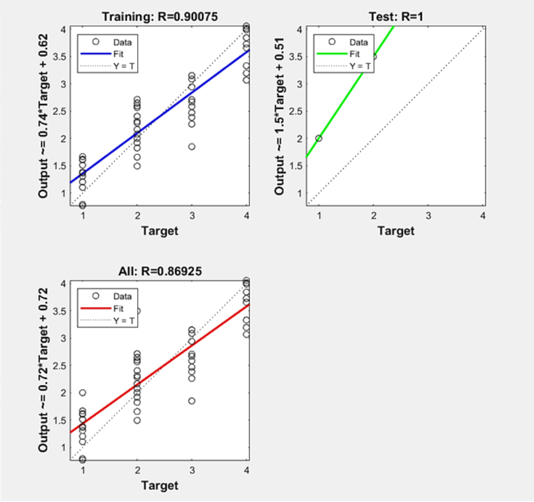

Figure 7 The regression graph for the Bayesian Regularization Algorithm.

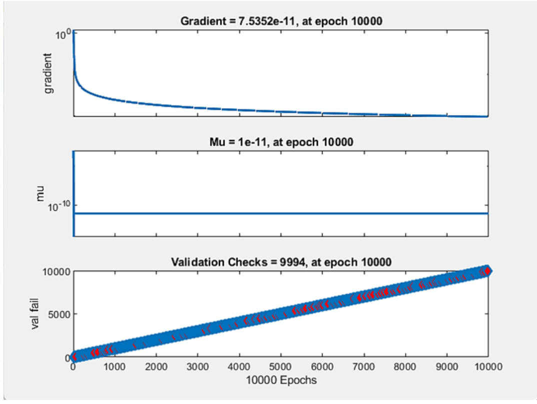

Figure 8 The training graph for the Levenberg-Marquardt Algorithm.

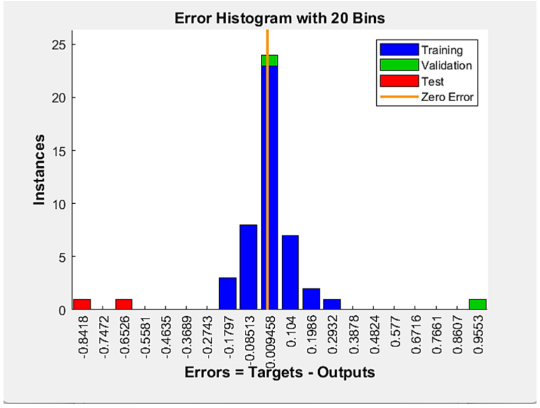

Figure 9 The distribution of error rates for the Levenberg-Marquardt Algorithm.

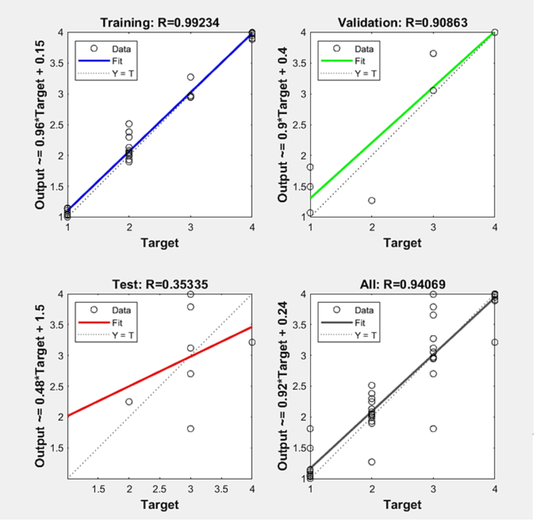

Figure 10 The regression graph for the Levenberg-Marquardt Algorithm.

RESULTS

In the diagnosis of neurodegenerative diseases such as ALS, Parkinson's, Huntington's, and healthy individuals, attempts were made to determine the disease using an ANN model based on walking parameters, and success rates were compared among ANN algorithms. The success rates of the algorithms used in the diagnosis of neurodegenerative diseases are as follows: Levenberg-Marquardt algorithm achieves 99%, Bayesian Regularization algorithm achieves 90%, and Scaled Conjugate Gradient algorithm achieves 85% success rate (Figure 11).

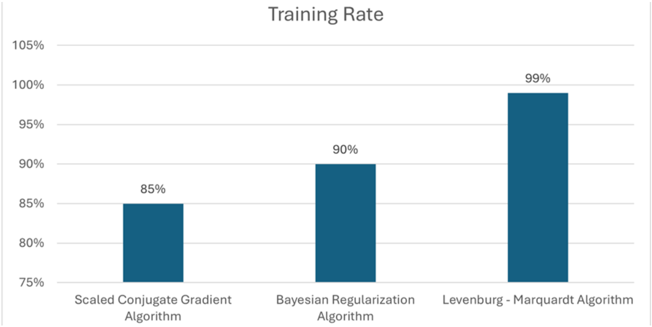

Figure 11 The success rates of the algorithms.

The Levenberg-Marquardt Algorithm is considered to provide the most successful diagnosis among the algorithms, with a success rate of 99%. When comparing the results of the study between the test and training datasets, it is observed that while the training data exhibit high success rates, the test data show lower success rates. This discrepancy is attributed to overfitting in the ANN algorithms due to the limited amount of data, indicating that the training did not achieve high performance. Therefore, it is suggested that future studies should utilize larger datasets to address this issue.

CONCLUSION

In this study, we explored the potential application of artificial neural networks (ANNs) for diagnosing neurodegenerative diseases based on walking parameters. Our findings demonstrate that ANNs, particularly utilizing the Levenberg-Marquardt Algorithm, can achieve a remarkable 99% success rate in disease diagnosis among individuals with ALS, Parkinson's, Huntington's, and healthy controls. This highlights the significant promise of ANNs as valuable tools in early disease detection and clinical decision-making.

While our study focused on walking parameters, the potential of ANNs extends to broader applications within neurodegenerative disease diagnostics. Future research could explore the integration of additional physiological, imaging, and genetic data into ANN models to enhance diagnostic accuracy and facilitate personalized treatment strategies. Furthermore, the successful implementation of ANNs in this context underscores the need for collaborative efforts between clinicians, data scientists, and engineers to translate innovative technologies into clinical practice. Establishing robust, validated ANN models for neurodegenerative disease diagnosis requires interdisciplinary collaboration and rigorous validation against diverse patient cohorts.

Availability of data and material

Not applicable.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The authors have no relevant financial or non-financial interests to disclose.

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Bibliometric Analysis of Publications on Action Recognition, Convolutional Neural Network, Video Surveillance During 2012-2021

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ABSTRACT Action recognition based on convolutional neural networks (AR-CNN) has been developing rapidly in recent years. It is of great significance to conduct a deep analysis to understand the recent development of AR-CNN. However, a limited number of studies examining the research status of this field could be found. Therefore, this study aims to quantitatively assess the publications related to the SciVal topic "Action Recognition; Convolutional Neural Network; Video Surveillance (T.561)" in computer vision research. This study focused on six aspects: literature distribution characteristics analysis, the development trend, citation analysis, collaborative analysis, keyword analysis, and thematic evolution, using VOSviewer and Bibliometrix. The relevant publications were retrieved from Scopus in the period 2012–2021. A total of 6633 publications were identified by 9088 different authors; 62% were conference papers, and 35% were research articles. China and the USA contributed 39.7% and 17.9% of the total publications, respectively. The authors' productivity demonstrated variability in alignment with Price's Law, yet exhibited consistency when evaluated under the framework of Lotka's Law. Ling Shao was the most productive author, with 48 papers (0.7%). Chinese Academy of Sciences was the most productive affiliation, with 259 papers (3.9%). The first Bradford site consisted of Computer Science Lecture Notes with 617 publications. A moderately significant correlation was revealed between the country's publications and GDP per capita. The overall results show that the number of AR-CNN-related documents has increased significantly in recent years, with rapid growth from 2016. Although publications on AR-CNN were published mainly in European journals, China led the scientific production.

KEYWORDS
Action recognition
Deep learning
Convolutional neural network
Video surveillance
Artificial intelligence
Bibliometric analysis

INTRODUCTION

Action recognition (AR) is used to decipher an action/activity component from a video or image scene. It is a fundamental and challenging topic in computer vision (Ahad 2011). It has drawn the attention of many researchers due to its varying applications, such as security systems, medical systems, virtual reality, autonomous vehicles, ambient intelligence, human behavior analysis, robotics, human-computer interaction, etc. (Khan *et al.* 2020; Sudha *et al.* 2017; Xia *et al.* 2015; Oh *et al.* 2011; Popoola and Wang 2012). At its very early stage, action recognition was used to categorize human actions, security reasons, and surveillance systems (Oh *et al.* 2011; Bobick and Davis 1996; Rosales and Sclaroff 2001; Karpathy *et al.* 2014). Later, with the breakthrough and fast development of deep learning technology, action recognition has advanced considerably. Much research was conducted based on deep learning to recognize human actions in videos (Simonyan and Zisserman 2014; Donahue *et al.* 2015; Zhou *et al.* 2018). Since videos are 3D Spatiotemporal signals, the main idea behind the majority of these studies is to extend Convolutional Neural Networks (CNNs) to include the temporal information contained in videos. CNN is a deep model that ob-

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tains complicated hierarchical features via convolutional operation alternating with sub-sampling operation on the raw input images (LeCun *et al.* 1998). Since CNN was adopted in video-based human action recognition (HAR), many extensions of CNN (such as deep neural network (DNN), Recurrent Neural Networks (RNNs), 3D CNNs, etc.) have been proposed to improve both the accuracy and efficiency of human action recognition from videos (Karpathy *et al.* 2014). This increasing interest in action recognition based on CNN (AR-CNN) resulted in numerous research papers. While bibliographic data for AR-CNN-related studies are increasingly available, how to review all research and discover the research trends in AR-CNN based on these bibliographic data represents a challenging research question. Thus, it is necessary to implement bibliometric analytical techniques to evaluate the growing literature on AR-CNN.

Bibliometrics is a useful tool to evaluate and quantify the growth of literature for a particular subject (A. 1969). There are three bibliometric studies in action recognition. Aryanfan etc., examined the characteristics of HAR literature from 1987 to 2015 based on the Web of Science Core Collection (WOS) (Bi *et al.* 2017). Chen and Deng analyzed the evolution of CNNs in many computer vision applications, such as fault and image recognition diagnosis, seismic detection, image classification, etc., by using the bibliometric method in literature from 2011 to 2020 (Chen and Deng 2020). Ci, etc., analyzes the publishing trends, major countries or regions, research topics, and research fronts based on computer vision and graphics papers from 2010 to 2020 (Ci *et al.* 2021). However, these studies remain at the general level for the subject AR-CNN and are limited to the WOS data only. Also, there is no analysis to reveal the research correlation between scientific output and Gross Domestic Product (GDP) per capita, the relationship between journals and the papers they publish, and the productivity of authors. That is why this study is focused on AR-CNN with different quantitative and qualitative parameters such as characteristics of subject literature, productivity, and relationship, international collaboration percentage, etc.

This study uses the Scopus database to conduct a bibliometric analysis of the 2012-2021 AR-CNN research. The objectives of this article are a multi-angle assessment of research productivity and an analysis of the significant publication patterns, research directions, and trends in the field of AR-CNN.

MATERIAL AND METHODS

The Scopus database was used for the bibliometric analysis of "Action Recognition; Convolutional Neural Network; Video Surveillance" (T.561). In order to reach reliable and accurate details on this subject, 6633 publications were obtained on September 26, 2022, for the period 2012-2021. Downloaded information included authors' names, paper titles, publishing years, document type, subject, the Scopus categories of the publication, names of journals, country, institution, and citations for each publication. Since the T.561 topic is only defined in Scival, not Scopus, a download strategy was developed for transferring data from Scival to Scopus using the Selenium Python library. The SciVal is based on output and usage data from Scopus, the world's largest abstract and citation database for peer-reviewed publications. The SciVal uses the Scopus data from 1996 to the current date, which covers 48 million publication records, 22,000+ journals, and 5,000+ publishers (SciVal 2023).

The general research performance of the retrieval literature was processed by Microsoft Excel 365. The VOSviewer software (1.6.18) was utilized to evaluate the co-authorships among countries and institutions and produce a keyword co-occurrence analysis. VOSviewer is a robust tool that uses clustering algorithms and functionalities based on the strength of the connections among items to facilitate network analyses (**?**). Also, Bibliometrix and its user interface, Biblioshiny, were used to generate a bibliometric map. Bibliometrix and R Shiny platform incorporate various analyses, such as overview, conceptual structures, intellectual structure, etc. (Aria and Cuccurullo 2017).

- Literature distribution characteristics, including categories, productive publication sources, authors, affiliations, countries, citations, and publication trends, were analyzed using statistical methods. Simple linear regression analysis was used to estimate publication numbers for the following years.
- The network analysis method was used to visualize scientific collaborations among authors, affiliations, and countries.
- Price's Law analysis, Bradford's Law, and Lotka's Law were used to explain scientific productivity and the relationship between authors and the quantities of their papers. The correlations between the Gross Domestic Product (GDP) per capita and publication productivity of countries on the topic T.561 were investigated with Spearman's rank correlation coefficient.
- Keyword analysis by the author Keyword analysis was conducted to provide important information about research trends that concern researchers. For deeper analysis, the thematic evolution was compared between two time periods, i.e., 2012-2018 and 2019-2021; it provides us with a global view of the changes.

Other databases, such as the WOS and Google Scholar, could also be considered for collecting bibliometric information, but Scopus has significant advantages. Scopus includes most journals indexed in the Web of Science (WOS) across various disciplines. As 99% of journals indexed in the WOS overlap with the Scopus, about 34% of journals indexed in the Scopus overlap with the WOS. This means that Scopus covers about 66% of its journals exclusively compared to WOS. In addition, in Natural Sciences and Engineering (NSE), the Scopus covers 38% of all Ulrich's journals in this field, while the WOS covers 33% (Mongeon and Paul-Hus 2016). Yang & Meho (2006) observed that the WOS should not be used alone for locating citations to an author or title and that Scopus and Google Scholar can help identify many valuable citations not found in the WOS. The WOS and the Scopus journal coverage results in variations in research output volume, rank, and global share in different countries. China and India are two significant exceptions, where research output volume in the Scopus is significantly higher than in the WOS. Considering its largest curated databases covering scientific journals, books, conference proceedings, etc., Scopus is a more convenient choice for a more detailed and comprehensive overview of the bibliographic data source (Kiduk and Meho 2006).

RESULTS

The distribution of subject categories

Throughout 2012–2021, 6633 publications of different types appeared: articles (2341, 35.3%), conference papers (4124, 62.2%), chapters (75, 1.1%), conference reviews (43, 0.65%), reviews (32, 0.48%), and others (18, 0.27%).

The Scival database covered 27 top-level and 334 lower-level subject areas based on the Scopus All Subject Journal Classification (ASJC). As shown in Figure 1, most of the publications related to AR-CNN focused on three top-level categories, including "Computer Science" (5981, 90.2%), "Engineering" (2291, 34.6%), and

"Mathematics" (1324, 20%). The first lower level is "Computer Vision and Pattern Recognition" (2284, 34.4%) for the "Computer Science" category, "Electrical and Electronic Engineering" (1118, 16.9%) for "Engineering" and "Theoretical Computer Science" (680, 10.3%) for "Mathematics". The results followed by Instrumentation (192, 2.9%) for Physics and Astronomy, General Materials Science (192, 2.7%) for Material Science, and Information Systems and Management (204, 3.1%) for Decision Sciences. It is noted that since a paper can be mapped to different categories, the total percentage in Figure 1 is more than 100%.

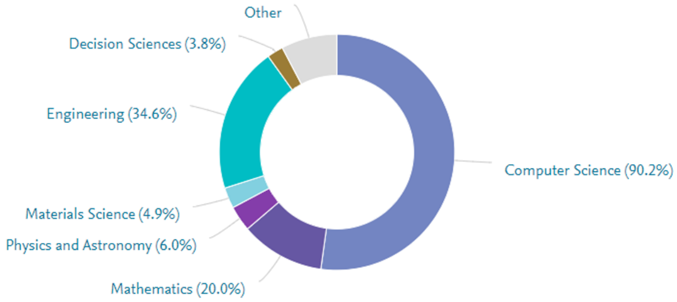

Figure 1 The distribution of subject categories

Development of publications

Figure 2 shows the trend of cumulative and annual publications related to AR-CNN research from 2012 to 2021 and the predictions for the next four years. An increasing trend was observed over the years, approximated by the linear growth curve following the equation $y = 85.85x + 295$ (where x is the number of points per year and y is the number of publications per year). This means that between 2012 and 2021, the data tended to be linear, with a linear annual growth rate of 86 publications per year. Based on the linear model, it could be estimated that 1240 (95% confidence interval; 1085-1395) publications could be published in 2022, while in 2025, this number is expected to increase to 1497 (1209-1785).

Since 2012, the number of publications has been observed to increase despite some fluctuations, revealing that research on AR-CNN has been a growing passion of researchers. More than half of the publications were published after 2018. One of the key reasons for this increase might be related to the improvements in deep learning algorithms, computer vision cloud services, and mobile devices.

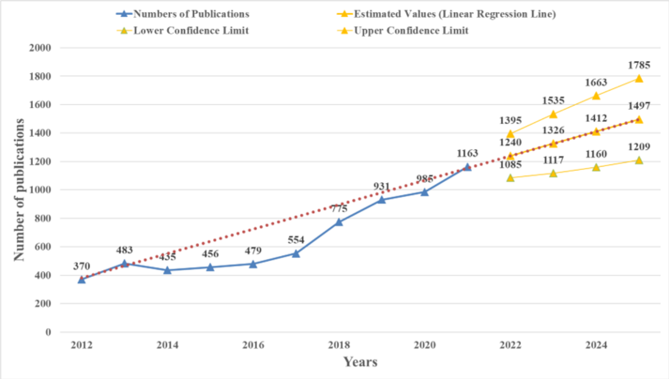

Figure 2 The number of publications by year on AR-CNN

Citations

Overall, 6633 publications received 130,616 citations with 1.76 field-weighted citation impact (FWCI). Table 1 shows the percentage of publications for each threshold based on the number of citations received. Only 6.9% (456) papers have received more than 50 citations, 8% (532) papers received more than or equal to 20 citations, and the remaining papers received less than 20 citations. However, the FWCI of AR-CNN is more than 1. The output is more cited than expected according to the global average.

Active Authors

A total of 6633 publications were produced by 9088 authors. Of these, 4183 authors published articles, some co-authors, and 6917 authors published conference papers. The top productive five authors in terms of citations per publication (CPP) were Andrew P. Zisserman (20 papers, 502 CPP), Du Tran (20 papers, 439.9 CPP), Rahul Sukthankar (15 papers, 380.2 CPP), Lorenzo Torresani (20 papers, 334.4 CPP) and Cordelia Schmid (33 papers, 234.1 CPP). The top 5 authors producing the highest number of publications were Ling Shao (48 papers, 0.72%), Limin Wang (39 papers, 0.59%), Cordelia Schmid (33 papers, 0.5%), Yu Qiao (32 papers, 0.48%), and Anastasios Tefas (32 papers, 0.48%).

Active Institutions

According to the results, 5208 organizations contributed to the analyzed publications. The top 10 organizations that contributed most to the literature were: the Chinese Academy of Sciences (259, 3.9%), CNRS (118, 1.78%), Shanghai Jiao Tong University (118, 1.78%), University of Chinese Academy of Sciences (109, 1.64%), Sun Yat-Sen University (96, 1.45%), Peking University (94, 1.42%), Beijing Institute of Technology (91, 1.37%), CAS - Institute of Automation (91, 1.37%), University of Electronic Science and Technology of China (80, 1.21%), and Institut National de Recherche en Informatique et en Automatique (77, 1.16%).

The top productive ten organizations in terms of CPP are Institut National de Recherche en Informatique et en Automatique (77 papers, 125.6 CPP), Chinese Academy of Sciences (259, 36.6 CPP), CAS - Institute of Automation (90, 32.7 CPP), CNRS (118, 26.9 CPP), University of Electronic Science and Technology of China (80, 15.6 CPP), University of Chinese Academy of Sciences (109, 15.5 CPP), Shanghai Jiao Tong University (118, 14.9 CPP), Peking University (94, 14 CPP), Beijing Institute of Technology (91, 10.7 CPP) and Sun Yat-Sen University (96, 10 CPP). Figure 3 shows the number of publications of the institution over time from 2012 to 2021, and there is an increasing trend, with slight fluctuations in individual years. It was noted that the outputs of government and academic institutions named the Chinese Academy of Sciences fluctuated with high figures in 2018.

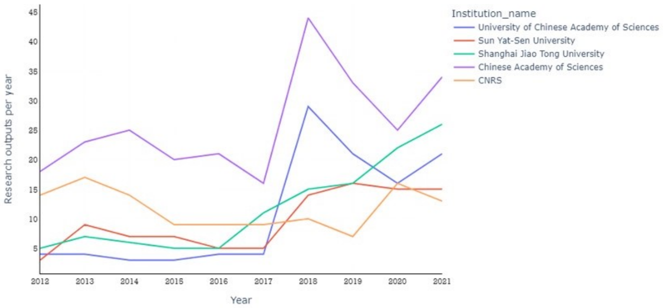

Figure 3 Affiliation production over time

Table 1 General citation structure

Number of citations	Number of publications	Publications %
$\geq$ 50 Citations	456	6.9
$\geq$ 20 Citations	532	8.0
< 20 Citations	5645	85.1

Active Sources

Six thousand six hundred thirty-three publications were published in a wide range of 488 journals, 1055 conference proceedings, 30 books, 23 book series, and one trade publication. The top 22 sources with the highest number of publications are shown in Table 2, and more than 40% of 6633 publications are from these 22 sources.

Lecture Notes in Computer Science (book series) was the most productive source, followed by three conference proceedings, as shown in Table 2. IEEE Access (journal) and Multimedia Tools and Applications (journal) ranked 5th and 6th most productive sources, respectively.

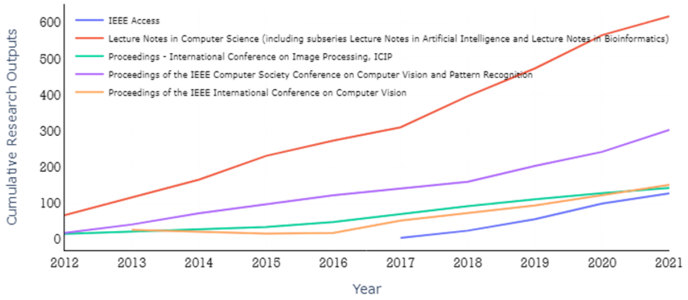

Figure 4 Top 5 journals with the highest number of publications

In Fig. 4, the trends of publication quantities of the top 5 productive journals during ten years were revealed. While the number of publications of the sources was close to each other in 2012, a divergence occurred over time. Especially since 2017, the rate of the annual increase of "Lecture Notes in Computer Science" has accelerated more than other sources, and the number of publications in "Lecture Notes in Computer Science" is almost equal to the total number of publications in the other four sources.

Top Cited Authors

Table 3 shows the top 15 most cited authors, with a minimum of 1500 papers.

Top 10 Publications by Number of Citations

Table 4 provides a detailed overview of the top 10 publications by the number of citations in the field of action recognition. The leading paper, "Learning Spatiotemporal Features with 3D Convolutional Networks" by Tran et al. (2015), has garnered a total of 4721 citations, averaging 590.13 citations per year and achieving a normalized total citation count of 133.77. This is followed closely by the work of Simonyan et al. (2014) on "Two-Stream Convolutional Networks for Action Recognition in Videos," which has received 4423 citations with an annual citation rate of 491.44 and a normalized citation count of 114.66. Notably, Karpathy et al.'s (2014) research on "Large-Scale Video Classification with Convolutional Neural Networks" has also made significant impact, with 4349 citations and a normalized total of 112.75. Other influential works include Ji et al.'s (2013) "3D Convolutional Neural Networks for Human Action Recognition" and Carreira et al.'s (2017) "Quo Vadis, Action Recognition? A New Model and the Kinetics Dataset," reflecting their substantial contributions to the field with normalized citation counts of 103.77 and 85.38, respectively. The table also highlights the works of Heng Wang et al., Feichtenhofer et al., and Yue-Hei Ng et al., illustrating the breadth and depth of research efforts in this domain. Overall, these publications represent critical advancements in the development and application of convolutional neural networks for action recognition, demonstrating significant academic influence and ongoing relevance in the research community.

COLLABORATION ANALYSIS

Active Countries

According to the retrieved results, the papers covered a total of 86 different countries (or territories). The network visualization map of 15 countries producing at least 35 publications is shown in Figure 5b. China ranked first with a dominant output of 2638 papers or a share of 39.7%. The USA had 1184 papers (17.9%), and India had 523 (7.9%), ranking second and third, respectively. Other top-ranked countries are the UK (6.1%), Japan (4.0%), France (3.7%), South Korea (3.5%), and Australia (3.5%).

The international cooperation analysis studied a network of the leading countries, plotted in Figure 5b. China showed 13.42 average citations and a total link strength of 753; the USA showed 46.56 average citations and a link strength of 600; the UK showed 42.63 average citations and a total link strength of 365; Australia showed 26.19 average citations with a link strength of 194, Singapore showed 20.48 average citations with a link strength of 156, France showed 46.12 average citations with a link strength of 150, Spain showed 16.24 average citations with a link strength of 136 and Pakistan showed 16.92 average citations with a link strength of 120.

The strongest link strength was evidenced by the USA and China, with a 260 link strength, followed by the UK and China with a 105 link strength, Australia and China with a 71 link strength, HongKong and China with a 71 link strength, the China and Singapore with a 68 link strength, the UK and the USA with a 41 link strength, and the UK and Spain with a 39 link strength.

Figure 6 shows the growth trends of publications for the top 5 productive countries from 2012 to 2021. Compared to the four countries, the trend in China has increased at a quicker pace after 2017. China's linear annual growth rate reached 16 publications per year from 2012 to 2018, up to 146 publications per year in 2018, and then 62 publications per year from 2019 to 2021. This marked increase in 2018 may be associated with China's efforts to

Table 2 Top 22 journals with the highest number of publications

No	Journals	Publication number	%	CiteScore 2021
1	Lecture Notes in Computer Science	617	9.3	2.1
2	Proceedings of the IEEE Computer Society Conference on Computer Vision and Pattern Recognition	325	4.9	44.6
3	Proceedings of the IEEE International Conference on Computer Vision	177	2.67	14.1
4	Proceedings - International Conference on Image Processing, ICIP	142	2.14	-
5	IEEE Access	127	1.91	6.7
6	Multimedia Tools and Applications	124	1.87	5.3
7	Proceedings - International Conference on Pattern Recognition	101	1.52	2.1
8	ACM International Conference Proceeding Series	96	1.45	1.0
9	IEEE Computer Society Conference on Computer Vision and Pattern Recognition Workshops	96	1.45	-
10	Neurocomputing	92	1.39	10.3
11	IEEE Transactions on Image Processing	81	1.22	16.4
12	Proceedings of SPIE - The International Society for Optical Engineering	78	1.18	0.9
13	Communications in Computer and Information Science	76	1.15	0.9
14	Advances in Intelligent Systems and Computing	75	1.13	-
15	Pattern Recognition	73	1.1	15.5
16	IEEE Transactions on Circuits and Systems for Video Technology	67	1.01	10.1
17	IEEE Transactions on Pattern Analysis and Machine Intelligence	61	0.92	36.6
18	Pattern Recognition Letters	60	0.9	8.6
19	Proceedings - ICASSP, IEEE International Conference on Acoustics, Speech and Signal Processing	58	0.87	5.8
20	Computer Vision and Image Understanding	56	0.84	9.9
21	International Journal of Computer Vision	51	0.77	16.8
22	Proceedings - IEEE International Conference on Multimedia and Expo	51	0.77	-

CiteScore is the ratio of citations of the document received in the current year to the total citations in the previous three years.

implement machine learning interventions in real-world settings, the general increased awareness of action recognition, and the effects of Project 985 (Xuefei 2014). The publications in the US tended to be linear, with an annual growth rate of 17 publications per year since 2016. The publications in India remained constant at around 85 per year during 2018-2020 and then increased at an annual growth rate of 30 publications per year. The growth trends of Japan and the United Kingdom remained constant during the last decade, with a low increase rate.

Figure 7 shows the distribution of publications in SCP (Singular country publications) and MCP (Multiple country publications) status by country. When viewed proportionally, it can be said that England, Australia, Pakistan, and Singapore published more than multiple countries.

General Patterns of Collaboration

Table 5 shows collaboration metrics by assigning publications as international, national, institutional, and single-authorship based on T.561 data. International collaboration measures the proportion of publications with at least one international co-author. National collaboration measures the proportion of publications carried out by several authors/institutions from a single country. Institutional

Table 3 Top 15 most cited authors (2012-2021) with characteristics of publication outputs

No	Name	Citations	Number of publications	Citations per Publication	Field-Weighted Impact	Citation	h-index
1	Zisserman, Andrew P.	9863	20	493.2	24.93		122
2	Schmid, Cordelia	7650	33	231.8	12.77		102
3	Torresani, Lorenzo	6526	20	326.3	15.13		36
4	Tran, Du	6437	15	429.1	19.4		17
5	Sukthankar, Rahul	5648	15	376.5	19.58		48
6	Wang, Limin	5368	39	137.6	11.68		29
7	Qiao, Yu	4861	32	151.9	11.87		52
8	Niebles, Juan Carlos	2554	25	102.2	6.08		33
9	van Gool, Luc J.	2242	18	124.6	10.83		123
10	Ghanem, Bernard	2076	26	79.8	6.04		40
11	Fei-Fei, Li	1955	18	108.6	7.28		87
12	Laptev, Ivan	1877	17	110.4	7.04		47
13	Shao, Ling	1852	48	38.6	3.05		75
14	Shah, Mubarak A.	1604	23	69.7	4.82		87
15	Fernando, Basura	1575	21	75	5.25		24

Field-Weighted Citation Impact: The ratio of citations received relative to the expected world average for the subject field, publication type, and publication year. The average world FWCI is 1.00

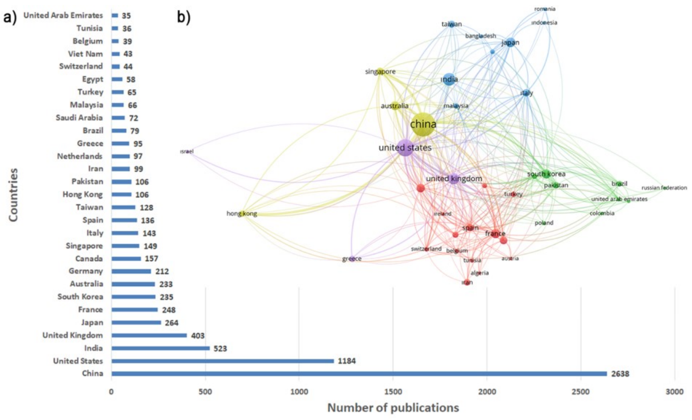

Figure 5 a) Bar chart showing the productivity of the top 15 countries in the world. b) Network visualization map for international cooperation of countries on Action Recognition, Convolutional Neural Networks, and Video Surveillance. Footnote: As the size of the circle increases, the number of publications increases. Clusters are separated by colors. The thickness of the lines expresses the strength of cooperation between countries.

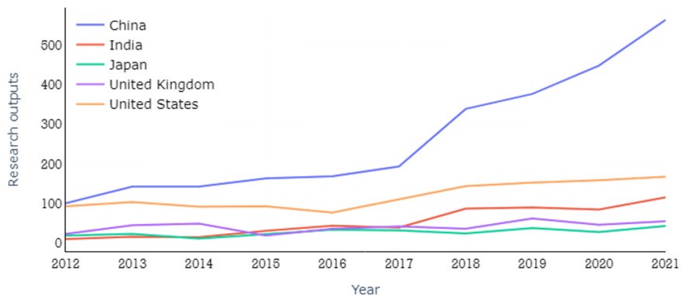

Figure 6 Country Production over Time

collaboration measures the proportion of publications carried out by several authors from the same institution in a single country. Most of the retrieved publications had only institutional collaboration (n=3132; 47.2%), followed by only national collaboration (n = 1909; 28.8%) and international collaboration (n =1385; 20.9%). The rest of the publications belong to the category "single authorship" or "no collaboration" (n=206; 3.1%). Nonetheless, in terms of impact, an international collaboration (31.7 citations/document, 2.64 FWCI) exceeds both national (20.4; 1.79) and institutional collaboration (14.2;1.42). Chinese Academy of Sciences was among the top for coauthorship collaboration between the institutions with the highest number of publications.

Table 4 Top 10 publications by the number of citations

Paper	Author	Year	Total (TC)	Citations	TC per Year	Normalized TC
Learning Spatiotemporal Features with 3D Convolutional Networks	Tran et al.	2015	4721		590.13	133.77
Two-Stream Convolutional Networks for Action Recognition in Videos	Simonyan et al.	2014	4423		491.44	114.66
Large-Scale Video Classification with Convolutional Neural Networks	Karpathy et al.	2014	4349		483.22	112.75
3D Convolutional Neural Networks for Human Action Recognition	Ji et al.	2013	3818		381.80	103.77
Quo Vadis, Action Recognition? A New Model and the Kinetics Dataset	Carreira et al.	2017	2910		485.00	85.38
Action Recognition with Improved Trajectories	Heng Wang et al.	2013	2474		247.40	67.24
Convolutional Two-Stream Network Fusion for Video Action Recognition	Feichtenhofer et al.	2016	1815		259.29	57.26
Beyond short snippets: Deep networks for video classification	Yue-Hei Ng et al.	2015	1513		189.13	42.87
Temporal Segment Networks: Towards Good Practices for Deep Action Recognition	Limin Wang et al.	2016	1337		191.00	42.18
Dense Trajectories and Motion Boundary Descriptors for Action Recognition	Heng Wang et al.	2013	1326		132.60	36.04

Field-Weighted Citation Impact: The ratio of citations received relative to the expected world average for the subject field, publication type, and publication year. The average world FWCI is 1.00

Table 5 Publications by the amount of international, national, and institutional collaboration

Metric	%Percentage	Number of publications	Citations	Citations per Publication	Field-Weighted Citation Impact
International collaboration	20.90%	1,385	43,880	31.7	2.64
Only national collaboration	28.80%	1,909	39,015	20.4	1.79
Only institutional collaboration	47.20%	3,132	44,494	14.2	1.42
Single authorship (no collaboration)	3.10%	206	704	3.4	0.52

Figure 8 shows network graphs of coauthorship relations among authors. Coauthorship relations represent whether an author has written a paper with another author. Figure 8 presents the three collaboration clusters among the authors with 50 or more publications. All the institutions in the red cluster belong to China. It can be seen that the cooperation between authors is mainly focused on the same country or neighboring countries.

SCIENTIFIC PRODUCTIVITY AND RELATIONSHIP ANALYSIS

Price's Law

Price's Law is the most commonly used indicator to analyze productivity in a specific discipline. It states that half of the literature on a subject will be contributed by the square root of the total number of authors publishing in that area. For AR-CNN over the entire period, at least 95 primary authors (the square root of 9088 authors) were required to publish 1939 papers, whereas according to Price's calculations, 95 authors were needed to produce 3316 papers (the

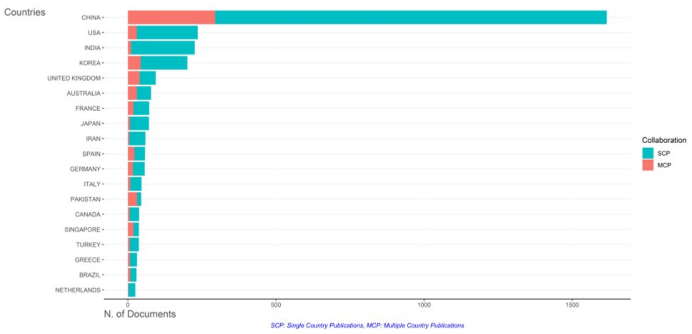

Figure 7 Corresponding Author's Country

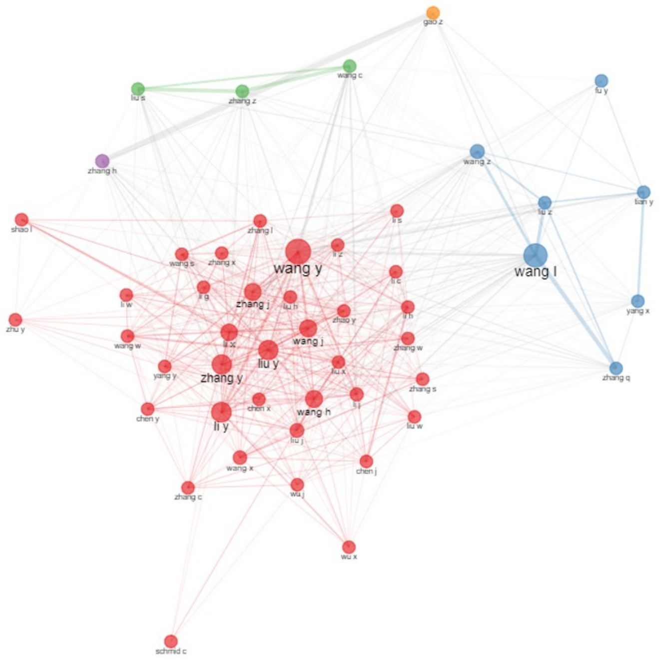

Figure 8 Network visualization of coauthorship collaboration

half of 6633 outputs). Therefore, our data did not support Price's Law.

Bradford's Law

Bradford's Law is a bibliometric indicator of the quantitative relationship between journals and their published papers (Bradford 1948). In this Law, the journals are arranged in descending order of productivity and divided into equal zones (core, allied, and alien). Each zone would contain a similar number of publications, but the number of journals would increase upon moving from one zone to another.

The total 6633 publications are divided into three groups. The first zone (core journals) contained 15 journals with 2260 (34%) publications. The second zone (allied journals) contained 144 journals with 2186 (33%) publications. The third zone (alien journals) contained 1433 journals with 2186 (33%) publications. The summary of the division of zones is as follows. Bradford's algebraic interpretation of the Law is 1: n: n^2. The connection of each zone in this study is 15:144:1433. Here, 15 is the number of journals in the core zone, and Bradford's mean multiplier is 9.78.

Hence,

$$15 : 15 * 9.78 : 15\,(9.78)^2$$

$$15 : 147 : 1433 \approx 1595$$

$$Percentage\ of\ Error = \frac{1595 - 1592}{1592} * 100 = 0.19\%$$

The error percentage is very low (0.19%); therefore, Bradford's Law fits the above data.

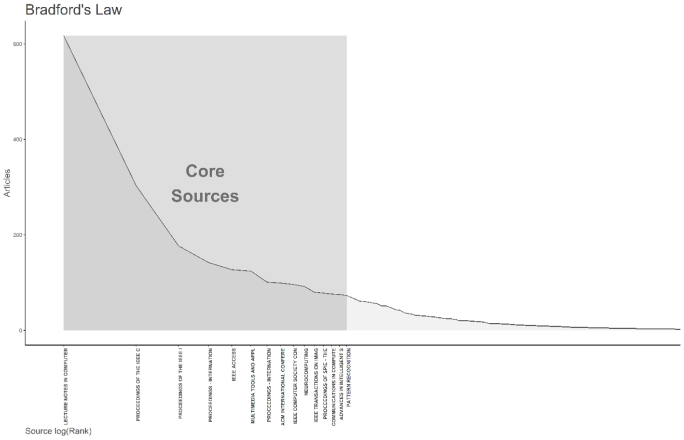

Figure 9 Scattering of Journals over Bradford Zone

Lotka's Law

Lotka's Law Lotka (1926) describes the frequency distribution of authors on scientific productivity in any given field. This Law is expressed as $Y = KX^{-b}$, where x is the number of contributing authors and y is the number of publications, whereas K and b are parameters to be estimated from data. According to this Law, the number of authors that publish n publications in a given subject field is inversely proportional to n^2. This means that for every 100 authors contributing to one publication, 25 will contribute 2, 11 will contribute three, and so on. According to Lotka's Law of Scientific Productivity, only six percent of the authors in a given field will produce more than ten publications. Using the Kolmogorov-Smirnov test (KS-test) of goodness-of-fit, we find that the null hypothesis that the A literature conforms to Lotka's law must be rejected at 0.01 level of significance.

After analyzing data, we determined that in CA, 5666 authors published one paper, which accounted for 62.3% of the total authors (9088), 1378 authors published two papers, which accounted for 15.2% and 640 authors published three papers, which accounted for 7%. This conclusion indicates that only six percent of the authors in AR-CNN will produce more than ten publications, as in Lotka's Law of Scientific Productivity. In other words, the scientific elite of researchers, each of whom publishes many papers, is responsible for advancing the field.

Correlation Analysis

Spearman's rank correlation test was used to assess the relationship between publication numbers and GDP per capita. The test resulted in a p-value of 0.002, rejecting the null hypothesis that there is no significant relationship between publications and GDP per capita at the significance level of 5%. The number of publications

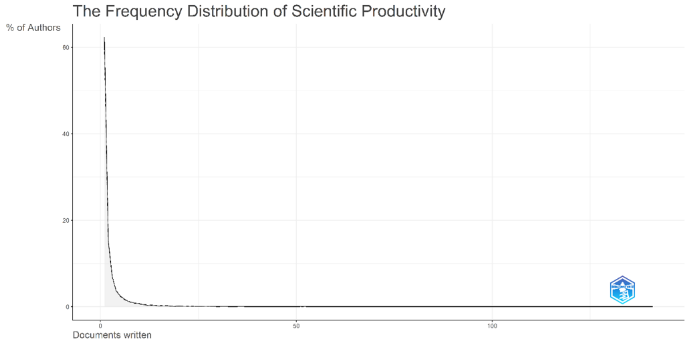

Figure 10 Lotka's Law on the productivity of authors

correlates significantly positively with GDP per capita (r=0.23). The correlation results by country have been found as r=0.72 for the United States, r=0.75 for Australia, r=0.99 for China, r=0.68 for Germany, r=0.96 for India, r=0.66 for Japan and r=0.92 for Pakistan. There is no significant relationship between publications and GDP per capita for other countries.

Keyword Analysis

A total of 8918 different author keywords were used in 6633 publications, and 514 keywords meet the threshold set at the 5-minimum number of occurrences for the keywords. 6991 author keywords appeared only once, 913 keywords appeared only twice, and 320 keywords appeared only three times. The number of keywords used more than three times was 694 (10.5%), which showed that the popular research topics in AR-CNN focused on a small field. A large number of once-only author keywords probably indicates a lack of continuity in research and a wide disparity in the research focuses. The clustering analysis between these keywords is given in the network visualization map (Fig. 11). According to the analysis of the frequency of keywords, the AR-CNN-related research was basically steady, and mainstream research was centered on the following methods: action recognition, human action recognition, and security systems. Except for the seven top keywords, the four frequently used keywords were optical flow, video analysis, feature extraction, and video classification. The keyword "optical flow" indicates the importance of analyzing moving agents, such as creatures or robots, to adapt to their environment.

Thematic Evolution

Figure 12 demonstrates the evolution of keywords in two different stages (2012-2018 and 2019–2021). The left side indicates the themes that were studied during 2012-2018. Six themes are listed in different sizes based on their usage. Themes include action detection, action recognition, deep learning, transfer learning, human action recognition, and feature extraction. Most of the research themes of the initial period were lumped together under these two large topics (human action recognition and action recognition) in the developing period. Feature extraction-related research lines took an important place in both stages. Figure 12 shows that words like transfer learning are highly connected to human action recognition.

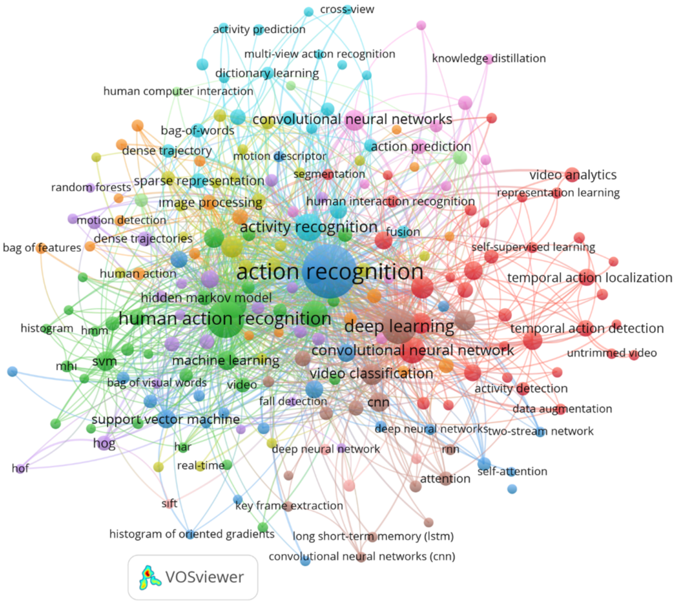

Figure 11 Keyword Analysis

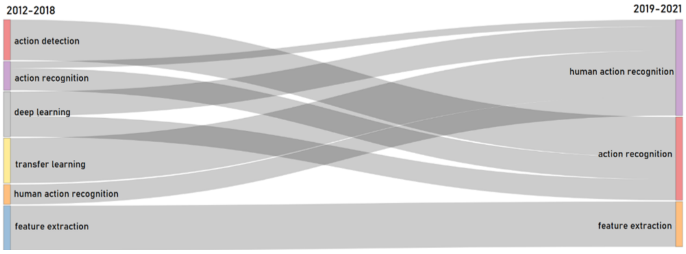

Figure 12 Thematic evolution of the AR-CNN

DISCUSSION

The objective of this study was to estimate the research productivity of the topic "Action Recognition; Convolutional Neural Network; Video Surveillance". The publications included in the study were collected from the Scopus database during 2012–2021. Of the 6632 publications, 62% were conference papers, 35% were research articles, and 3% were others (chapters, conference reviews, etc.).

When the number of publications is evaluated by years, it is seen that there is a linear increase in the number of publications, with a significant increase since 2017. According to the regression analysis, AR-CNN has attracted serious concerns, and more and more publications have been published in the last four years. China ranked first with the highest number of publications, accounting for 39.8% of worldwide publications. It can be predicted that its predominant position will be further enhanced in the next few years. The Chinese Academy of Sciences published the largest number of papers when considering institutions. Through the coauthorship analysis of countries, this study determined that China was at the center of international cooperation. The strongest link strength was evidenced by the USA and China, with a 260 link strength, followed by the UK and China, with a 105 link strength. According to Lotka's Law, authors' production was consistent, meaning that the number of authors who wrote a single paper was approximately 60%. The number of publications is significantly positively correlated with GDP per capita for the United States, Australia, China, Germany, India, Japan, and Pakistan. There is no significant relationship between publications and GDP per capita for other countries. Based on an analysis of article keywords, mainstream research was centered on the following keywords: action recognition, human action recognition, and security systems.

CONCLUSION

This study aims to quantitatively evaluate the publications on the topics of SciVal's "Action Recognition; Convolutional Neural Network; Video Surveillance (T.561)" in computer vision research between 2011 and 2021. It has been observed that there is generally an increase in the annual number of studies produced from 2011 to 2021. AR-CNN has a FWCI above 1 and is cited more than expected based on the global average, with the most prolific author in terms of citations per publication (CPP) being Andrew P. Zisserman (20 articles, 502 CPP). The first organization that contributed the most to the literature was the Chinese Academy of Sciences (259, 3.9%), while the most productive organization in terms of CPP was the Institut National de Recherche en Informatique et en Automatique (77 articles, 125.6 CPP). Lecture Notes in Computer Science was the most productive source. Zisserman, Andrew P. was the most prolific author in the FWCI and h-index, citing per publication. "Learning Spatiotemporal Features with 3D Convolutional Networks" was the most cited publication. China ranked first with an output of 2638 articles or a share of 39.7%. The most productive countries in terms of the number of publications are developed or overpopulated countries. The participation of researchers in multinational studies in developing or underdeveloped countries may enable them to conduct more research on this subject.

Availability of data and material

Not applicable.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The authors have no relevant financial or non-financial interests to disclose.

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Machine Learning Interpretability in Diabetes Risk Assessment: A SHAP Analysis

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ABSTRACT Diabetes continues to be a complicated and prevalent metabolic illness, providing a serious burden to public health. While machine learning approaches like extreme gradient boosting (XGBoost) provide intriguing options for diabetes prediction, their 'black-box' nature typically limits clinical interpretability. To overcome this gap, our work applied SHapley Additive exPlanations (SHAP) to give insights into the XGBoost model's predictions. The dataset utilized in this research comprised of 253,680 patients and contained 21 parameters, such as General Health Status, High Blood Pressure Status, Age, and Body Mass Index. After feature selection using Recursive Feature Elimination (RFE), 15 important characteristics were discovered. In the test set, the XGBoost model obtained an accuracy of 86.6%, precision of 54.1%, recall of 17.0%, and an F1-score of 25.9% for the Original dataset. For the RFE dataset, the model displayed an accuracy of 86.6%, precision of 54.9%, recall of 16.5%, and an F1-score of 25.3%. SHAP analysis found that General Health Status, High Blood Pressure Status, Age, and Body Mass Index were the most important characteristics in both the Original and RFE datasets. This work provides as a platform for transparent and clinically applicable predictive modeling, assisting in early diabetes identification and preventive healthcare.

KEYWORDS
Explainable AI
Diabetes
Recursive feature elimination

INTRODUCTION

Diabetes, marked by chronic high blood sugar levels, is a pressing global health concern. Its prevalence continues to rise, leading to increased risks of cardiovascular diseases and other severe health issues. The World Health Organization (WHO) states that around 1.28 billion adults aged 30–79 years suffer from diabetes, predominantly in low- and middle-income nations (Diabetes - World Health Organization (Organization *et al.* 2019). Yet, less than half receive proper diagnosis and treatment, with a mere one in five effectively managing their condition (Mihai *et al.* 2022). Such disparities highlight the pressing need for better diabetes prevention, diagnosis, and management.

In the last decade, the allure of machine learning in refining predictive models for diabetes has captivated researchers (Lin *et al.* 2022; Gómez-Peralta and Abreu 2022; Qin *et al.* 2022; Shankaracharya 2017; Afsaneh *et al.* 2022). This has given birth to innovative methods for predicting various outcomes related to diabetes, from individualized risk evaluations to disease behaviour. These methods provide crucial insights into risk factors, pushing the frontier of tailored healthcare. However, many machine learning tools are criticized for their opaque "blackbox" methodologies (Carreras *et al.* 2021). For diabetes prediction, this opacity means healthcare professionals might struggle to grasp the biomarkers and elements that drive predictions. Considering the intricate relationships between diabetes risk factors, this lack of clarity can limit the models' clinical and public health value.

Several biomarkers critical to diabetes' onset and progression are recognized in medical literature (Gómez-Peralta and Abreu 2022). Dyslipidemia, notable for its impact on cholesterol, is a recognized cardiovascular risk, and its ties with diabetes are well-documented (Gutch *et al.* 2017). Other factors, like electrolyte imbalances (high sodium, low potassium), iron metabolism, vitamin B12, and HbA1c levels, are also significantly linked with diabetes (Hasan *et al.* 2021).

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To enhance model transparency, the research community has pivoted towards explainable artificial intelligence (XAI) methodologies (Hasan *et al.* 2021). Notably, SHapley Additive exPlanations (SHAP) have risen in prominence which demystifies both global and local feature significance, offering a clearer understanding of diabetes risk factors, and aiding more informed medical and public health decisions (Gong *et al.* 2022).

This study delves deep into the existing literature on diabetes prediction, emphasizing transparent machine learning methods. SHAP is employed to elucidate an XGBoost model's predictions, utilizing a commonly available diabetes dataset from The Behavioral Risk Factor Surveillance System. Study involves 253.680 participants with their diabetes status and relevant clinical data. This includes chronic illnesses, medications, and other markers. Firstly, one of the tree-based machine learning models called XGBoost is selected due to its better performance. This is followed by employing SHAP explanations to uncover novel links between diabetes risk and biomedical parameters. This work enriches the understanding of machine learning models in diabetes prediction and sets the stage for transparent, clinically pertinent predictive modeling in diabetes research and care. The paper is structured as follows:

- The Methodology section delves into our research design, discussing data gathering, analytical methods, the XGBoost model, RFE(Recursive Feature Elimination) feature selection method and the use of SHAP for enhancing interpretability.
- The Results section shows our results, concentrating on the performance measures of the XGBoost model in both the Original and RFE datasets. It also digs into the SHAP analysis, emphasizing the most relevant factors like General Health Status, High Blood Pressure Status, Age, and Body Mass Index in both datasets. The section further covers the modest differences in accuracy, precision, recall, and F1-score between the Original and RFE sets, proving the efficiency of our feature selection approaches like RFE in diabetes prediction.
- A comprehensive discussion interprets our results, underlining the significance of transparent machine learning in diabetes research and healthcare choices in Discussion section.
- Finally, Conclusion section highlights the benefits of transparent machine learning in diabetes prediction, addresses constraints, and suggests future research directions to elevate diabetes risk evaluation, ultimately aiming for superior diabetes care and preventive medicine for better public health.

METHODOLOGY

In this work, two variations of the Behavioral Risk Factor Surveillance System (BRFSS) dataset, a yearly telephone survey conducted by the Centers for Disease Control and Prevention (CDC), were subjected to a thorough statistical analysis. The original dataset has two categorical outcome classes: '0,' which denotes the lack of diabetes or the presence of gestational diabetes alone, and '1,' which denotes either prediabetes or diabetes. There were originally 21 feature variables in this dataset, which included a variety of behavioral and health characteristics. Recursive Feature Elimination (RFE) was used as a feature selection strategy to narrow the feature space and improve the model's ability to forecast. A second dataset was created as a result, however only 15 of the most useful features were kept. On both the original and the RFE-selected datasets, subsequent SHapley Additive exPlanations (SHAP) studies were performed to clarify the impact of each variable on the predictive model. This divided method provided a sophisticated assessment of feature relevance and offered insightful information on the characteristics most responsible for the likelihood of developing prediabetes or diabetes. These findings provide healthcare professionals with a strong analytical framework that enables more focused interventions based on the recognized important variables.

70% of the dataset is allocated for training, while the remaining 30% is used for testing, leading to a 70/30 data split. The 'Discussions' section also presents findings from a tenfold cross-validation, providing insights into the model's stability. Model interpretation is further enhanced using SHAP (SHapley Additive exPlanations).

Model Training

In this section, a detailed description of the classifier that has been implemented for the purpose of categorizing the diabetes dataset has been presented. A classifier, a fundamental machine learning algorithm, is utilized to partition the input data into predefined categories. In our specific context, the classifier employs the patient's features as input to discern the presence or absence of diabetes.

High levels of accuracy in predicting diabetes based on a wide range of attributes, including high blood pressure status, high cholesterol levels, cholesterol check status, Body Mass Index, stroke status, heart disease or attack status, physical activity status, heavy alcohol consumption, general health status, mental health status, difficulty walking or climbing stairs, gender, age category, education level, and income level are delineated in Table 1. Models like XGBoost, AdaBoost, Random Forest, and other tree-based standards provided excellent and comparable outcomes in the studies. XGBoost has been chosen as the main model despite alternative models having equivalent performance that has been demonstrated. XGBoost is regarded as the outstanding model due to its usability and practical efficiency, which are especially well-suited to the study objectives. It is the best option for addressing the complexity faced in our work in diabetes forecasting because of its exceptional computational speed mixed with strong predictive skills.

eXtreme Gradient Boosting (XGBoost)

The XGBoost classifier builds upon the Gradient Boosting classifier, which also emphasizes speed and performance. One of the notable features of XGBoost is its regularized learning, which helps to smooth out the final learned weights and prevent overfitting. Overfitting occurs when the model performs well on the training data but poorly on the testing data due to learning both the information and noise from the training data (Fitriyani *et al.* 2020).

The objective function $L(\theta)$ of the XGBoost can be written as:

$$L(\theta) = \sum_{i=1}^{n} l(y_i, \hat{y}_i) + \sum_{k=1}^{K} \Omega(f_k) \tag{1}$$

where n is the number of training instances, y_i is the actual value for the i^{th} training instance, $\hat{y}_i$ is the predicted value for the i^{th} training instance, $l(y_i, \hat{y}_i)$ is the training loss, which measures the difference between the predicted and actual values for each training instance, K is the number of trees, f_k is the k^{th} tree, and $\Omega(f_k)$ is the regularization term for the k^{th} tree, which penalizes the complexity of the model to avoid overfitting.

The regularization term $\Omega(f_k)$ can be further defined as:

$$\Omega(f_k) = \gamma T + \frac{1}{2}\lambda \|w\|^2 \tag{2}$$

Where T is the number of leaf nodes in the k^{th} tree, w is the vector of scores on the leaf nodes in the k^{th} tree, and γ and λ

Table 1 Model Metrics and Confusion Matrixes

Model	Accuracy	Precision	Recall	F1-Score	Confusion Matrix	
XGBoost	0.8656	0.5413	0.1701	0.2588	64092	1513
					8713	1786
Adaboost	0.8650	0.5402	0.1955	0.2871	63858	1747
					8446	2053
Random Forest	0.8599	0.4788	0.4789	0.1748	63608	1997
					8663	1836
Decision Tree	0.7979	0.2930	0.3289	0.3099	57274	8331
					7045	3454
E. Boosting Machine	0.8654	0.5662	0.1664	0.2573	64266	1339
					8751	1748
Naive Bayes	0.7718	0.3166	0.5647	0.4057	52809	12796
					4570	5929
Logistic Regression	0.8652	0.5395	0.5395	0.1585	64184	1421
					8834	1665
KNN	0.8468	0.3948	0.2066	0.2713	62279	3326
					8329	2170
SVM	0.7798	0.2088	0.2184	0.2106	57117	8488
					8264	2235

■ **Table 2 Variable names, their indications, and value scales along with patient data.**

Variable Name	What It Indicates	Value Scales	Pt6	Pt156	Pt34	Pt265
Diabetes_binary	Diabetes Status	0=no diabetes, 1=prediabetes/diabetes	0.0	1.0	1.0	0.0
HighBP	High blood pressure status	0 = no high BP, 1 = high BP	1.0	1.0	1.0	1.0
HighChol	High cholesterol levels	0 = no high cholesterol, 1 = high cholesterol	0.0	1.0	1.0	0.0
CholCheck	Cholesterol check status	0 = no check in 5 years, 1 = yes	1.0	1.0	1.0	1.0
BMI	Body Mass Index	Continuous Scale	30.0	47.0	24.0	36.0
Smoker	Smoking status	0 = no, 1 = yes	1.0	1.0	1.0	1.0
Stroke	Stroke status	0 = no, 1 = yes	0.0	0.0	0.0	0.0
HeartDiseaseorAtc	Heart disease or attack status	0 = no, 1 = yes	0.0	0.0	0.0	1.0
PhysActivity	Physical activity status	0 = no, 1 = yes	0.0	0.0	0.0	0.0
Fruits	Fruit consumption	0 = no, 1 = yes	0.0	1.0	0.0	1.0
Veggies	Vegetable consumption	0 = no, 1 = yes	0.0	0.0	0.0	1.0
HvyAlcoholCons	Heavy alcohol consumption	0 = no, 1 = yes	0.0	0.0	0.0	0.0
AnyHealthcare	Healthcare coverage	0 = no, 1 = yes	1.0	1.0	1.0	1.0
NoDocbcCost	Avoided doctor due to cost	0 = no, 1 = yes	0.0	0.0	0.0	0.0
GenHlth	General health status	1=excel, 2=very good, 3=good, 4=fair, 5=poor	3.0	3.0	2.0	3.0
MentHlth	Mental health status	1-30 days	0.0	0.0	0.0	0.0
PhysHlth	Physical health status	1-30 days	14.0	0.0	0.0	2.0
DiffWalk	Difficulty in walking	0 = no, 1 = yes	0.0	1.0	0.0	1.0
Sex	Gender	0 = female, 1 = male	0.0	0.0	0.0	0.0
Age	Age category	1 = 18-24, 9 = 60-64, 13 = 80 or older	9.0	11.0	12.0	11.0
Education	Education level	1 = Never attended, 6 = College graduate	6.0	6.0	3.0	5.0
Income	Income level	1 = less than $10,000, 8 = $75,000 or more	7.0	5.0	3.0	4.0

are regularization parameters that control the complexity of the model. Large weights are penalized by the regularization term, which also encourages the model to have more streamlined and comprehensible structural elements. The goal of the model is to minimize this loss over the entire training set. Given that our dataset is also noisy, XGBoost is one of the appropriate classifiers for it Shao and Hu (2022). The values of the hyperparameters are given in Table 3.

Recursive Feature Elimination (RFE)

Finding the ideal subset of features for a particular machine learning study is the goal of the feature selection method known as recursive feature elimination (RFE)Zhang *et al.* (2022). When using RFE, a model is fitted to the data, and the features are then ranked according to how important or relevant they are to the prediction. The least significant characteristics are then gradually removed by RFE until the target number of features is obtained or a stopping requirement is satisfied. By lowering the dimensionality and complexity of the data, as well as by removing noise and multicollinearity among features, RFE can enhance the effectiveness and performance of machine learning models.Chen and Jeong (2007)

Recursive Feature Elimination (RFE) is a feature selection algorithm commonly employed in machine learning for identifying a subset of most predictive features. Given a dataset $\mathcal{D} = \{(x_1, y_1), \ldots, (x_n, y_n)\}$ with n samples, where each $x_i \in \mathbb{R}^d$ is a d-dimensional feature vector and y_i is the corresponding label, RFE aims to minimize a loss function $\mathcal{L}(f(x;\theta), y)$ by selecting the most relevant features. The optimization objective is $\theta^* = \arg\min_\theta \sum_{i=1}^{n} \mathcal{L}(f(x_i;\theta), y_i)$. The algorithm starts by fitting a predictive model $f : \mathbb{R}^d \rightarrow \mathbb{R}$ parameterized by θ to the entire feature set. It then ranks the features based on their importance, often calculated as $\text{Importance}(j) = \left|\frac{\partial \mathcal{L}}{\partial x_j}\right|$ for each feature j, and recursively eliminates the least important ones. This process continues iteratively until the desired number of features is retained. The computational complexity of RFE is generally $O(d \times p)$, where p is the complexity of the base estimator used for ranking features. RFE is particularly useful when model interpretability and simplicity are as crucial as predictive performance, although it can be computationally expensive for high-dimensional data.

Several machine learning models that offer some kind of feature importance metric can be used with recursive feature elimination (RFE). This comprises linear models with coefficients, tree-based techniques with feature significance scores, and support vector machines (SVMs) with their support vectors. It's important to keep in mind, though, that RFE functions as a wrapper technique and requires the fitting of a new model for each subset of characteristics. This might require a lot of work and increase the risk of model overfitting. Table 2 provides more information on the 15 relevant parameters that were chosen for our investigation using RFE.

Model Interpretation with SHAP

To augment the transparency of our XGBoost model and provide clinically meaningful interpretations, we employed SHapley Additive exPlanations (SHAP) as an interpretability tool. SHAP is rooted in cooperative game theory, aiming to fairly allocate "payouts" or contributions among features for a given prediction. Mathematically, the Shapley value ϕ_i of a feature i is computed as:

$$\phi_i(f) = \sum_{S \subseteq N \setminus \{i\}} \frac{|S|! \cdot (|N| - |S| - 1)!}{|N|!} [f(S \cup \{i\}) - f(S)]$$

where $f(S)$ is the prediction of the model for feature subset S, and N is the set of all features. These Shapley values represent the marginal contribution of each feature to a specific prediction, enabling us to decipher both global and local feature importance.

The application of SHAP to our XGBoost model adhered to a systematic methodology. Initially, specific data preprocessing steps tailored for SHAP analysis were executed. Utilizing the SHAP library, Shapley values for each feature across all data points were computed. These values were aggregated to form global feature importance metrics, which can be mathematically represented as:

$$\text{Global Importance}(j) = \frac{1}{n} \sum_{i=1}^{n} |\phi_{ij}|$$

where ϕ_{ij} is the Shapley value of feature j for data point i, and n is the total number of data points. This provided an overarching view of the most and least impactful features in diabetes prediction. Interestingly, our analysis revealed that certain biomarkers, traditionally not emphasized in diabetes literature, played a significant role in model predictions.

SHAP also excels in local interpretability, enabling us to dissect individual predictions. For example, in case studies of specific patients, the SHAP values highlighted the biomarkers that were instrumental in classifying them as high-risk or low-risk for diabetes. This local interpretability is invaluable for clinicians, as it provides personalized insights into each patient's risk factors. Mathematically, local interpretability can be examined through the individual Shapley values ϕ_{ij}, providing a nuanced understanding of how each feature contributes to a specific prediction.

In XGBoost, SHAP values may be particularly useful for comprehending how various characteristics interact with one another. The authors' modification of SHAP values to take interaction effects into consideration led to the idea of SHAP interaction values. These interaction values guarantee the explanations of each of XGBoost's unique estimations for interaction effects. In order to highlight important interactions that XGBoost captures but that could otherwise go undetected, SHAP interaction values discriminate between main effects and interaction effects for specific model predictions.He *et al.* (2023)

An efficient tool for understanding XGBoost models is the SHAP values. They constitute a significant theoretical breakthrough by overcoming consistency problems and permitting the separate assessment of main and interaction effects for individual model predictions.This might highlight important interactions that XGBoost has recorded but that were otherwise missed. Data scientists are now better prepared to develop models that are more clear and intelligible thanks to the introduction of SHAP values in XGBoost.Gao *et al.* (2023)

RESULTS

Results of Classifications

First, two separate sets were created from the original dataset after a data preparation step. The original collection, referred known as the "Original Set," had 253,680 samples and kept all 21 features. The second set, referred to as the "RFE Set," was created by choosing 15 important features from the initial 253,680 samples using recursive feature elimination (RFE).

RFE was used to improve feature selection and reduce model complexity. This approach chose 15 characteristics, which are listed in Table reftab:attributes, including high blood pressure status, high cholesterol levels, cholesterol check status, body mass index, and others.

■ **Table 3 Hyperparameter values for the model.**

Hyperparameter	Value
eta (learning rate)	0.3
n_estimator (number of gradient-boosted trees)	100
Gamma (min split loss)	0
Max depth	6
Min child weight	1
Max delta step	0
subsample	1
Sampling method	Uniform

The two sets—'Original' and 'RFE'—were each put through an XGBoost classifier separately to evaluate the precision and robustness of our feature selections, as shown also in Table reftab:analysis-results. Despite some variations in the measures, the classifier performed well on both sets of data.

The classifier's performance for the 'Original' set was accuracy of 86.6%, precision of 54.1%, recall of 17.0%, and F1-score of 25.9%.

Similar results were obtained for the 'RFE' set, where the classifier's accuracy was 86.6%, precision was 54.9%, recall was 16.5%, and F1-score was 25.3%.

These findings validate the efficacy of our feature selection approaches by showing that both feature sets are useful for classification, although with minor changes in accuracy and recall measures.

Explaining Model with SHAP

Machine learning algorithms have emerged as effective tools for disease prediction in the evolving healthcare landscape. However, the 'black-box' nature of these models often makes it challenging to interpret their predictions and understand the relative importance of different input factors. To address this issue, interpretability tools as SHAP have gained popularity. SHAP values provide a nuanced understanding of the factors influencing illness risk by quantifying the impact of specific attributes on the model's prediction. In this context, we explore the intricate network of health factors affecting the likelihood of developing hypertension, a common and complex cardiovascular disease. Our goal is to analyze the interaction of various health metrics, ranging from medication use and standard risk factors to less obvious influencers, and how they collectively influence the model's predictions using patient-specific SHAP values. This investigation highlights how machine learning interpretability tools can enhance our understanding of disease prediction and potentially guide therapeutic decisions.

study highlights the primary factors impacting hypertension across various dataset modifications through the analysis of global SHAP values. Several common trends and intriguing variances are observed. The average magnitude of the SHAP values for each feature over the entire dataset is evaluated, as depicted in Figure 1a.

To acquire a better understanding of how each feature effects the model's predictions, SHAP (Shapley Additive Explanations) values were generated. Among all the characteristics, General Health Status, High Blood Pressure Status, Age, and Body Mass Index emerged as the most significant in both the Original and RFE datasets. In the Original dataset, the SHAP values were notably 0.674 for General Health Status, 0.523 for High Blood Pressure Status, 0.413 for Age, and 0.401 for Body Mass Index. Similarly, in the RFE dataset, the comparable SHAP values were 0.673 for General Health Status, 0.530 for High Blood Pressure Status, 0.411 for Age, and 0.404 for Body Mass Index as also shown in figure 1. These values provide as a quantifiable indication of the average influence each of these qualities has on the model's output, therefore underlining their relevance in diabetes prediction.

These results validate the success of our feature selection techniques by showing the resilience of the chosen features in predicting diabetes, regardless of the feature set employed.

A more sophisticated knowledge of the model's prediction ability is revealed when the individual SHAP values are thoroughly analyzed and compared to the actual health situations of particular patients. Negative SHAP values for General Health Status were seen starting with Patient 6, who was correctly identified as not having diabetes (True Negative),as shown in the Figure 2, -1.3621 in the "Original" set and -1.4022 in the "RFE" set. These data support the model's accurate prediction of a decreased risk of diabetes, together with a negative SHAP value for high blood pressure status (-0.5726 in "Original" and -0.5969 in "RFE").

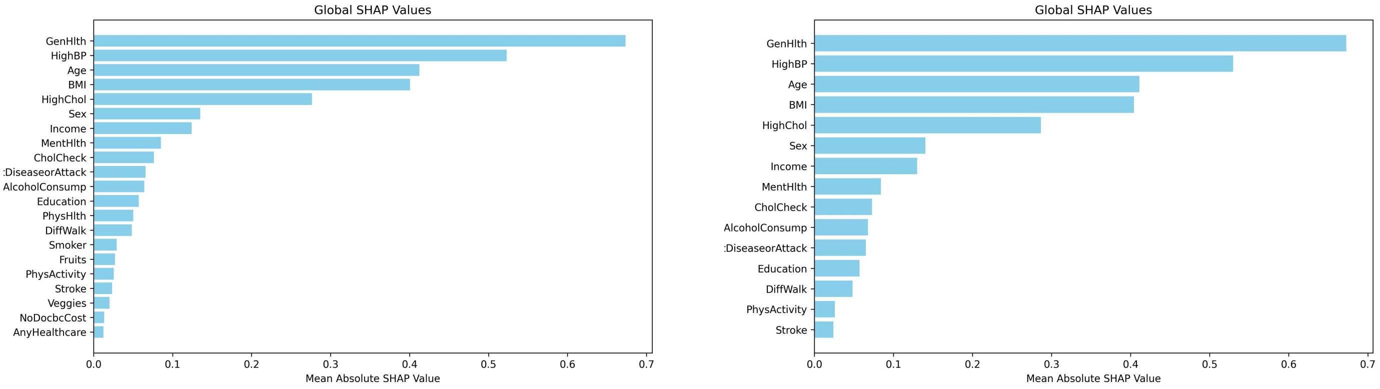
Patient 156 had substantial positive SHAP values for BMI, 0.9521 in the "Original" set and 0.8867 in the "RFE" set, and was appropriately diagnosed as having diabetes (True Positive).As shown in the figure 2, positive SHAP values for High Blood Pressure Status (0.5819 in 'Original' and 0.6005 in 'RFE') are confirmed to have a significant influence in the model's ability to diagnose diabetes accurately.

However, the model's forecasts did not show infallibility. Positive SHAP readings for High Blood Pressure Status were found in both sets for Patient 34, who was incorrectly diagnosed as not having diabetes (False Negative), as shown in the Figure 3, namely 0.5234 in the "Original" and 0.5418 in the "RFE". These were countered by a negative SHAP value for General Health Status (-0.5440 in 'Original' and -0.4934 in 'RFE'), indicating that these competing signs may have caused the inaccurate prediction to be confused.

Similar positive SHAP readings as shown in the figure 3, for

Table 4 Attribution of the dataset and patient details with RFE Selection

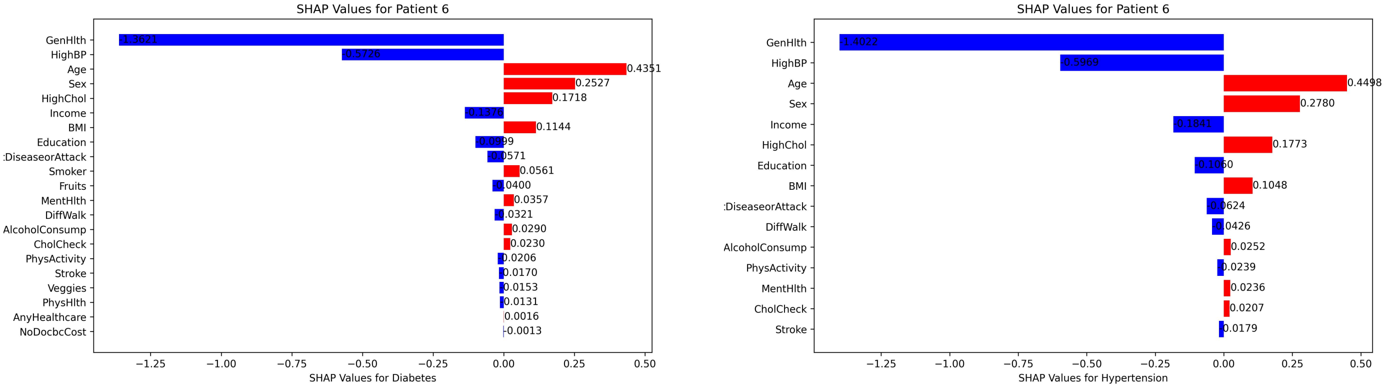
No.	Attribution	Variable	RFE	Pt6	Pt156	Pt34	Pt265
1	High blood pressure	HighBP	Picked	1.0	1.0	1.0	1.0
2	High cholesterol levels	HighChol	Picked	0.0	1.0	1.0	0.0
3	Cholesterol check status	CholCheck	Picked	1.0	1.0	1.0	1.0
4	Body Mass Index	BMI	Picked	30.0	47.0	24.0	36.0
5	Smoking status	Smoker		1.0	1.0	1.0	1.0
6	Stroke status	Stroke	Picked	0.0	0.0	0.0	0.0
7	Heart disease or attack	HeartDorA	Picked	0.0	0.0	0.0	1.0
8	Physical activity status	PhysActivity	Picked	0.0	0.0	0.0	0.0
9	Fruit consumption	Fruits		0.0	1.0	0.0	1.0
10	Vegetable consumption	Veggies		0.0	0.0	0.0	1.0
11	Heavy alcohol consmp.	HvyAlcoholC	Picked	0.0	0.0	0.0	0.0
12	Healthcare coverage	AnyHealthcr		1.0	1.0	1.0	1.0
13	Avoided doctor due to cost	NoDocbcCos		0.0	0.0	0.0	0.0
14	General health status	GenHlth	Picked	3.0	3.0	2.0	3.0
15	Mental health status	MentHlth	Picked	0.0	0.0	0.0	0.0
16	Physical health status	PhysHlth		14.0	0.0	0.0	2.0
17	Difficulty in walking or climbing stairs	DiffWalk	Picked	0.0	1.0	0.0	1.0
18	Gender	Sex	Picked	0.0	0.0	0.0	0.0
19	Age category	Age	Picked	9.0	11.0	12.0	11.0
20	Education level	Education	Picked	6.0	6.0	3.0	5.0
21	Income level	Income	Picked	7.0	5.0	3.0	4.0



(a) Global SHAP Values

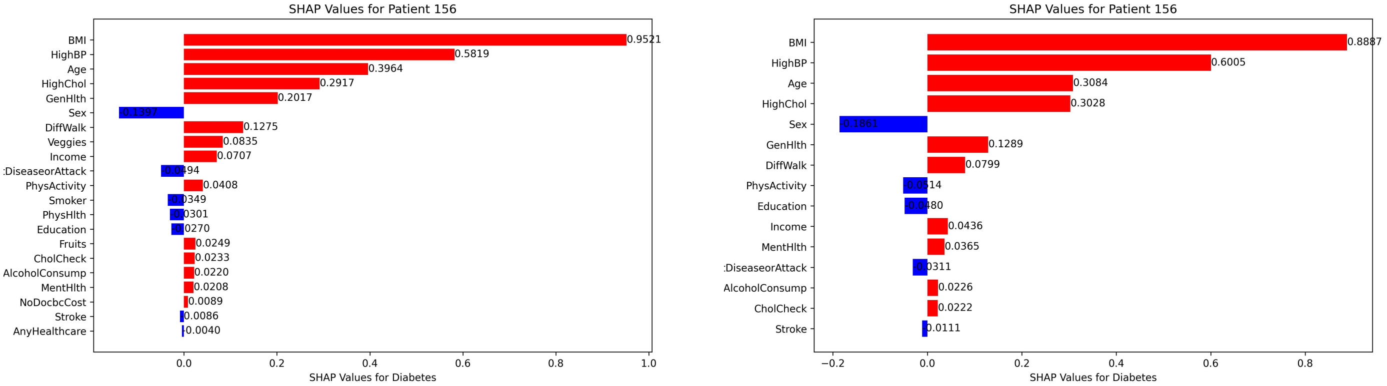
(b) Global SHAP Values (RFE)

Figure 1 Comparison of Global SHAP Values



(a) Local SHAP values for original dataset

(b) Local SHAP values for RFE dataset



(c) Local SHAP values for original dataset

(d) Local SHAP values for RFE dataset

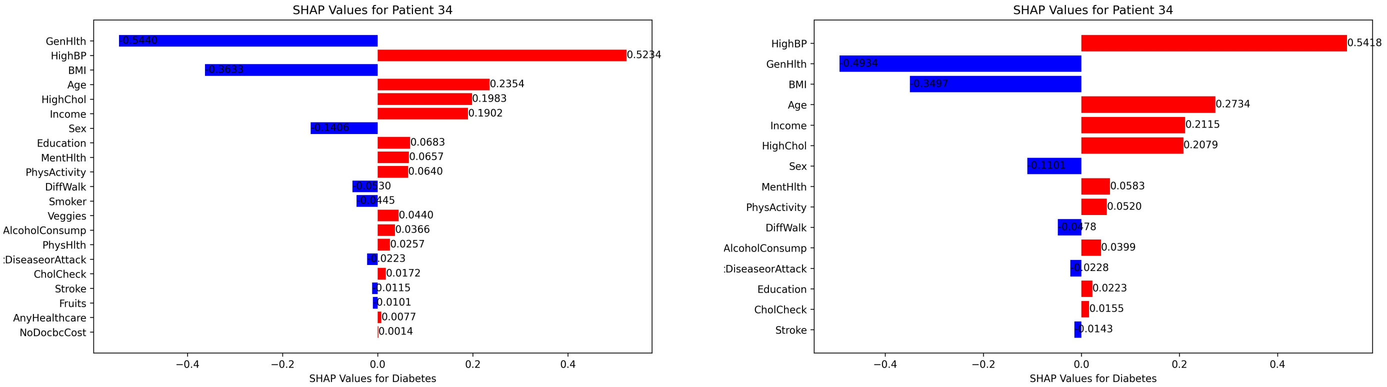
Figure 2 Comparison of local SHAP values for Patient 6 and 156

BMI (0.5051 in 'Original' and 0.5029 in 'RFE') and High Blood Pressure Status (0.5122 in 'Original' and 0.4965 in 'RFE') were reported in the case of Patient 265 who was misdiagnosed as having diabetes (False Positive). Despite these signs, the model overestimated the danger, which led to an inaccurate prognosis.

These distinct studies confirm the robustness of the feature selection while also highlighting potential areas where more model fine-tuning may be necessary for more precise and dependable predictions.

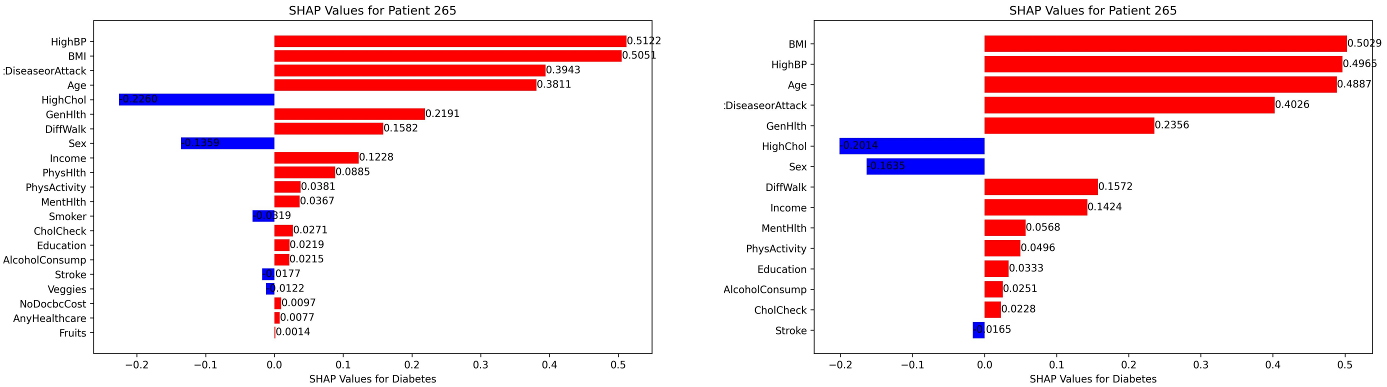
SHAP Dependences for Variables

In the study, the clarification of how individual features influence the model's predictions was provided by SHAP dependence plots. Additionally, how these relationships are modulated by other in-



(a) Local SHAP values for original dataset

(b) Local SHAP values for RFE dataset



(c) Local SHAP values for original dataset

(d) Local SHAP values for RFE dataset

Figure 3 Comparison of local SHAP values for Patient 34 and 265

teracting variables was indicated by the color of each point on the plots. A comprehensive understanding of the key variables and their interactions that drive the model's decisions was offered by these plots.

Two distinct sets were utilized for this analysis: the 'Original' set, which encompasses all 21 variables, and the 'RFE' set, a refined subset containing 15 selected features. In both sets, the identification of the most impactful features was made: General Health Status (GenHlth), High Blood Pressure Status (HighBP), Age, and Body Mass Index (BMI), listed in descending order of their importance. A more comprehensive understanding of the implications of these critical variables was enabled by the utilization of both sets, thereby enriching the interpretability of the model.

It must be noted that rigorous statistical analysis has not been applied to the SHAP values, which are intended to provide an initial understanding of the relationships between the variables and diabetes risk. For example, a greater likelihood of diabetes was suggested by higher SHAP values for General Health Status and High Blood Pressure Status in both sets, as illustrated in the dependence plots.

Regarding Age, an increase in the risk of diabetes as age increases was indicated by the SHAP values. This is consistent with broader medical understanding, in which older age is linked to a higher likelihood of developing chronic conditions, including diabetes.

Similarly, a link between elevated Body Mass Index (BMI) values and a higher risk of diabetes was established, corroborating existing medical literature that associates obesity with diabetes.

In summary, the validation of the efficacy of the feature selection process was achieved through the SHAP dependence plots generated from both the 'Original' and 'RFE' sets. Nuanced insights into how these selected variables interact to influence the model's predictive capabilities were also offered.

DISCUSSION

In the current work, the efficacy of machine learning methods in predicting diabetes risk was examined, with a special emphasis on the XGBoost classifier. Two unique datasets were employed: the 'Original' set, encompassing all 21 variables, and the 'RFE' set, a refined subset of 15 chosen characteristics. The SHAP dependent charts were developed to give subtle insights into the correlations between various variables and the model's prediction capabilities. It was discovered that General Health Status (GenHlth), High Blood Pressure Status (HighBP), Age, and Body Mass Index (BMI) were the most impacting factors in both groups. These results accord with current research, strengthening the assumption that these characteristics are key markers of diabetes risk.

The investigation also demonstrated that the XGBoost classifier performed with a high degree of accuracy on both the 'Original' and 'RFE' sets. However, it should be noted that the model's performance indicators, such as accuracy and recall, differed marginally across the two sets. This implies that although feature selection

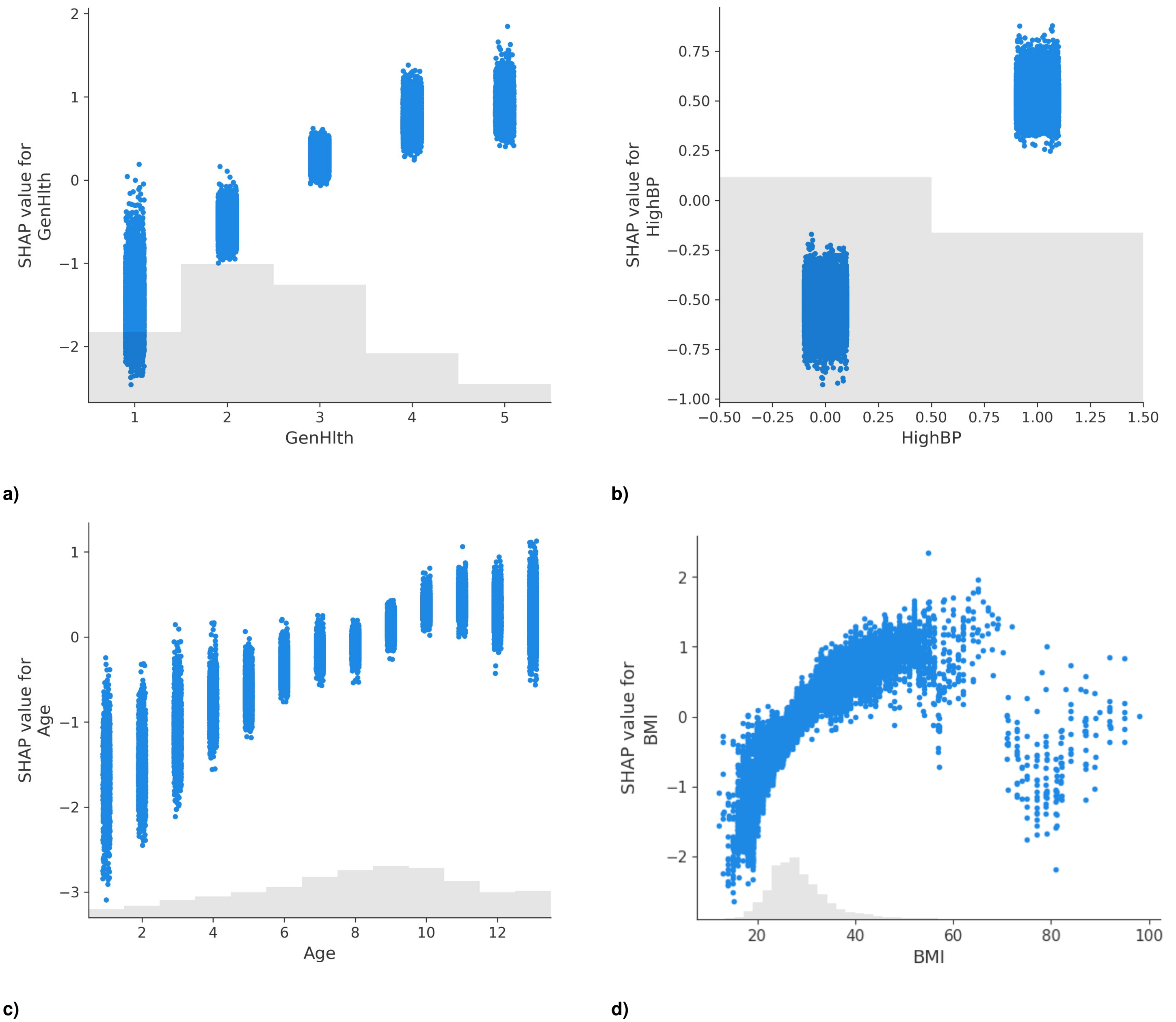


Figure 4 Dependence plots in original dataset for variables **a)** General health status, **b)** High blood pressure, **c)** Age, **d)** Body Mass Index (BMI)

strategies like RFE may be efficient in decreasing model complexity, they may not necessarily lead to a substantial gain in predictive accuracy. Therefore, the option between employing all accessible data or a subset of chosen features should be made carefully, considering the unique aims and restrictions of the study.

One of the disadvantages of this research is the absence of comprehensive statistical analysis done to the SHAP values. While the SHAP dependency plots give helpful early insights into the correlations between factors and diabetes risk, they are not a replacement for a complete statistical study. Future study might benefit from a more in-depth investigation, potentially adding additional statistical approaches to confirm the results further.

In conclusion, this work adds to the expanding corpus of research on the application of machine learning algorithms in healthcare. It reveals that XGBoost, when trained on well chosen characteristics, may be a strong tool for predicting diabetes risk. The insights gathered from the SHAP dependent plots give an extra layer of interpretability to the model, making it more transparent and perhaps more trustworthy in a clinical environment. Further study is required to confirm these results across diverse demographics and healthcare systems.

CONCLUSION

In our comprehensive research journey into the domain of machine learning interpretability, an emphasis on diabetes risk assessment was pronounced, leveraging the usability of SHAPley analysis. Drawing from the Behavioral Risk Factor Surveillance System (BRFSS) dataset, the study precisely analyzed two distinct variations (original and feature selected) of the dataset, which is a renowned annual telephone survey collected by the Centers for Disease Control and Prevention (CDC). The dataset presented a separation in its outcome classes, defining the presence of diabetes, offering a granular understanding of this pervasive disease. Firstly, encompassing 21 varied feature variables, the dataset provided a kaleidoscopic view of a many of behavioural and health characteristics. Identifying the potential for refinement, we harnessed RFE as a strategic tool for feature selection. This not only rationalised our feature space but significantly augmented our model's prediction ability. In conclusion our efforts underscore the enormous benefits of adopting a transparent machine learning paradigm, especially in the diabetes prediction.

The horizon of future endeavours, our study gazed into several areas of research. The profound depth of the BRFSS dataset hints at the potential for uncovering more intricate patterns and correlations, thereby exploring diabetes risk prediction. While our current methodologies have proven the usability, the dynamic nature of healthcare mandates continuous evolution. This could clear in the form of integrating more sophisticated machine learning algorithms, or perhaps investigating the distinctions of SHAP to loosen more complex model behaviors. Collaborative research performed with medical professionals could surface the real-world results for the application of our models, offering concrete benefits to patients. It is aspired by amalgamating feedback from the clinics, refining methodologies, and developing innovation, to redefine the landscape of machine learning in diabetes risk assessment.

Availability of data and material

Not applicable.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The authors have no relevant financial or non-financial interests to disclose.

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