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REVIEW

Artificial intelligence on biomedical signals: technologies, applications, and future directions

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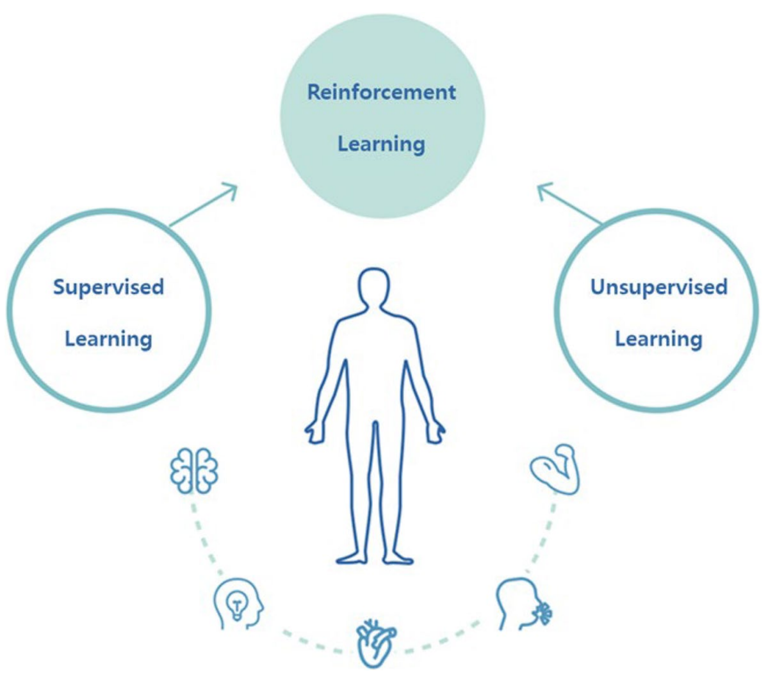
Abstract

Integrating artificial intelligence (AI) into biomedical signal analysis represents a significant breakthrough in enhanced precision and efficiency of disease diagnostics and therapeutics. From traditional computational models to advanced machine learning algorithms, AI technologies have improved signal processing by efficiently handling complexity and interpreting intricate datasets. Understanding physiological data, which requires highly trained professionals, is now more accessible; in regions with limited access, AI tools expand healthcare accessibility by providing high-level diagnostic insights, ultimately improving health outcomes. This review explores various AI methodologies, including supervised, unsupervised, and reinforcement learning, and examines their synergy for biomedical signal analysis and future directions in medical science. By capturing a comprehensive overview of the current state and prospects of AI-driven healthcare, this paper highlights the transformative potential of AI in analyzing biomedical signals.

Graphical Abstract



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Highlight

• This review shows an extensive examination of the integration of AI in the analysis of biosignals to enhance diagnostics and therapeutics.
• The summary details the development and utilization of AI techniques, such as supervised, unsupervised, and reinforcement learning.
• This paper also covers the critical factors that impact the design and implementation of AI algorithms for processing bio-signals.

Keywords Artificial intelligence · Biomedical devices · Signal analysis · Healthcare · Diagnostics · Therapeutics

Introduction

At the forefront of healthcare innovation, the integration of artificial intelligence (AI) into the biomedical signal (biosignal) marks a significant breakthrough, reshaping the methodology of medical diagnostics and therapeutic care. The increasing complexity of medical data, especially with the rise of personalized medicine, has made it difficult for human experts to analyze without assistance. Extracting meaningful information from high-dimensional biosignal data was challenging due to long, variable signals and the need for manual input requirements from highly trained professionals [1, 2]. Systems with AI can accurately process complex and voluminous data, significantly improving the diagnoses accuracy by identifying subtle differences across biomarkers. AI's ability to manage and interpret this data helps identify disease markers faster and with greater precision [3, 4]. This capability enhances diagnostic processes, shortens the time required for data analysis, and provides critical support in emergency settings where quick decision-making is essential for addressing biosignal abnormalities [5, 6]. Biomedical signals, such as electroencephalograms (EEG) and electrocardiograms (ECG), are essential to medical diagnostics. EEGs are extensively utilized in neurological studies to monitor brain activity, diagnose conditions like epilepsy, and assess cognitive states [7, 8]. The analysis and interpretation of EEG data face significant challenges due to the large volume of information involved [9]. Similarly, ECGs are critical in cardiology for detecting heart abnormalities, such as arrhythmias, which can be life-threatening if not identified promptly [10, 11]. The large amounts of data generated from these signals require efficient processing and analysis methods to extract relevant information and provide accurate diagnoses [12, 13]. The automation of repetitive processes, including classification and anomaly detection in biological signals, has been greatly aided by AI [14]. Different AI methodologies have distinct applications and strengths in biosignal analysis. Supervised learning, a method where models are trained on labeled data, is widely used for tasks classifying normal and abnormal heartbeats in ECG data. Unsupervised learning, which deals with unlabeled data, helps identify hidden patterns and anomalies in biosignals without prior outcome knowledge. Reinforcement learning, where models learn through trial and error by receiving feedback from their actions, is increasingly applied to complex decision-making tasks in dynamic and uncertain environments [5, 15]. AI technologies, driven by conventional computation models to advanced machine learning (ML) algorithms, have transformed biosignal processing and applications by a) handling data complexity and volume, [3, 4] b) advancing capabilities for interpreting complex datasets, [5, 16, 17] and c) enhancing personalized recognition and recommendation. These innovations in AI not only refine the interpretation of physiological data but also suggest more predictive solutions and interfaces for human health issues [4, 18]. By automating routine tasks, AI frees medical professionals to focus on more complex aspects of patient care, optimizing overall healthcare delivery (Fig. 1) [19–21]. Furthermore, in regions with a shortage of trained medical professionals, AI tools can offer high-level diagnostic insights that would otherwise be unavailable, democratizing healthcare knowledge and improving health outcomes in under-resourced settings [5, 16]. This review explores supervised, unsupervised, and reinforcement learning, as well as the synergy between machine learning and biomedical engineering, highlighting AI's efficiency in medical practice and its role in setting new standards in healthcare delivery. It begins with traditional supervised learning approaches and progresses through unsupervised and reinforcement learning methods, outlining the trajectory and impact of AI on the interpretation of complex biological data. Each section covers the architecture, key methodologies, and performances of these approaches. Additionally, this review included a summary table (Table 1) that outlines the advantages, applications, and commonly used algorithms for Supervised Learning, Unsupervised Learning, and Reinforcement Learning. Table 2 provides essential details on the characteristics, applications, and relationships between these learning methods. Finally, the review discusses inherent challenges and future directions in medical science, offering a comprehensive view of the

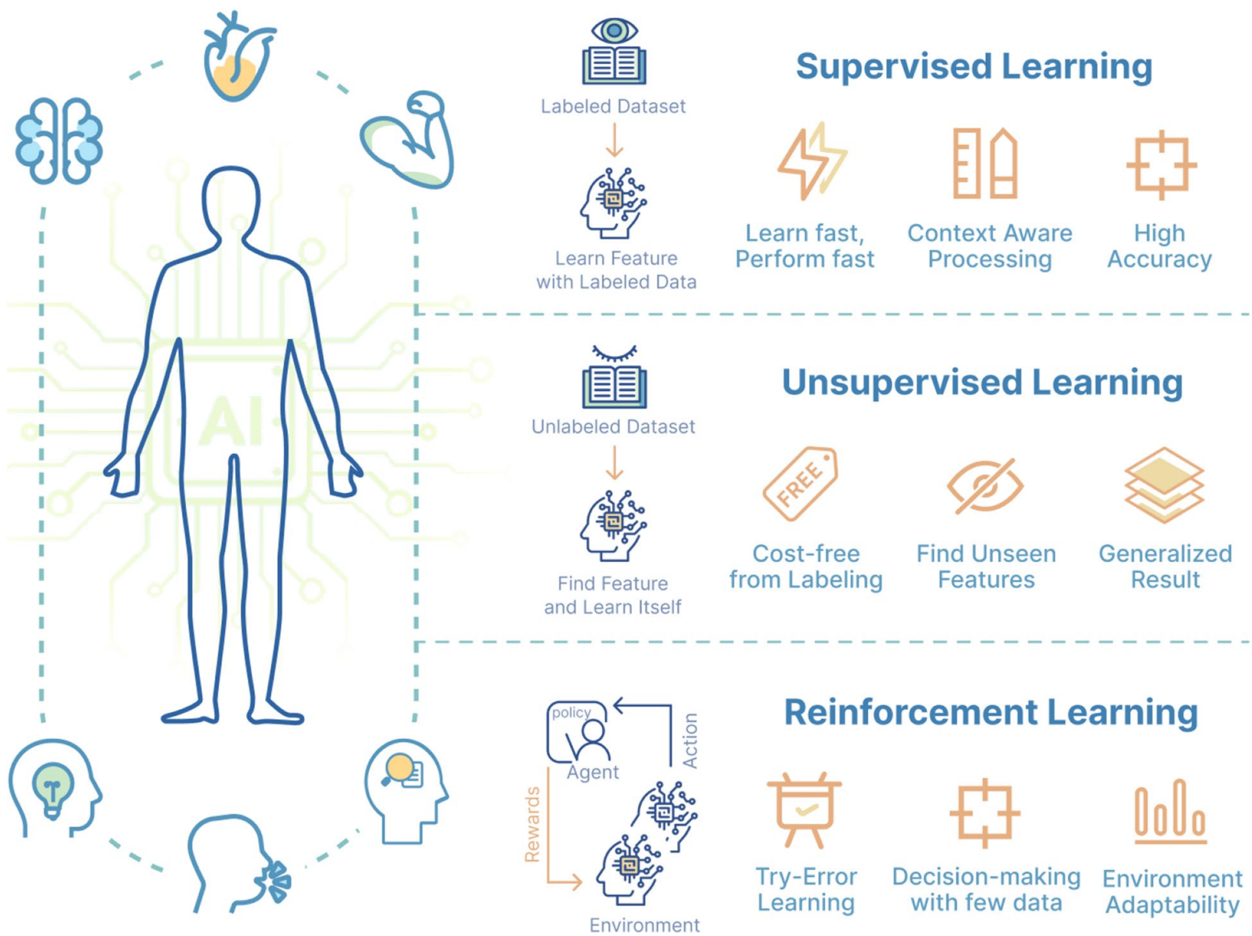

Fig. 1 Overview of AI on biomedical signal analysis

current state, applications, and prospective advancements in AI-driven healthcare.

Supervised learning

Overview

Machine learning, a subset of artificial intelligence, empowers systems to learn from data, recognize patterns, and make decisions with minimal human intervention [22]. It involves training algorithms on data sets to allow them to make predictions or take actions based on what they have learned [22, 23]. Traditional machine learning algorithms like Support Vector Machines (SVM), Random Forest, and other gradient boosting algorithms are instrumental in developing models that interpret complex patterns in the context of AI-powered biosignal. For instance, they can be used to identify subtle changes in Electrocardiogram signals that indicate the onset of cardiac conditions, capture Electromyography (EMG) signals for neuromuscular disorder, and analyze Electroencephalogram signals for signs of neurological states and disorders. Other gradient boosting algorithms are utilized to forecast the symptoms of disease and states. They have demonstrated efficacy in capturing distinctive patterns and characteristics of biosignals with relatively low computational overhead, setting a foundational stage before the advent of more complex models such as Convolutional Neural Networks.

Support vector machine

Support Vector Machine (SVM) has been notably effective in biosignal applications due to its efficiency in handling high-dimensional spaces and its ability to perform classification tasks by finding the optimal hyperplane that maximizes the margin between different classes [22]. Siuly et al. designed a robust feature extraction method based on sample entropy and spectral entropy for the classification of EEG signals [24]. Here, SVM is utilized to classify EEG signals

Table 1 Comparison of AI learning types in biomedical signal analysis

Learning type	Algorithms	Advantages	Disadvantages	Applications
Supervised Learning	**Conventional ML** - SVM - RF - Gradient boosting **DL** - CNN - RNNs (LSTM, GRU) - TCN	**a.** High accuracy in classification tasks **b.** Ability to handle high-dimensional data **c.** Effective in identifying subtle patterns **d.** Improved model interpretability	**a.** Requires large, labeled datasets **b.** Can be biased by training data **c.** High computational cost for complex models	**a.** ECG/EEG/EMG signal classification - Heartbeat classification in ECG - Seizure detection in EEG - Hand gesture recognition with EMG **b.** Disease diagnosis - Arrhythmia detection - Epilepsy detection
Unsupervised Learning	**Conventional ML** - K-means - PCA **DL** - Auto Encoder - t-SNE, UMAP	**a.** Identifies intrinsic patterns in data **b.** Reduces dependency on labeled data **c.** Efficient in feature extraction **d.** Handles complex and noisy datasets	**a.** Results can be less interpretable **b.** Requires significant data preprocessing **c.** Less precision in predictive tasks	**a.** Clustering for patient stratification - Cluster patient by arrhythmia types - Cluster symptoms of epilepsy patients **b.** Dimensionality reduction - feature extraction from complex EEG - reduce high dimensional biosignal
Reinforcement Learning	**Conventional RL** - Q-learning - A2C - Policy Gradient Method **DL aided RL** - DQN, DDQN	**a.** Adaptability to dynamic environments **b.** Continuous learning and optimization **c.** Reduces need for extensive labeled datasets **d.** Handles sequential decision-making	**a.** High complexity **b.** Requires extensive training time **c.** Risk of suboptimal policies, **d.** if not carefully tuned	**a.** Dynamic treatment regime (DTR) - Optimizing deep-brain stimulation strategy to treat epilepsy **b.** Optimization of healthcare processes - Optimal treatment to sepsis - Personalized treatment for diabetes **c.** Control systems - Control lower limb press system to enhance blood flow

Table 2 Characteristics of AI methods and relationships with other learning methods in biomedical signal analysis

Learning Type	Parameter Characteristics	Data Characteristics	Relationship to Other Learning Types
Supervised Learning	**a.** Requires tuning of hyperparameters **b.** Sensitive to overfitting	**a.** Requires labeled data **b.** Large datasets needed for training	**a.** Provides labeled data for semi-supervised and reinforcement learning **b.** Combined with unsupervised learning for feature extraction and preprocessing
Unsupervised Learning	**a.** Fewer tuning parameters **b.** Focus on dimensionality reduction	**a.** Works with unlabeled data **b.** Requires large datasets for better insights	**a.** Preprocess data for supervised learning **b.** Used in reinforcement learning to identify state spaces
Reinforcement Learning	**a.** High number of parameters for policy optimization **b.** Balance for Exploration vs. exploitation	**a.** Optimized for sparse and noisy data **b.** Can handle various data forms	**a.** Utilizes supervised learning for policy improvement **b.** Incorporate unsupervised learning for better exploration strategies

for different mental states, using entropy-based features from the time and frequency domains. Support Vector Machines are used to classify ECG data by learning to differentiate between different types of heartbeats, such as normal beats and those indicative of arrhythmia [25]. SVM works by mapping ECG signal data into a high-dimensional space and then finding the hyperplane that best separates the different classes (e.g., normal vs. arrhythmic). This classification is achieved by maximizing the margin between the nearest points of each class, referred to as support vectors [25]. This capability demonstrated the ability of SVM to accurately classify EEG and ECG data, thereby expanding the potential application of AI in the diagnostic process.

Random forest

Random Forest is an ensemble learning technique that employs multiple decision trees to enhance predictive accuracy and mitigate overfitting, thereby enabling the classification and prediction of various medical conditions from biosignals. Prior studies utilized the analysis of random subsets of features from complex ECG data to effectively predict cardiac arrhythmias, distinguishing arrhythmic segments from normal ones with high accuracy and minimal data preprocessing [26]. Chen et al. showcased fuzzy entropy (FuzzyEn), which use fuzzy set concepts to effectively characterize the complexity of short, noisy EMG signals, thereby improving the accuracy of SVM predictions [27]. This research introduces the Random Forest's ability to maintain higher similarity degrees and reduce data length dependency, making it particularly effective for analyzing complex signal patterns.

Gradient boosting algorithms

Gradient Boosting Algorithms such as XGBoost (eXtreme Gradient Boosting), CatBoost (Categorical Boosting), and LightGBM(Light Gradient Boosting Machine) operate on the principle of boosting [28]. They combine multiple weak decision trees sequentially to create a strong predictive model for AI-powered biosignal analysis [12, 28]. Each tree is added to correct the errors of its predecessors, aiming to minimize a loss function that measures the discrepancy between predicted and actual values. XGBoost is renowned for its speed for computational resource usage and the accuracy of the final model [29]. The iterative refinement makes it particularly effective for complex regression tasks, including biosignal processing for healthcare applications [30]. XGBoost has been extensively applied to analyze high-sample biosignals, such as ECG [31] and EEG [32] physiological data, to detect abnormalities and predict cognitive states. Its capability to manage large datasets and high-dimensional features makes it especially well-suited for biosignal analysis, where the data is inherently complex and multi-dimensional [29, 33]. CatBoost differentiates itself by handling categorical data, making it highly applicable in healthcare datasets that often include numerical and categorical variables [34]. CatBoost's algorithms are designed to effectively handle the challenges posed by categorical data, avoiding the need for extensive data preprocessing and minimize the risk of overfitting [34]. This feature is especially beneficial for biosignal data intertwined with patient metadata, allowing for more nuanced signal-based feature predictions [28, 35]. LightGBM stands out for its speed and efficiency, particularly in handling large-scale datasets. It's gradient-based one-side sampling and exclusive feature bundling techniques reduce the volumn of data to be processed while maintaining high accuracy [34]. It offers faster training times without compromising the model's performance, making it an enhanced choice for real-time biosignal monitoring systems [34].

Advancements in biosignal analysis

The application and prior studies of SVM, Random Forest, XGBoost, CatBoost, and LightGBM in biosignal analysis proposed an advancement in personalized algorithms. The iterative learning process for algorithms and blending the model allows for the development of accurate models that are suited for the dynamic and complex nature of biosignals. It pioneers the development of predictive models that can offer early warnings and statistics about potential health issues, recommend early treatments to individual patients, and ultimately improve patient outcomes. However, the reliance on labeled and human intervention data in these machine-learning approaches presents limitations in scenarios where labeled examples are scarce or costly to obtain. Moreover, with advances in sensing modalities, wearable sensors [36], and advanced medical settings, diverse biosignal and data fusion methodologies have been integrated into biosignal analysis systems, and there is an emerging need for real-time monitoring and proactive analytic tools. This emphasizes the need for exploring supervised and unsupervised learning methods to expand the potential for AI-based analysis of biosignals that can analyze multiple structured biosignal features.

Convolutional neural network

Convolutional neural networks (CNNs), widely recognized for their ability to analyze structured, grid-like data such as images and time-domain signals, have become increasingly prevalent in the analysis of biomedical signals [37]. Their applicability proves high efficiency in the complex analysis of biomedical signals like ECG, EMG, and EEG. It is because these signals are characterized by high frequency and intricate patterns, presenting significant challenges in data processing and interpretation [12]. CNNs address these challenges by learning spatial hierarchies of features through convolutional filters, which compress and preserve essential information while reducing data dimensionality [38]. This process ensures minimal data loss and lower computational demands, making CNNs particularly valuable in biosignal processing where precision and efficiency are needed [12]. The advancement of CNNs in biosignal analysis has been further enhanced by models such as AlexNet, GoogleNet, VGGNet, and ResNet. These models have introduced innovations like inception modules, factorization, and residual blocks, which enhance the networks' ability to process large and complex datasets. These improvements are especially beneficial when dealing with the nuanced and detailed nature of biosignals [39–41].

Advanced models of CNNs

The development of advanced image classification models like AlexNet, GoogleNet, VGGNet, and ResNet has marked significant advancements in the utilization of CNN for biosignal analysis [42]. These models have been enhanced with techniques that not only enrich the feature maps extracted by CNNs—such as GoogleNet's Inception module and VGGNet's factorizing convolution—but also address critical challenges like parameter reduction and the gradient vanishing problem through innovations like residual blocks. For instance, in the application of CNNs to cardiology as shown in Fig. 2A, models have been developed to classify symptoms of heart diseases using ECG signals [42]. As the depth of CNNs increases, the gradient vanishing problem tends to occur; however, this has been effectively mitigated by implementing residual blocks. This approach not only enhances classification performance but also adds non-linearity to make feature maps more informative, resulting in an interpretable model that can promptly explain the reasoning behind its classifications. This demonstrates how advanced CNN models, through integrations such as module or residual blocks, have improved the accuracy and interpretability of ECG-based heart disease classification, offering more reliable diagnostic tools.

Signal processing and models

Biosignals like ECG, EMG, and EEG contain numerous data points due to their high frequencies and complex patterns. Efficient feature extraction from high-dimensional biosignals and low data loss are crucial for accurate AI-driven classification and forecasting, making CNNs an ideal choice for these tasks [12, 47]. The CNNs operate with reduced computational demands, speed up the training process, and process complex patterns by learning spatial hierarchies of features from input data, making CNNs particularly suitable for biosignal-driven classification and applications [12, 48, 49]. CNNs have significantly transformed the analysis of biosignals due to their ability to process structured data efficiently. Kim, et al. [43] suggested a CNN-based user identification system with EMG, as shown in Fig. 2B. Even though people may pose the same gestures, their EMG signals vary, and this characteristic is used in user identification systems. The study converted EMG signals into 2D spectrograms and utilized CNNs to extract the features from the spectrogram for classification. The CNNs performed successfully, achieving a classification accuracy of 97.5%. These successful applications of CNNs to biopotential-based user identification highlight the model's potential for enhancing the accuracy and reliability of personalized biomedical signal analysis.

Signal compression with CNNs

Moreover, CNNs also prove valuable in signal data compression, an effective process for handling long data generated by devices that record biopotential signals like ECG or EEG [12]. The theoretical foundation of CNNs is based on their ability to capture spatial hierarchies in data, enabling the efficient reduction of dimensionality without compromising essential features. For example, CNNs have been used to classify heartbeats from ECG signals represented as spectrograms, effectively detecting cardiac anomalies [50, 51]. This application not only highlights the ability of CNNs to compress biopotential data without losing vital information but also highlights their potential in automated classification systems, which can identify and analyze biosignals such as heart sounds or brain waves more effectively [13, 48, 49]. Furthermore, the multi-layered structure of CNNs allows for the extraction of both low-level and high-level features, ensuring that even subtle patterns within the data are captured, which is crucial for detecting complex medical conditions. These advancements exemplify how CNNs, through their fast computation capabilities and efficient data representations, contribute significantly to the field of AI-powered biosignal analysis, solving problems that were previously unmanageable and pushing the boundaries of achieving medical diagnostics and monitoring [52, 53].

Spectrogram classification with CNNs

CNNs have transformed the analysis of biosignals, leveraging their capabilities in both spectrogram classification and signal data compression to address previously challenging issues in the field. A spectrogram, which represents the spectrum of frequencies of a signal over time, is used in analyzing audio signals, including biosignals like EEG [44, 54] and EOG [55]. CNNs are particularly suited for

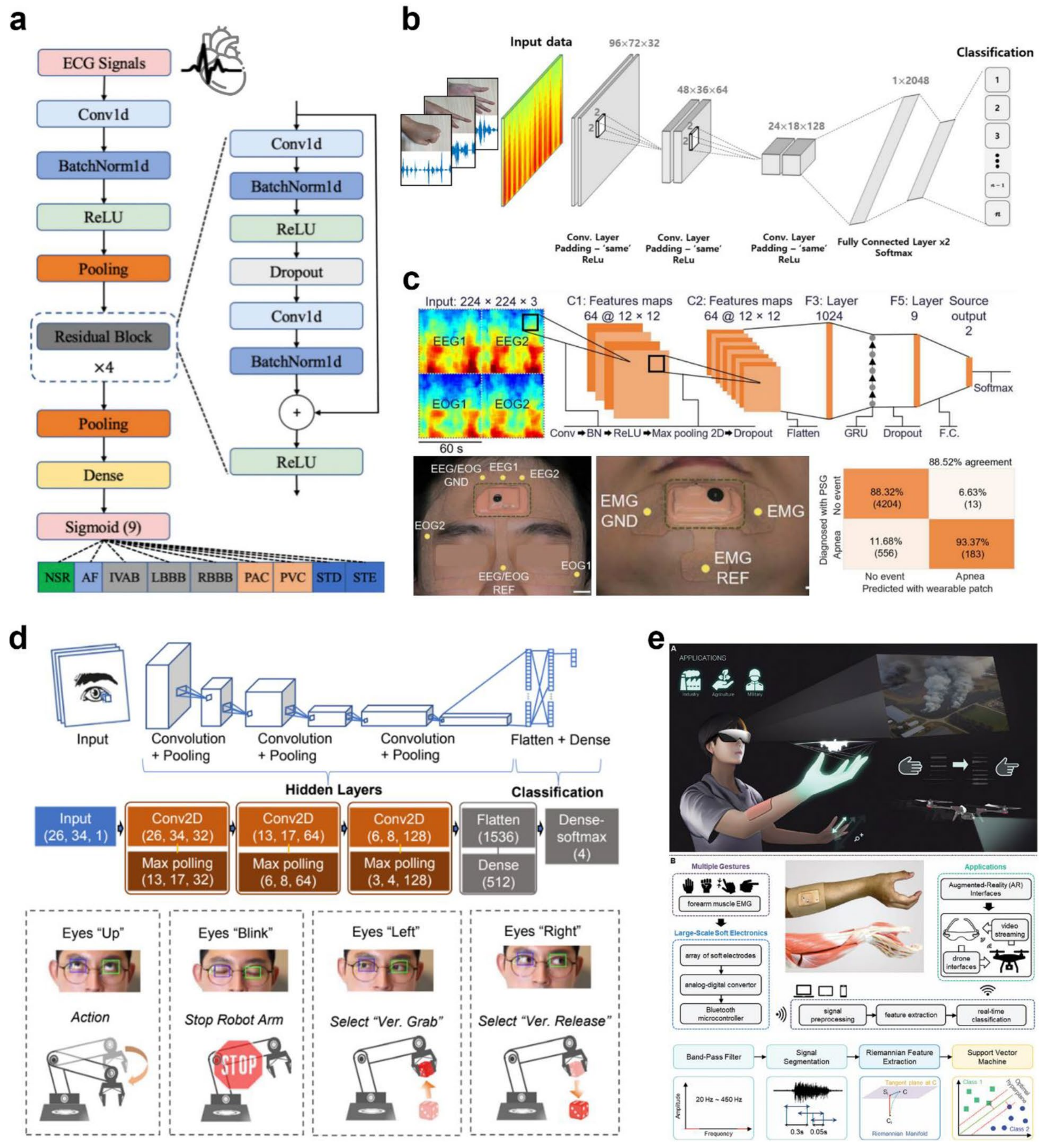

Fig. 2 **A** Residual blocks of a CNN used in an interpretable symptom diagnosis model for ECG signals [42], **B** Basic architecture of a CNN-based classification model for authentication using hand gesture-driven EMG signals [43], **C** Sleep apnea classification using CNN with EEG and EOG signals [44], **D** CNN applied in an HMI to control a robotic arm via gaze and eye tracking [45], **E** AR-enabled human–machine interfaces, illustrating the integration of AR technologies for enhanced interaction and control [46]

these tasks due to their ability to efficiently capture both temporal and frequency-related features embedded within the spectrogram. In prior applications as shown in Fig. 2C, CNNs have shown exceptional utility in complex classification tasks such as sleep apnea detection from EEG and EOG signals measured by wearable sensors [44]. These models employ ReLU activation functions which, compared to traditional tanh functions, provide up to six times faster computation speeds. The implementation of techniques such as ReLU activation and dropout layers not only enhances computational efficiency but also ensures that the models remain resilient against overfitting, making them well-suited for real-world applications where data variability can be a significant challenge. Additionally, the integration of dropout layers prevents overfitting, thereby improving the model's accuracy. These advancements demonstrate how CNNs, with their ability to efficiently process spectrograms, have significantly enhanced the accuracy and speed of detecting multiple conditions from biosignals, leading to more effective health monitoring systems.

Human machine interface

In addition to their applications in biosignal analysis, CNNs have been effectively integrated into Human–Machine Interface (HMI) systems. Figure 2D illustrates the use of CNNs to track eye movements and control robotic arms, showcasing their real-time processing and interaction capabilities [45]. The efficiency of CNNs in fast processing enables them to encode signals into compressed formats and decode them with minimal loss, facilitating precise intention transmission of biosignal data. Another example in Fig. 2E demonstrates next-generation HMI using AI for gesture recognition with EMG signals measured by wearable sensors [46]. These systems convert raw EMG signals directly into feature maps for classification, highlighting the potential of enhancing the accuracy and practicality of real-world applications [56, 57]. Combining CNNs with other algorithms, such as Support Vector Machines (SVMs), can further improve the overall accuracy and extend the applicability of these systems in various fields, including augmented reality and advanced sensor technologies [58, 59]. These integrations illustrate how CNNs can advance the precision and functionality of Human–Machine Interface systems, highlighting more responsive and accurate applications in the field of assistive technologies.

Cardiac systems with CNNs

In prior studies, various activation functions, such as the ReLU function used in AlexNet, have demonstrated their efficacy in enhancing the accuracy and computational speed of cardiac diagnostics. These advancements highlight the potential of CNNs to transform cardiac health monitoring by enabling real-time analysis of intricate patterns in cardiac signals. Prior research highlights the application of CNNs in continuous authentication-enabled cardiac biometric systems [60]. These systems integrate advanced CNN models with cardiac signal analysis to provide a high-accuracy, real-time biometric authentication method that combines with other analytical tools, enhancing both security and user convenience in medical and other user specific applications [61]. This integration of CNNs with signal analysis not only enhances the precision of biometric authentication but also improves real-time security measures, making it more applicable for handling sensitive medical and personalized healthcare environments.

Recurrent neural network

Biosignals are a representative form of time series data that have a sequential order over a certain period of time. Due to this characteristic, the hidden features within that order must be considered. For example, ECG is measured with a certain frequency and has specific peak points called P, Q, R, S, T that indicate cardiac movements and each peak point appears sequentially. Symptoms from most cardiac diseases showed anomalies at ECG sequential patterns, e.g., LBBB (Left Bundle Branch Block) and RBBB (Right Bundle Branch Block). In other words, experts start by finding anomalies at ECG when detecting symptoms of heart disease [62]. Recurrent Neural Networks (RNNs) are the AI methods capable of considering sequential orders. RNNs train data sequentially using recursive hidden states that memorize information from prior steps and use it to calculate present states, allowing them to understand the context of the data. This enables RNNs to consider sequential order and have a crucial role in deep-learning-based biosignal processing [63, 64]. For example, RNNs are used to recognize sleep disorders by analyzing EMG and ECG signals through iterative peak detections [65]. However, RNNs have certain limitations, particularly when dealing with long-term dependencies, which necessitate the development of more advanced models [66].

Advanced models of RNNs

In analyzing biosignals, long-term consideration of the signals is often required. While RNNs provide an effective solution to this issue, basic RNNs have the 'long-term dependencies problem' or 'gradient descent problem,' where they lose information from past steps [66]. In the context of biosignals, the loss of past information can lead to critical misunderstandings or errors in treatment. Long short-term memory (LSTM) networks solve this problem by incorporating multiple gates in their architecture that can retain and process information from previous steps [67]. Additionally, the LSTM network can be trained both in one direction and backward, enabling LSTM to use past information more effectively, and this approach is known as Bidirectional LSTM (BiLSTM). For example, their effectiveness in biosignal processing is well demonstrated in a study using RNN and BiLSTM for pain recognition with EMG and ECG data [68]. The study showed that BiLSTM based model outperformed basic RNN models, although the authors noted that feature selection had a greater impact than the algorithm itself. The Gate Recurrent Unit (GRU) is a simplified version of LSTM that retains the ability to capture dependencies over long sequences while offering faster training times and reduced computational loads [69, 70]. As a result, LSTM and GRU networks have been effectively applied in detecting arrhythmias in ECG signals and predicting epileptic seizures from EEG data by analyzing temporal sequences and identifying abnormal patterns indicative of medical conditions [71, 72]. Another advanced algorithm, Temporal Convolutional Networks (TCNs), is a CNN-based approach capable of handling the sequential order of datasets [73]. TCNs utilize a hierarchy of temporal filters to capture intricate patterns and dependencies in sequential data. More specifically, TCN uses causal convolution and dilated convolution to effectively handle sequential data, allowing them to maintain a 'large effective history' or a 'longer effective memory' with these methods. Moreover, TCNs have a relatively simple architecture compared to RNNs, LSTMs and GRUs. Due to these advantages, TCNs have emerged as a powerful tool for biosignal processing with fewer parameters, faster computation, and competitive performance. For instance, Zou L. et al. used TCNs to detect sleep apnea with ECG, EOG, EEG, leg-EMG, and other signals, showing better performance in per-recording detection compared to CNN, CNN-GRU, or LSTM models [74]. Another study by Ingolfsson, T. M. et al. demonstrated that TCNs provided a more balanced performance with fewer parameters on cardiac arrhythmia detection using ECG compared to LSTM based model [75].

Signal processing with CNNs

Biosignals (ECG, EMG, EEG, EOG, etc.) are often collected in uncontrolled environments. Due to their inherent variability and external factors, particularly, biosignals from wearable devices tend to have more contaminants, even as the demand for data collection from these devices increases. For better accuracy and analysis, denoising (or removing contaminants from the signal) is important. While conventional filtering methods, such as the Butterworth filter, which is preferred for medical applications, still show strong performance, denoising with Deep Learning (DL) methods has gained attention recently [76, 77]. Simple Neural Network (NN) and CNN have demonstrated their effectiveness in denoising biosignals alongside performances with LSTM and GRU. Dias, M. et al. developed an ECG denoiser using GRU and Bidirectional GRU (BiGRU) in an industrial setting [78]. This study trained and tested their model on a public database, PTB-XL and MIT-BIH Noise Stress Test database, which are representative of ECG data, and achieved impressive results with small parameters—a key advantage of GRU. In addition to denoising, Machado J. et al. showed the classification of contaminant types in EMG signals using RNN [79]. This study classified contaminants into five categories: white Gaussian noise, power line interference, movement artifacts, ECG, and clean EMG, across three SNR levels, and achieved excellent performance.

Cardiac system with RNNs

The cardiac system is a complex collection of signals and a crucial part of the healthcare system. ECG signals have visible information that can easily be analyzed, but they also contain hidden information. One of the key pieces of hidden information that many researchers aim to uncover is time-perspective data [64, 80]. While CNNs have shown great performance in analyzing ECG signals, such as detecting arrhythmias and classifying ECG signals based on cardiac movements, RNNs are also being actively researched because they can consider the sequential properties of the data [64, 80]. Figure 3A illustrates the basic unit of an RNN and its application in ECG rhythm classification [81]. The researchers developed three models—RNN, LSTM, and GRU—and compared their performance. Initially, they found that RNNs did not train properly, as the gradient norm showed a large increase. However, the use of LSTM and GRU models resulted in better performance without encountering the same problem. ECG beats exhibit variability in both temporal and morphological aspects, depending on the patient, making ECG classification more challenging [81]. DL methods, especially RNNs, have shown superior performance in addressing this issue. Boda, S. et al. demonstrated the use of RNNs for ECG beat classification [82]. They developed three models (RNN, LSTM, and GRU) to classify ventricular ectopic beats and supra-ventricular ectopic beats. Among these, LSTM showed the best performance, and with hyperparameter tuning (a single LSTM layer of 50 hidden nodes), the model proved applicable to continuous monitoring applications.

Motion recognition

Human motion recognition is widely used in biomedical analysis and Human–Computer Interfaces. It can assist patients with disorders in communicating with others and enable AR/VR environments for remote treatment systems. However, recognizing human motion is quite challenging due to the presence of significant noise and hidden features in the sequential data. RNNs can address these challenges. Song, Y. et al. used BiLSTM with CNN to recognize hand gestures from EMG signals captured by a wrist-worn device [83] (Fig. 3B). This study utilized CNN to compress and extract features from 6-channel EMG signals and

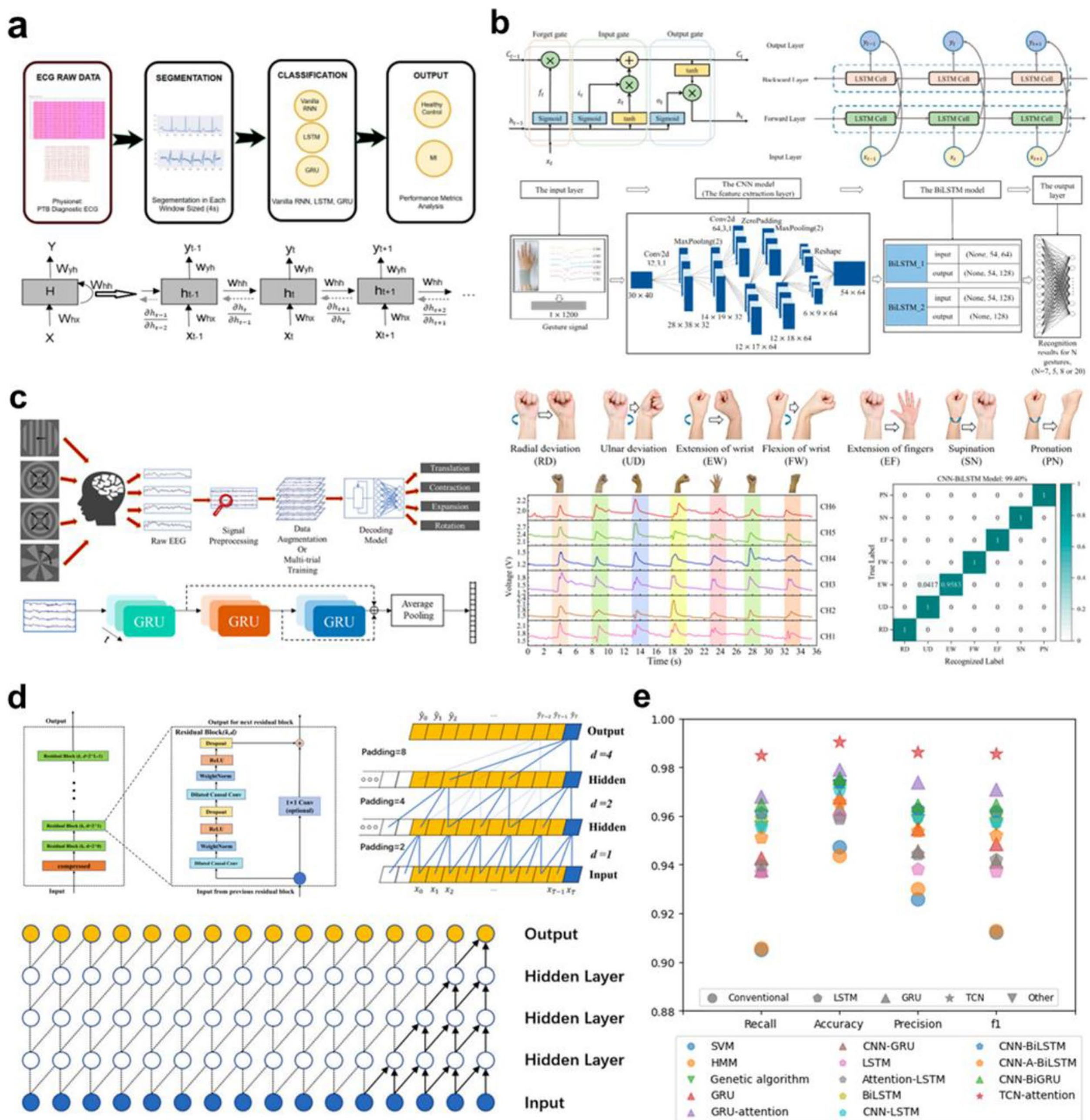

Fig. 3 **A** Summary of ECG rhythm classifier using RNNs and the basic structure of RNN [81], **B** Architecture of LSTM and Bidirectional LSTM for hand gesture recognition with EMG measured at a wearable wrist sensor [83], **C** Decoding visual motions from EEG using GRU [84], **D** Architecture of TCN for EMG compression [85], **E** Performance of various time-series algorithms on human activity recognition tasks with the WISDM dataset [86]

used parallel BiLSTM to train the model with sequential information to recognize 20 gestures. Koch, P. et al. also used CNN-LSTM (or Conv-LSTM) for hand gesture recognition using surface EMG [87]. They also utilized GRU cells to reduce LSTM parameters and computing time, as GRUs use gating units to control sequential information within the unit without requiring separate memory cells. Wei, X. et al. reported human activity recognition based on TCN, and Fig. 3E demonstrates a comparison of the performance with other algorithms (SVM, CNN, GRU, LSTM, etc.) on the WISDM dataset [86]. This study demonstrated that TCNs can compress and extract features without losing time-related information, highlighting their effectiveness in handling sequential data for accurate analysis and classification.

Other applications

There are various other applications of RNNs in biosignal processing. Yang D. et al. demonstrated visual motion recognition by decoding EEG using GRU [84] (Fig. 3C). This study collected 31 channels of EEG while four types of motion (translation, contraction, expansion, rotation) were displayed at 60-s intervals. The developed GRU-based model achieved impressive performance with an average accuracy of 73.72%. Another application involving signal compression and reconstruction with TCN was reported by Zhang, L. et al., and Fig. 3D presents the architecture of a TCN for EMG compression, highlighting its ability to manage and analyze long-term dependencies in biosignals [85]. In summary, the application of RNNs, their advanced variants LSTMs and GRUs, and TCNs in biosignal analysis leverages the strength these networks in processing sequential data. These networks can uncover complex patterns in time-series biosignals, leading to more accurate and reliable diagnostic tools and monitoring systems.

Limitations of RNNs

RNNs, designed with a recursive structure, process data sequentially. This means that to calculate the output at any given time step, all prior steps must be computed first. This inherently sequential nature leads to slow learning speeds, as the model must backpropagate through all previous states to update the weights, a process that becomes increasingly complex as the depth of the network grows [88]. RNN series models have enabled deep learning models to consider the time-series characteristics of data. However, they still face notable limitations. Traditional models, such as CNNs and other machine learning algorithms, while effective for various biosignal tasks, struggle with long sequences and intricate temporal dependencies. RNNs and their variants were developed to address these issues but continue to face challenges with slow learning speeds and the effective capture of long-term dependencies. These models often struggle with encoding long sequences due to their fixed-length representation of input data, which can lead to potential information loss even with bidirectional methods. RNNs also struggle with accurately learning the context of long sequences [66]. As the length of the input data increases, the importance of past data points diminishes, leading to a significant difference in importance between earlier and current data points. This issue is exacerbated by the long-term dependency problem, where gradients can diminish to near zero, making it difficult for the model to learn long-range dependencies. Although methods such as LSTM, GRU, and Bidirectional RNNs have been introduced to mitigate these issues, they do not provide a complete solution. These models attempt to maintain important information over long sequences but still face limitations in fully capturing the context and importance of data points across extended time frames. From the perspective of TCN, it showed better performance compared to RNN, LSTM, and GRU, as illustrated in Fig. 3E. However, TCN also has limitations. It requires the entire raw sequence when performing tasks, which means it needs a significant amount of memory. This requirement can limit the application of TCN in mobile devices, such as portable ECG measurement devices.

Transformer

Traditional models such as CNNs and other machine learning algorithms have been highly effective for various biosignal tasks but face limitations when handling long sequences and capturing intricate temporal dependencies. RNN series models, including LSTM, GRU, BiRNN, and BiLSTM, were developed to address these issues. However, they still suffer from slow learning speeds and difficulty in capturing long-term dependencies effectively [66, 88]. These models often struggle with encoding long sequences due to their fixed-length representation of input data, which can lead to potential information loss even with bidirectional method.

Transformer's solutions

Transformer suggest solutions for the limitations of RNNs. The Transformer model, introduced by Vaswani et al., represents a significant evolution in deep learning, particularly for Large Language Models (LLMs) [89]. The model is built on an attention mechanism that allows it to weigh the importance of different parts of the input data variably. This mechanism enables the Transformer to focus on relevant segments of the input sequence when making predictions, thereby enhancing its efficiency and performance in sequence processing.

Parallel processing

One of the key advantages of the Transformer model over RNNs is its ability to process data in parallel, which significantly reduces learning time [89]. While RNNs process data sequentially, Transformers use attention mechanisms that allow for simultaneous processing of all input data. This parallel processing capability addresses the slow learning speed limitation of RNNs. The technique of positional encoding enables transformers to compress complex data while preserving its sequential characteristics, effectively capturing the order of inputs. Moreover, the self-attention mechanism in transformers calculates the importance of each signal or feature, allowing for the visualization of these importance scores. This provides deeper insights into which features drive the model's predictions or classifications.

Learning context with positional encoding and multi-head attention

With its attention mechanism, the Transformer model introduces an additional layer of sophistication in handling biopotential signals. Unlike RNN-based approaches, the Transformer can manage long-range dependencies in data without the constraints of sequential processing. This capability allows for a more comprehensive analysis of biopotential signals, where the relevance of specific segments can vary significantly across the time series. By focusing on the most informative parts of the signal, the Transformer model can potentially improve the detection and classification of anomalies and conditions in real-time, offering insights that are not readily apparent through traditional methods. From the perspective of 'how the transformer solves the limitations,' the transformer learns data in parallel to decrease the learning time compared to RNN, which learns the data sequentially. Second, they understand the context of input data by using positional encoding and the multi-head attention method. Positional encoding enables the model to understand the sequential information of the input data by adding positional information when calculating attention scores (in other words, encoding). Multi-head attention is like investigating the input data with multiple investigators. For example, when learning ECG signals for the arrhythmia classification model, we can set one investigator to check the LBBB as more important than other symptoms and set other investigators to check the RBBB as more important, and so on. After the investigation, each investigator reports how much the signal has emphasized symptoms more than other symptoms. The model derives the results of arrhythmia classification results by collecting information from investigators. Therefore, the model can be trained by multiple perspectives and get more information compared to other algorithms. Le, M. D. et al. also showed the powerful efficacy of the transformer mechanism (positional encoding and multi-head attention) in detecting arrhythmia in ECG. They used a transformer to re-weight the features by a proper ratio and showed high accuracy and F1 score compared to other simple RNN, 1D-CNN, 2D-CNN, or SVM models [90]. In another study, Islam, M. R. et al. also used a transformer mechanism to detect arrhythmia in single-lead ECG. They used an attention mechanism to stress a more informative segment of ECG and used positional encoding to train the model with the context of sequence in the ECG dataset. The multi-head attention mechanism is also used to enhance the features from ECG (feature map of ECG) by contextualizing the long-range dependencies and enabling parallel processing.

Applications

With these assets, transformers showed powerful performance on biosignals. Transformers offer several advantages when applied to biosignal monitoring and disease detection. Their ability to process data in parallel makes them ideal for real-time applications, enhancing the model's ability to identify anomalies and conditions accurately. ECG researchers recently used a transformer in their study [91–97]. As shown in Fig. 4A, Ji, C. et al. a study developed a transformer block-based model for the ECG classification model [98]. The model showed a 9-class classification task comprising 9 NSR, AF, IAVB, LBBB, RBBB, PAC, PVC, STD, and STE and showed the state-of-the-art CPSC 2018 publicly available ECG dataset. They suggested multi-scale grid attention and self-attention mechanism to extract multi-lead features and multi-scale temporal features, so that the model captured abnormalities in ECG signals efficiently. Compared to other conventional methods, the transformer and attention algorithm enabled extracts the features from different scales at other leads. The multi-head attention mechanism improves the detection and interpretation of complex patterns in biosignals, where large datasets need to be handled efficiently and accurately. The transformer showed great performance on hand gesture recognition based on EMG (including sEMG; surface EMG) [99–102]. In Fig. 4B, Núñez Montoya, B., et al. showed the hand gesture recognition model based on transformer algorithm [100]. They used 6 channel unfiltered EMG signals as input data and performed 4-class classification task. Even though they did not use the conventional filters, which are often used to remove powerline noise and contact noise, the transformer extracted features well and showed successful performance. In other words, transformer is able to extracts features in noisy environments. Song R. et al. also used transformer on analyzing sEMG to silent speech recognition [103]. They developed patch-type sEMG sensors, attached them to the candidates' neck and collected sEMG data while the candidates saying words. Developed transformer model which recognize the words showed better performance compared to LSTM based speech recognition model. They noted that multi-head attention makes the model extract more expressive sequence representation by relating all the frame-pairs so that it can draw the dependencies between different frames. Compared to transformer, LSTM trains the sEMG data in order and in compressing the information loss, leading to poor performance. Transformer is applied well on EEG research for example, emotion recognition, person identification, brain activity classification, epilepsy

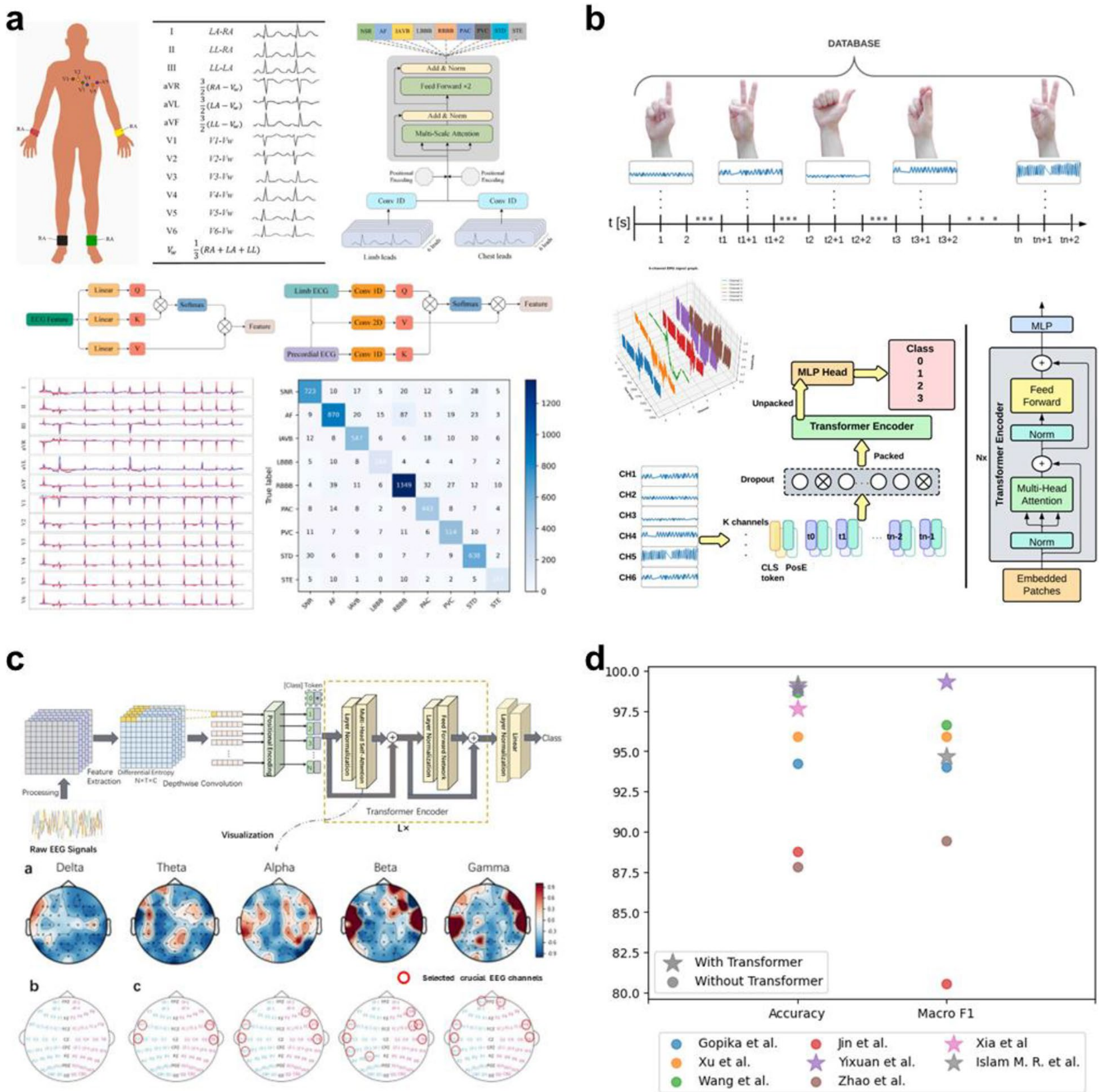

Fig. 4 **A** transformer-based 12-lead ECG arrhythmia detection model; multi-scale grid transformer network [98], **B** hand gesture classification using a transformer algorithm for an anthropomorphic robotic hand [100], **C** EEG-based emotion recognition and visualizing crucial EEG channels using transformer-based neural network [109], **D** accuracy of arrhythmia classification with 5 classes with or without using a transformer [97, 113–119]

detection [104–108]. Not only transformer can solve the limitations mentioned above, but also has other assets comes from using attention algorithm. When training or performing the task, the model calculates attention scores that means what feature, or which part of the signal has the importance of the produced results. In other words, attention-based algorithms not only perform task effectively, but also enhance model explainability. Studies on biosignals have demonstrated the explainability of their models using transformers or attention mechanisms [96, 108–112]. Figure 4C showed that Guo, J. Y. et al. reported emotion recognition model based on transformer algorithm [109]. They not just reported the powerful performance of transformer algorithm, also showed visualization of crucial EEG channels for emotion recognition model. Most emotion recognition models reported their advanced architecture and performance; however, they are treated as black-box model that learning processes are difficult to interpret. In this study they showed the importance of each input data using multi-head attention mechanism while recognizing emotions and based on the importance, they visualized on EEG channel maps. Transformers can be used with other algorithms CNN, ML algorithms, other unsupervised algorithms and their combinations showed good performance. Figure 4D showed the powerful performance of transformer on the DEAP dataset [97]. In the figure, the model with transformer showed high performance compared to the model without using transformer [113–119]. Because of the characteristics of transformer (multi head attention mechanism, positional encoding, scale encoding), the algorithm can extract important information from intricate signals and also have faster learning in the same time.

Unsupervised learnings

Overview

Unsupervised learning is one of main anatomy of machine learning. It trains system with unlabeled data, in other words, it trains data itself. It has various algorithms that are commonly used to extract features (or dimensionality reduction), clustering. Traditional unsupervised methods like Principal Component Analysis (PCA) extract features or reduce the dimension from complicate biosignals. Not like supervised learning, unsupervised learning showed efficacy on extracting features in noisy signal data without using preprocessing, whereas supervised learning commonly used conventional signal processing methods like Butterworth, wavelet transform, etc. before analyzing it. For instance, they can extract generalized features from intricate and noised EEG signals for identifying the emotion of subjects or classifying emotions, reduce the multi-lead ECG signals for anomalies of ECG and extract common and generalized feature from EMG for human activity recognition. Other algorithms like K-means, Density-Based Clustering of Applications with Noise (DBSCAN) are the representative of clustering algorithms on the dataset without any corresponding target values. For example, they can be used to cluster the arrhythmia patient by their symptoms they have based on ECG signals, cluster EEG signals to detect epileptic seizure. These cases showed the demonstration of efficacy in extracting core feature from complex biosignals resulting in generalized outcome, not case-dependent one, and suggestion for next concept of complex algorithms like Auto Encoders (AEs). PCA has been used in biosignal application for its ability to feature extraction from high-dimension space via dimensionality reduction. Their main goal of PCA in the field of biosignal is to convert complex signals into simplified and useful data for the training model. Gupta, V. et al. used PCA to analyze noisy and different morphologies of ECG signals [120]. PCA extracted optimal features on noisy ECG, and they developed algorithms to detect R-peaks. K-means algorithm is clustering the dataset with the k-number of clusters. It calculates the distance between each data point and center points and set the point that minimize mean of the distance. K-means algorithm plays a convenient and simple tools for analyzing biosignal as only thing to use this algorithm is set the number of k [121–123]. Elgendi, M. et al. used this clustering method to find the relationship between biosignals (ECG, EMG, etc.) with driving stress [124]. The study showed that the ECG consistently correlated with the stress marker noting that ECG is the important biosignal for assessment of driving stress. Not only k-means, t-SNE (t-distributed Stochastic Neighbor Embedding) and UMAP (Uniform Manifold Approximation and Projection) also are reported for their usage on clustering biosignals at high-dimensional space [125–127]. Sikder, N. et al. analyzed human activity recognition samples with t-SNE to find trend on clustered dataset before develop the recognition model [128]. Xia X. et al. also used t-SNE for analyzing taste related EEG features extracted by the model and the results showed that the features clustered by the tastes [129]. Not only their results are just for seeing their clustering results, also can be used to train the system as feature [130, 131]. For example, UMAP can be used for dimensionality reduction while preserving the local and global structures of original dataset [132]. Leal, A. et al. used this ability of UMAP to reduce dimensions of seizure dataset including EEG signals and successfully identified preictal patterns of patients. Unsupervised learning can overcome the limitations of research on biosignals, for example, lack of labeled dataset, high cost for data label in medical environments. In addition, since they train the system without corresponding label, they can show more generalized results compared to supervised learning methods on same task (classification, forecasting, etc.) [133]. Furthermore, as the computing power increases and various type of large-scale dataset stacks, research on more generalized foundation model for biosignals like Chat GPT on the field of Large-scale Language Model (LLM) is noticed and unsupervised learning can be the solution for how to train the model since well-developed foundation model enables zero-shot learning which perform tasks successfully on unseen or untrained cases [134, 135]. This suggests that even under different biosignal monitoring setup like wearable sensor, hospital-level monitoring or at home IoT monitoring system, we can efficiently develop AI model fits each environment via fine tuning or using foundation model itself.

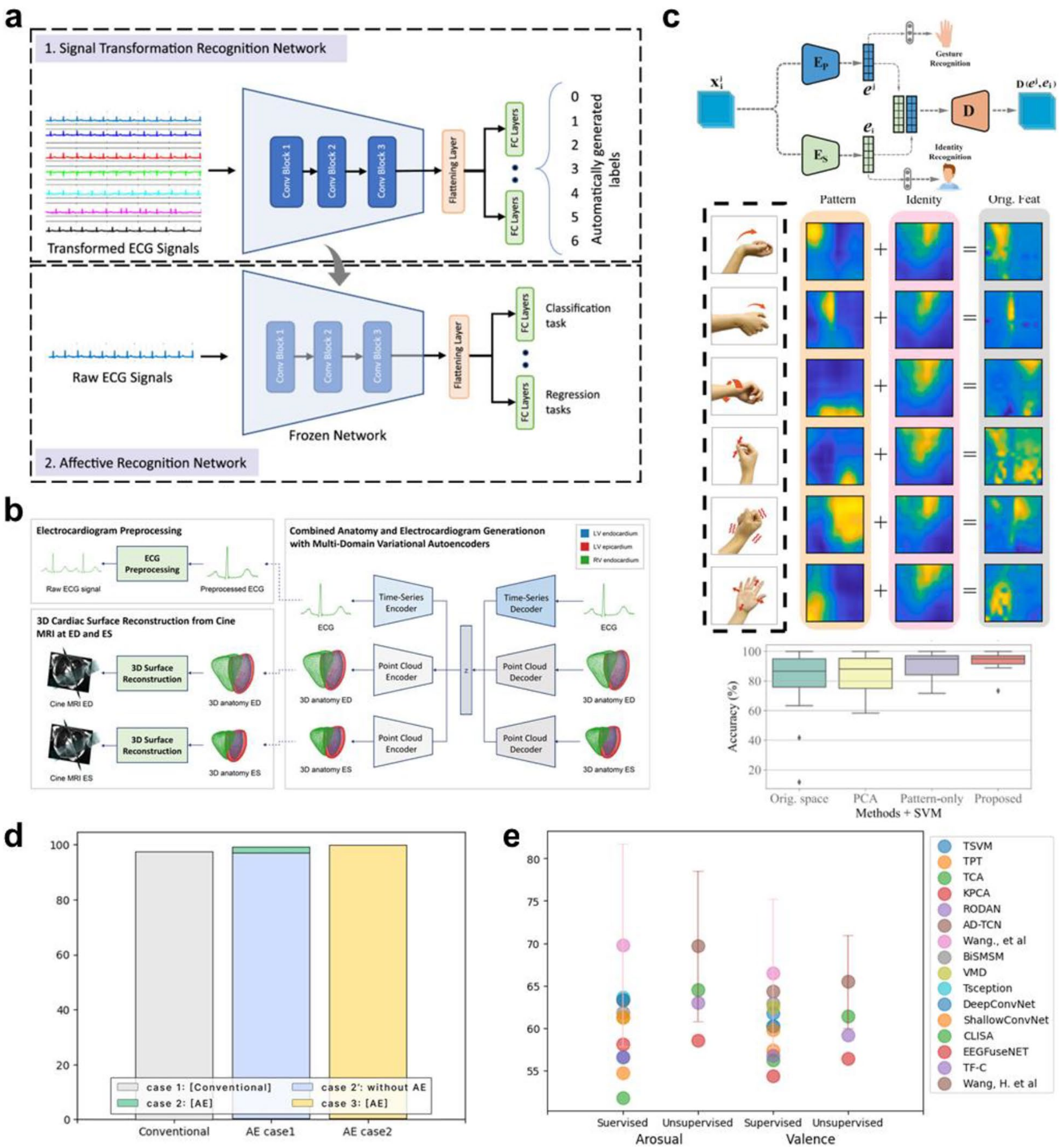

Fig. 5 **A** Self-supervised representation learning for detection of maternal and fetal stress from the maternal abdominal ECG [148], **B** multi-domain variational autoencoder for biventricular anatomy and ECG representation [146], **C** robust EMG pattern recognition with self-supervised learning [147], **D** ECG-based heartbeat classification performance compared with the conventional method, with or without using autoencoder [149], **E** Performance of emotion classification on DEAP dataset using supervised or unsupervised learning on two states (arousal and valence) [150]

Self-supervised learning on biosignals

Self-supervised learning is basic concept of unsupervised learning that learns meaningful features from unlabeled data. Figure 5A showed usage of self-supervised learning on detection of maternal and fetal stress from abdominal ECG. They trained the model with representative features showing generalized results and good performance. Another example showed that Eom S. et al. used self-supervised algorithms with 6 biometric signals as pre-training model which can increase the popularity via using ignored unlabeled data [136]. They reported their self-supervised method showed better performance compared to traditional machine learning methods, SVM and CNN. Fourmani, N. M. et al. also reported self-supervised metric on EEG pretraining [137]. Since pretrained self-supervised metric needs low prior knowledge and ease to get generalization, the reported metric showed better performance on 5 public dataset (DREAMER [138], Crowdsourced [139], STEW [140], TUAB [141], TUEV [142]) and 1 private dataset compared to each state-of-the-art models. Auto Encoder (AE) is representative algorithm of self-supervised learning. AE trains itself by comparing re-constructed another me, original dataset. AE has simple structure, encoder, and decoder. The encoder compresses the high-dimensional input data to low-dimensional data (or vector), and the decoder reconstructs the input data from compressed low-dimensional data. It trains with reconstruction error that showed the model knows the features represent input data. In other words, AE can extract features that represent dataset itself without any supervised method. For this ability, AE develop generalized result avoiding data-dependency which most of any other algorithm usually has and this works on biosignals as well [143–145]. Figure 5B showed the example of using AE on the ECG signals and cardiac 3D-images. Beetz, M. et al. and this showed powerful feature extraction ability of AE [146]. They successfully showed the results of reconstruction of 3D cardiac image and ECG signals via AE. Another example in Fig. 5C shows that suggested robust hand gesture recognition model via feature disentanglement. Fan, J. et al. used only an encoder to extract the pattern-specific and subject-specific components [147].

Optimized treatment for biosignals

The model trains without any supervised method when extracting features resulting in development of generalized hand gesture recognition and task-independent biometric identifier. Not only expecting generalized results from the AE model, but AE is also expected for denoising biosignals [151]. In many studies so far, researchers use conventional filters like Butterworth high, low, band-pass filter to see what they want to see or highlight particular frequency-range of signals. We know there is irreplaceable part of conventional signal processing, however, AE enables denoise on biosignals [152]. Nurmaini, S. et al. showed the denoising the ECG signals with Denoising Auto Encoder (DAE) and also used AE for feature extraction [149]. They remove the noise from ECG with DAE as DAE trains the features that represent the signal, so that AE can reconstruct the denoised signals. Therefore, as shown in Fig. 5D, they showed that ECG-based heartbeat classification model using AE showed better performance compared to the model without AE. Wang, H. et al. reported emotion recognition based on EEG [150]. This study used self-supervised representation learning and compared performance of their model with other research on DEAP dataset as shown in Fig. 5E. Supervised learning showed slightly better performance on average accuracy on each state of emotion (arousal and valence), however, self-supervised learning (unsupervised learning) showed smaller standard deviations compared to supervised learning methods. This showed that unsupervised learning can show more generalized, not-subject-dependent results, on the other hand, supervised learning can produce better performance on personalized model.

Other advanced models and applications

Transfer learning is algorithm that develops the model with pre-trained model. As pre-trained model shared its pre-trained knowledge between related tasks, transfer learning can train the system with small resources like power source, calculation time etc. Transfer learning showed their efficacy and high performance in the field of biosignals [118, 126, 153–155]. Weimann, K. et al. used transfer learning for arrhythmia classification model. They noted the limitations about difficulties to collect a large number of labeled ECG recordings to train the model and transfer learning with the pre-trained developed with public dataset was suggested to solve the limitations. This showed the pretraining improves the target task by up to 6.57% reducing the number of the labeled dataset need for transfer learning. However, transfer learning needs well-tuned, big(deep) structured pre-trained model to make the model have powerful performance. For example, in the perspective of image classification, ResNet50 is used for various image classification model showing good performance so far. In the field of ECG classification, Murugesan, B. et al. showed the deep structured arrhythmia classification model using convolutional long-short term memory and their structure have been used for other deep structured model [156]. This suggested that deep structured model also is validated on biosignal field, not only image classification field. Moreover, unsupervised learning method can help large scale model have more generalized representative features from biosignals. Biosignal data varies by subject and its measuring environments, even if they have same symptoms. However, unsupervised learning can propose the solution for the variability characteristics of biosignal dataset. Not like supervised learning, unsupervised learning learns from dataset itself, so that they train

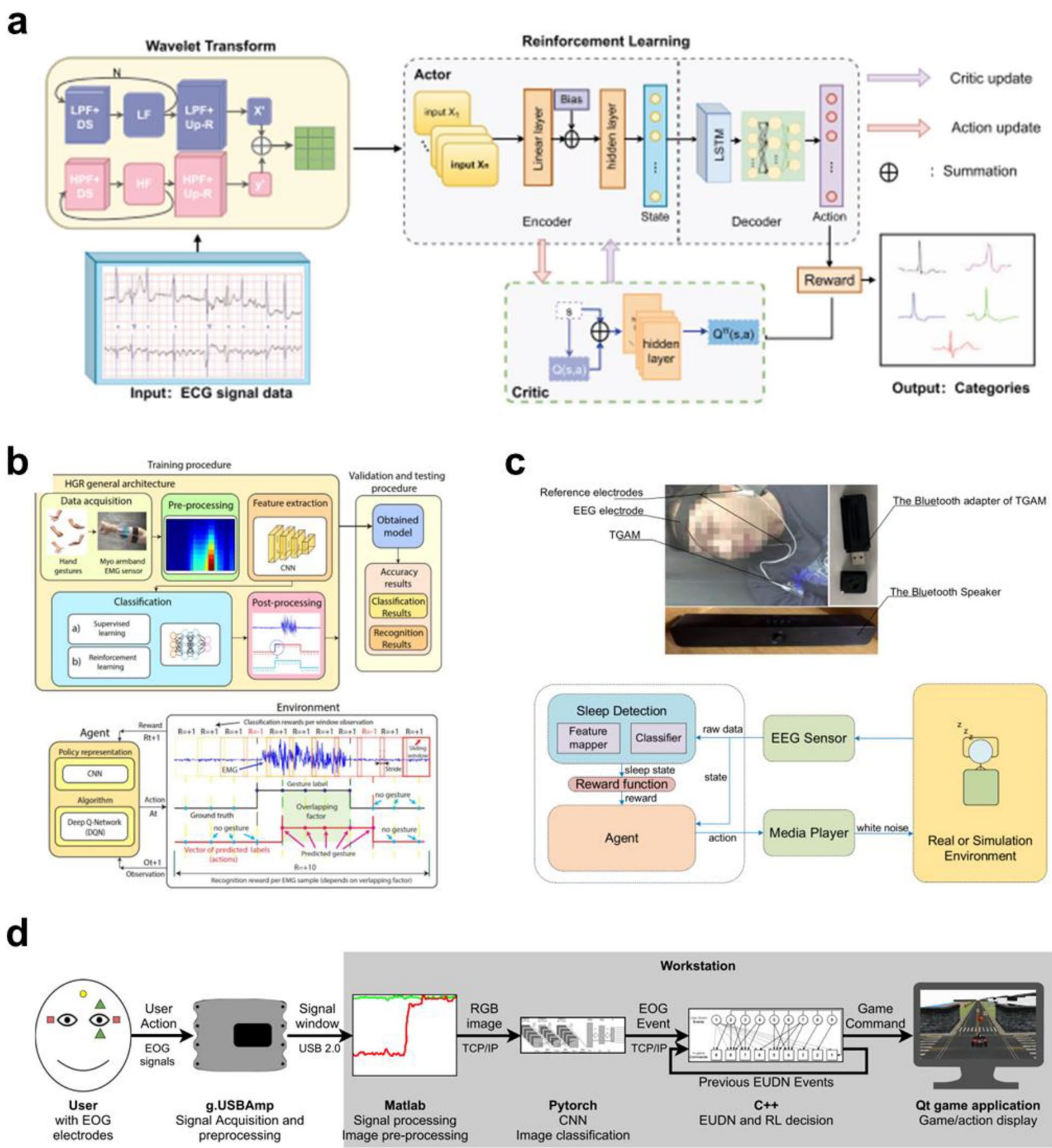

Fig. 6 **A** ECG classification using Actor-Critic based reinforcement learning [165], **B** EMG-based hand gesture recognition system and its architecture of reinforcement learning [166], **C** Sleep improvement control using simple reinforcement learning [167], **D** Eye-driven computer games with EOG signals assisted with reinforcement learning [168]

more generalized representative features from it. In addition, masked modeling, which block random or designed part of the input data to make the system learns generalized features, is also used to have more generalized representative features [136, 137, 146, 150, 157]. Unsupervised learning may be the key for the generalized foundation model for biomedical field like Chat GPT for language processing field.

Reinforcement learning

Overview

Reinforcement Learning (RL) is a branch of artificial intelligence in which an agent learns to make decisions by taking specific actions within an environment to maximize a cumulative reward [158]. Unlike supervised learning, which depends on labeled data, RL uses a trial-and-error approach to discover the most effective strategies, making it particularly well-suited for dynamic and complex tasks such as biosignal processing [159]. RL has gained significant attention for its potential to optimize and enhance various aspects of biosignal analysis and medical diagnostics. This adaptability is demonstrated in arrhythmia classification (Fig. 6A) and hand gesture recognition using EMG signals, where RL agents iteratively refine their strategies based on feedback [160–163]. Key advantages include RL's ability to adjust to data changes, optimize models through continuous learning, and handle complex tasks involving sequential decision-making, making it invaluable for real-time biosignal analysis and improving healthcare outcomes. Reinforcement learning offers several key advantages in biosignal processing. One of the primary strengths of RL is its adaptability. RL can dynamically adjust to changes in the data and environment, making it ideal for real-time biosignal analysis where conditions can vary. This adaptability ensures that RL models remain effective even when new or unexpected patterns emerge in the biosignal data. Additionally, RL agents continuously improve their performance through feedback. By iteratively learning from the outcomes of their actions, RL agents optimize their strategies, leading to models that can deliver more accurate and reliable predictions. Another significant advantage of reinforcement learning is its capacity for autonomous learning. RL reduces the need for extensive labeled datasets, as the agent learns from interactions with the environment rather than relying solely on pre-labeled data. This characteristic is particularly beneficial in biosignal processing, where acquiring labeled data can be challenging and time-consuming [164]. Furthermore, RL excels in handling complex tasks that involve sequential decision-making and long-term dependencies. These tasks are common in biosignal processing, where understanding the temporal relationships and patterns within the data is crucial for accurate analysis and diagnosis.

Advanced model of RLs

Q-learning is an off-policy method (or model-free reinforcement learning) commonly used in biosignal processing. Q-learning can find optimized policy under a finite Markov decision process. Using simple Q-learning, Fatima, R. et al. classified the ECG without explicit instructions or predefined rules [169]. However, finding Q-value needs a lot of computing power and time if the model is not simple. Dealing with biosignals usually requires complex and deep networks. To solve this problem, Deep Q-Network (DQN) or Double Deep Q-Network (DDQN) is used in biosignal processing. DQN is the algorithm that combines Q-learning and DL to find optimized Q-values using deep neural networks. DDQN is an improved version of DQN that uses two separate networks (replay memory, target network) for Q-value estimation and action determination, expecting more stable and accurate results. Ming, Y. et al. used DQN to estimate drowsiness and drive safety with EEG [170]. The DQN model showed more generalized results than the LSTM model, and it showed great performance. Li, D. et al. also used DDQN for emotion recognition with EEG while showing how the brain works in reward learning during the generation and processing emotion [171]. The DDQN model also showed more generalized performance than the DL models. Another algorithm, A2C, is also used in biosignal processing. A2C combines actor and critic methods in which the actor decides actions to take, and the critic evaluates the actions. As they update their policy and value function simultaneously, the model trains more stable and faster way and expecting. Zhu, M. et al. used A2C for arrhythmia detection from ECG (Fig. 6A) [165]. The classification model showed an interaction between the actor and critic network for the efficient processing of temporal information of ECG signals and capturing temporal correlations, showing superior performance compared to traditional ML/DL methods.

Applications on biosignals

RL has been effectively used to enhance the performance of hand gesture recognition models using EMG signals, demonstrating its utility in human–computer interaction and assistive technologies (Fig. 6B). Figure 6B demonstrates the use of RL in optimizing deep learning models for hand gesture recognition using EMG signals [166]. The training procedure involves data acquisition, pre-processing, feature extraction, and classification. The RL agent iteratively refines its policy based on feedback from the environment, improving the model's accuracy in recognizing hand gestures. This approach illustrates the flexibility and adaptability of RL in handling various biosignal types and improving model performance through continuous learning. RL is also used for human machine interfaces in biosignal processing that control various disease symptoms by controlling treatment devices. Che, N. et al. showed the use of DQN for sleep improvement framework for insomnia treatment with EEG collected hairband type wearable device (Fig. 6C) [167]. The DQN model controls the white noise lite to make the patient sleep and reduces the average time to sleep by 131.4 s. Santelices, I. B. et al. showed another example of RL, which controls intermittent pneumatic compression by applying external compression on lower limbs to enhance blood flow [172]. RL uses ECG, heart rate, and blood velocity as input and determines the compression timing of the device by the users, which means RL can make adaptive decisions. In other examples using biosignals but not for control treatment, Perdiz, J. et al. reported the use of RL on eye-driven computer games (Fig. 6D) [168]. Figure 6D depicts the frameworks of RL-based control to computer games with EOG.

Optimized treatment with RLs

RL shows strength in decision-making problems and RL can contribute to complex decision-making problems in healthcare system, medical or clinical treatment regime that needs sequence of decisions to determine [173–175]. Recent RL not only make a decision, also provides optimized treatment to the patients. Wu X. et al. used value-based DDQN for optimal treatment of sepsis [176]. The model is trained with adaptive dynamic weights Q value function, which enables improvement for accurate decision-making and the developed model showed 95.83% of survival rate on MIMIC-III dataset. Job, S. et al. also used DDQN for optimal treatment for critical patients [177]. They used LSTM-GRU for deriving representations from the patients and used DDQN to determine optimal treatment strategies and showing great performance. Other optimized treatments on diabetes control and antiretroviral therapy in HIV are supported by RL.

Others

Not just developing AI-powered model using biosignals, but by using RL to optimize deep learning models, researchers have achieved significant improvements in the accuracy and robustness of arrhythmia classification systems. Ismael, H. et al. showed the use of RL for optimizing hyper-parameters of arrhythmia DL model [178]. The process begins with signal acquisition and processing, where raw biosignals like ECG are collected and pre-processed. The RL agent then interacts with the environment, receiving rewards based on the accuracy of its predictions and updating its policy to improve performance. This iterative learning process continues until the agent optimizes its strategy for arrhythmia classification. By effectively managing these complexities, RL enhances the overall capability of biosignal processing systems. Bostani, A. et al. also used RL on ECG classification model however, RL is used to regulate the learning process [179]. An interesting finding in use of RL on biosignals is that RL can be used for robustness and explainability for signals. Sarkar, S. et al. reported RL frameworks that focuses on identifying sensitive regions while inducing misclassification with minimal distortion and variants of the distortions [180]. The RL agent is trained to add distortion to the most sensitive region of the data which shows high possibility that leads to misclassification with minimum number of steps. In other words, the accurate localization of the sensitive region of the signal is treated as critical region, explainable region. Overall, reinforcement learning represents a powerful approach for advancing biosignal processing and medical diagnostics. Its ability to adapt, optimize, and autonomously learn from interactions with the environment makes it an invaluable tool in the quest for more accurate and efficient healthcare solutions. As research in this field continues to evolve, RL is poised to play a critical role in the development of next-generation medical technologies and intelligent diagnostic systems.

Discussion

Each AI methodology—supervised learning, unsupervised learning, and reinforcement learning—makes significant contributions to the analysis of biomedical signals. Supervised learning demonstrates high accuracy when a clear relationship exists between inputs and expected outputs. In other words, with a well-labeled, high-quality dataset, it is possible to achieve strong performance across a variety of tasks. Table 3 presents examples of how supervised learning is applied to biomedical signals and describes the corresponding performance outcomes. It can be observed that all tasks involve expected outputs. For instance, CNNs compress complex biomedical signals with minimal information loss, achieving high performance in tasks such as ECG personal recognition, seizure detection in EEG, and hand gesture recognition using EMG. Moreover, due to CNNs' efficient signal compression capabilities, they are often combined with models such as LSTM, GRU, and Transformers, leading to further improvements in biomedical signal processing. For example, in the arrhythmia detection task using the MIT-BIH dataset, the integration of CNNs with Transformers yields superior performance compared to the use of Transformers alone. RNNs and their variants, such as LSTM and GRU, along with Transformers, have the capability to learn sequential features from datasets, which is essential for tasks like human activity recognition in complex EEG signals, decoding silent speech from EMG, and interpreting imagined speech from EEG. In contrast, unsupervised learning learns directly from the data itself, enabling the model to capture a wide range of information from the dataset. This approach is advantageous because it can extract latent features that may not be immediately apparent, capturing the data's most generalizable and representative aspects. This characteristic is particularly beneficial when dealing with complex and noisy biomedical signals. Table 4 provides examples of how unsupervised learning is applied to biomedical signals and outlines the associated results. For instance, PCA allows for the safe extraction of features from complex EMG signals, which can then be utilized in tasks such as speech recognition or hand gesture recognition through supervised learning methods. Autoencoders (AE), on the other hand, compress the dataset and use the latent space information as features for supervised learning tasks

Table 3 Summary of supervised learning on biomedical signals

Architecture	Target signal	Target task	Dataset	Performance	Reference	Year
CNN + Genetic programming	ECG	ECG personal recognition	PTB [181], CYBHi [182]	99% 81%	[183]	2021
CNN	EEG	Seizure detection and classification	Bonn [184]	98.22% (3 class)	[185]	2021
CNN	EMG	Hand gesture recognition	Original	99.75% (12 class) (Average accuracy)	[186]	2023
CNN + LSTM	EEG	Human activity recognition	UCI-HAR [187], DSA [188]	95.66% ± 0.63 (6 class) 92.95 ± 0.47 (19 class) (Average accuracy)	[189]	2023
CNN + GRU	EEG	Human activity recognition	UCI-HAR [187], WISDM [190], PAMAP2 [191]	96.20% (6 class), 97.21% (6 class), 95.27% (12 class) (Average accuracy)	[192]	2021
Transformer	ECG	ECG heartbeat classification for arrhythmia	MIT-BIH [193], PTB [181]	98% (5 class) (Average accuracy)	[95]	2024
CNN + CRM + BiTransformer[a]	ECG	ECG heartbeat classification for arrhythmia	MIT-BIH [193]	99.35% ± 0.16 (5 class) (Average accuracy)	[94]	2024
Transformer	EMG	Estimating finger joint angles by sEMG[b]	Original	0.970 (R^2) 21.104° (RMSE[c])	[99]	2024
Transformer	EMG	Decoding silent speech from sEMG[b]	Original	92.39% ± 4.17% (Average accuracy)	[103]	2023
Transformer	EEG	Multi-tasking workload classification	STEW [140]	95.32% (2 class) 89.01% (3 class) (Average accuracy)	[194]	2024
CNN + Transformer	EEG	Decoding imagined speech in EEG	Original	45.9% (13 class) (Average accuracy)	[106]	2022

[a]Bidirectional Transformer

[b]Surface EMG

[c]Root Mean Square Error

or detect anomalies through the reconstruction error of the AE. Since the latent space contains generalized feature information, AEs perform well across diverse patients. Furthermore, transfer and contrastive learning demonstrate strong and generalized performance in biomedical signal analysis. Unlike supervised and unsupervised learning, reinforcement learning learns through a trial-and-error process. As it learns by discovering the appropriate actions and optimal policies, reinforcement learning is not restricted to a specific dataset but can adapt to various environments, offering the potential for more generalized outcomes. This adaptability allows reinforcement learning to be effective even in scenarios where data is scarce or unavailable. Additionally, reinforcement learning is particularly advantageous for decision-making problems. Table 5 illustrates various applications of reinforcement learning in biomedical signal processing. For example, through Q-learning, it is possible to learn the optimal policy and perform tasks such as ECG classification for arrhythmia in conjunction with supervised and unsupervised learning methods. By applying various deep learning techniques to DQN for Q-value calculation, reinforcement learning also shows strong performance in tasks such as estimating driver drowsiness from EEG, distinguishing EEG patterns in epilepsy patients, and recognizing emotions through EEG. The ability to adapt to different environments allows reinforcement learning to perform well

Table 4 Summary of unsupervised learning on biomedical signals

Architecture	Target signal	Target task	Dataset	Performance	Reference	Year
PCA KNN	EMG	Speech recognition	Private	88.8% (3 class) 74.6% (5 class) (Average accuracy)	[195]	2021
PCA LDA RF	sEMG	Hand gesture recognition with domain adaptation	Private	75.55% (average accuracy)	[196]	2022
CAE	ECG	Heartbeat classification	MIT-BIH [193]	99.99% (5 class) (Average accuracy)	[197]	2024
VAE	EEG	Seizure identification	Upenn [198] (kaggle), TUH [199], MIT [200]	83% (accuracy)	[201]	2022
VAE + CNN	Human activity data	Abnormal emotion detection	DREAMER [138], DRIVEDEB [202], MAHNOB-HCI [203], WESAD [204], Private	0.546 (F1-score) 0.612 (F1-score) 0.726 (F1-score) 0.789 (F1-score) 85% (Accuracy)	[205]	2023
RCVAE[a]	EEG	Epileptic seizures prediction with EEG	CHB-MIT [8]	96.17% (Accuracy)	[206]	2022
LSTM AE	ECG	Anomalous ECG detection	ECG5000 [207, 208]	98% (Accuracy)	[209]	2023
Transformer + AE	ECG	Inter-patient ECG arrhythmia classification	MIT-BIH, INCENTIA 11 K [210]	97.93% (Average accuracy)	[211]	2023
CNN + CORAL[a] + Transfer learning	sEMG	Hand gesture recognition with domain adaptation	Original	90% (10 class) (Average accuracy)	[126]	2024
Contrastive learning	ECG	Arrhythmia classification	PTB-XL [212] (Used for pre-train), ICBEB2018 [213], PhysioNet2017 [214]	79.33% (5 class) 83.7% (5-class) (AUC[f])	[215]	2024

[a]Convolutional Auto Encoder: CAE in Architecture column

[b]Long Short-Term Memory Auto Encoder: LSTM AE in Architecture column

[c]Variational Auto Encoder: VAE in Architecture column

[d]Residual Convolutional Variational Auto Encoder: RCVAE in Architecture column

[e]CORrelation Alignment: CORAL at CNN+CORAL+Transfer learning in Architecture column

[f]macro-averaged area under the receiver operationing characterstic curve

in tasks such as implementing an adaptive Kalman filter or in adaptive brain control tasks. Finally, reinforcement learning demonstrates high performance in tasks such as treatment response classification for depression patients and determining optimal treatment strategies to prevent or accurately treat sepsis in critically ill patients, thanks to its powerful decision-making capabilities. Although all three methodologies exhibit strong performance in biomedical signal processing, they all require high-quality datasets. In supervised learning, accurate data labeling is needed to achieve optimal results. In unsupervised learning, well-refined data is necessary to extract accurate features. Even reinforcement learning, which is often cited as requiring minimal or no data, still necessitates high-quality datasets for decision-making problems. For example, when determining optimal treatment strategies for ICU patients, various data types, including treatment records, medication records, age, gender, weight, and other biomedical signals, are typically used together. The diverse nature and often inconsistent recording of these data types can present significant challenges in determining the most accurate optimal treatment. Even within the same biomedical signal processing task, there are differences between each methodology. For example, as shown in Tables 3, 4, and 5, all three methodologies perform well in arrhythmia classification, yet methods based on CNNs demonstrate slightly superior performance. While supervised

Table 5 Summary of reinforcement learning on biomedical signals

Architecture	Target signal	Target task	Dataset	Performance	Reference	Year
Q-learning	ECG	ECG classification	SNOMED [216]	0.904 (Average accuracy)	[169]	2024
GraphRL	ECG, PPG	Heart rate prediction	WESAD [204]	0.56 (GraphRL) 0.95 (GRU) 1.02 (GRU-based RL) (Mean Absolute Error)	[217]	2024
WTDRL (Actor-Critic)	ECG	Arrhythmia classification	MIT-BIH [193]	99.01% (Average accuracy)	[165]	2023
RL	EEG	Adaptive Brain Control	Private	0.0151 (Mean Square Error)	[218]	2021
RL	EEG	Classifying treatment response in depression	Private	95.28% (Average accuracy)	[219]	2024
Deep Q-learning	EEG	Drowsiness estimation of Driver	Private	1.16 (RMSE on response time of driver)	[170]	2021
DDQN	EEG	Emotion recognition	DEAP [220], DREAMER [138]	[Valence / Arousal] 98.35% / 98.17% 92.60% / 92.30% (Average accuracy)	[171]	2023
AFM-DQN	EEG	Focal/non-focal EEG classification	BB[a] [221], Bonn [184]	95.87% 97.5% (Average accuracy)	[222]	2023
A2C	EMG	Wrist Motion Prediction	Private	92% (Average accuracy)	[163]	2020
WD3QNE	Critical care data (Vital signs, ECG, etc.)	Optimal treatment of sepsis	MIMIC-III [223]	95.83% (Survival rate)	[176]	2023
DRL	ICU data (ECG, Respiration, etc.)	Optimal treatment for critical patients	MIMIC-III [223]	0.0558 (MAE)	[177]	2024

[a] Bern-Barcelona EEG database

learning can be expected to deliver high performance within a given dataset, it may struggle to maintain this performance with unseen data. On the other hand, unsupervised learning may yield more generalized features, thereby offering reasonable performance with unseen data. Due to its ability to adapt to different environments, reinforcement learning can also be expected to perform reasonably well with unseen data. However, reinforcement learning may require substantial computational time and resources to derive an adaptive optimal policy for each environment.

Conclusion and perspective

The integration of AI into biomedical signal analysis represents a groundbreaking advancement in healthcare. AI technologies, ranging from traditional machine learning algorithms to sophisticated deep learning models, have demonstrated remarkable efficacy in processing complex data. These advancements have enabled more accurate diagnosis, faster data analysis, and personalized treatment recommendations. Implementing supervised learning techniques has laid a robust foundation for AI-driven biosignal analysis [5, 7]. These methods have proven their capability to handle high-dimensional data, identify subtle patterns, and deliver high accuracy in classification tasks. Table 1 provides a comprehensive overview of these AI methodologies, showcasing the advantages, applications, and commonly used algorithms in supervised, unsupervised, and reinforcement learning. Furthermore, adopting CNNs and RNNs has enhanced the ability to interpret complex temporal and spatial data. The emergence of transformer models and self-supervised learning algorithms has further expanded the horizons of AI in biosignal processing [224–226]. Transformers, with their attention mechanisms, have shown superior performance in managing long-range dependencies, offering deeper insights into biosignal data. Self-supervised learning approaches, particularly autoencoders, have demonstrated their potential in extracting meaningful features from unlabeled data, thus reducing the dependency on extensive labeled datasets. Table 2 further elaborates on the characteristics, applications, and relationships between these learning methods, highlighting their specific roles in enhancing the analysis of complex biosignal data. Unsupervised learning methods have shown significant promise in biosignal analysis [120, 122, 125]. These methods can extract features and detect patterns from complex and noisy data without requiring labeled examples, making them particularly valuable in scenarios where annotated datasets are scarce or costly. By identifying intrinsic structures within the data, unsupervised learning can enhance the understanding and interpretation of biosignals, leading to more robust diagnostic models [227]. Reinforcement learning offers another innovative approach suited for dynamic and complex tasks. Applications of RL in biosignal analysis include optimizing deep learning models for tasks like arrhythmia classification and hand gesture recognition. Table 1 also highlights the adaptability and potential of reinforcement learning in dynamic biosignal processing tasks, showcasing how it can address challenges where data variability is a significant factor. Recent advances in computing, such as neuromorphic computing and quantum computing, have the potential to further enhance AI capabilities in biosignal analysis [228, 229]. Neuromorphic computing, which mimics the human brain's neural structure, offers significant improvements in processing speed and energy efficiency for AI tasks. Quantum computing can revolutionize the analysis and interpretation of vast amounts of biosignal data [230]. Systemic improvements in healthcare infrastructure are also changing the adoption of AI in biosignal analysis [231]. Advances in wearable technology, IoT devices, and cloud computing have enabled continuous monitoring and real-time data processing, providing access to AI-driven insights anytime, anywhere [232]. These developments are accelerating the integration of AI into healthcare systems, enhancing the speed and accuracy of diagnostics, and expanding the reach of AI applications in diverse medical environments [233].

Looking forward, the future of AI in biomedical signal analysis is promising, with several key trends and opportunities: 1) The integration with wearable sensors and devices offers in-depth data-centric healthcare by continuous biosignals. Integrating AI with these technologies will enable real-time monitoring and early detection of health conditions, facilitating proactive healthcare management and services. 2) AI's ability to analyze individual-specific biosignals will drive the development of personalized treatment plans. This personalized approach will enhance the efficacy of treatments and improve patient outcomes by aligning interventions based on individual physiological patterns. 3) The continuous evolution of AI algorithms will lead to more ever-growing diagnostic tools that can accurately predict and diagnose various medical conditions. This will be particularly beneficial in areas with limited access to specialized medical expertise. 4) The synergy between AI and biomedical engineering will broaden interdisciplinary collaborations, solving more complex biomarker and medical challenges. Collaborative efforts will drive advancements in AI algorithms, sensor technology, and biosignal interpretation techniques. Despite significant progress, challenges remain in advancing biosignal analysis with AI. Obtaining high-quality, annotated biosignal data is difficult due to privacy concerns, data variability, and manual annotation requirements. AI models, especially deep learning algorithms, often act as black boxes, necessitating enhanced interpretability and transparency to build medical professionals' trust and ensure ethically responsible use [234]. Navigating regulatory and ethical consideration is also essential for AI integration, including compliance with regulations, patient privacy protection, and addressing ethical AI decision-making concerns. Developing AI models that generalize across diverse patient populations and clinical settings is challenging, requiring scalable and contextually applicable solutions for effective real-world implementation [235]. AI holds great promise in the biomedical field, going beyond mere analysis to understanding and predicting patient intentions and health outcomes. However, the lack of predictive solutions and interface limitations hinder the current state of AI in healthcare, and after addressing these challenges, future trends are expected to shift towards [236]. In conclusion, AI has enormous potential to advance medical diagnostics and patient care through biosignal analysis. Addressing these challenges and leveraging technologies will enable AI to revolutionize biosignal processing, improving healthcare outcomes and quality of life.

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Declarations

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