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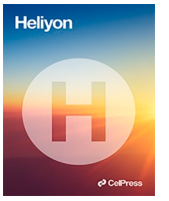

Research article

SleepMI: An AI-based screening algorithm for myocardial infarction using nocturnal electrocardiography

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ABSTRACT

Myocardial infarction (MI) is a common cardiovascular disease, the early diagnosis of which is essential for effective treatment and reduced mortality. Therefore, novel methods are required for automatic screening or early diagnosis of MI, and many studies have proposed diverse conventional methods for its detection. In this study, we aimed to develop a sleep-myocardial infarction (sleepMI) algorithm for automatic screening of MI based on nocturnal electrocardiography (ECG) findings from diagnostic polysomnography (PSG) data using artificial intelligence (AI) models. The proposed sleepMI algorithm was designed using representation and ensemble learning methods and optimized via dropout and batch normalization. In the sleepMI algorithm, a deep convolutional neural network and light gradient boost machine (LightGBM) models were mixed to obtain robust and stable performance for screening MI from nocturnal ECG findings. The nocturnal ECG signal was extracted from 2,691 participants (2,331 healthy individuals and 360 patients with MI) from the PSG data of the second follow-up stage of the Sleep Heart Health Study. The nocturnal ECG signal was extracted 3 h after sleep onset and segmented at 30-s intervals for each participant. All ECG datasets were divided into training, validation, and test sets consisting of 574,729, 143,683, and 718,412 segments, respectively. The proposed sleepMI model exhibited very high performance with precision, recall, and F1-score of 99.38%, 99.38%, and 99.38%, respectively. The total mean accuracy for automatic screening of MI using a nocturnal single-lead ECG was 99.387%. MI events can be detected using conventional 12-lead ECG signals and polysomnographic ECG recordings using our model.

1. Introduction

Myocardial infarction (MI) is the most common cardiovascular disease (CVD), accounting for more than 70% of CVD-related mortality in approximately 17.7 million people annually [1]. MI is caused by prolonged myocardial ischemia and is characterized

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by acute myocardial injury due to abnormal cardiac biomarker levels [2]. Therefore, an early detection of MI is important for preventing sudden death. Several diagnostic methods, such as electrocardiography (ECG), magnetic resonance imaging [3], and echocardiography [4], may be used to detect the risk of MI. ECG is the most common physiological signal that used to diagnose MI because it directly records the electrophysiological activity of the human heart. In addition, ECG provides the most informative physiological signal and many vital signs, such as cardiac activity, respiration [5], and body movement [6].

Nocturnal polysomnography (PSG) is the gold standard method for diagnosing sleep disorders, such as insomnia [7], sleep-related breathing disorders [8], sleep-related movement disorders [9], parasomnias [10], hypersomnolence [11], and circadian rhythm disorders [12]. PSG can objectively evaluate sleep disorders using several bio-signals, such as electroencephalography (EEG), electrooculography (EOG), ECG, and respiration, recorded during sleep [13]. In a previous study, diagnostic nocturnal PSG has shown the possibility of diagnosing sleep disorders and chronic diseases [14]. If PSG adapted some AI models, it can be used not only as a diagnostic tool but also as a preventive or pre-screening tool for comorbidities such as sleep apnea, CVD, and other chronic diseases.

In recent years, many alternative methods have been studied for the automatic detection of MI using ECG signals. These methods can be classified into resource signal and analytical methods. Generally, ECG signals are used in all these studies as the main source signal, with variations such as those in single-lead ECG [15], standard 12-lead ECG signals [16], and portable ECG signals [15]. In addition, all these studies applied representative machine learning techniques, such as support vector machine (SVM) [17], k-nearest neighbor (KNN) [18], decision tree [19], and popular deep learning models, including simple convolutional neural networks (CNN) [20], ResNet [21], and DenseNet [22], for MI detection. Acharya et al. proposed novel methods for automated detection of MI based on canonical machine learning (ML) [20] and the recent deep learning (DL) approach [23]. In ML-based research, the following three different features have been extracted from ECG waveforms: discrete wavelet transform (DWT), discrete cosine transform (DCT), and empirical mode decomposition (EMD). Thereafter, these authors applied dimension reduction with locality-preserving projection, and finally, KNN was performed for the detection of MI. In contrast, DL-based research directly trains the CNN model using raw ECG signals without handcrafted features and classifiers by comparing the performance with and without ECG signal noise. These studies proposed novel and exemplary methods for MI detection from ECGs. However, all these studies used ECG that measured daytime or daily activity. To the best of our knowledge, only a few studies have been conducted on MI detection based on nocturnal ECG signals.

In this study, we propose a novel approach for the automatic screening of MI using nocturnal ECG signals from PSG recordings. The proposed sleep-myocardial infarction (sleepMI) algorithm was designed using artificial intelligence models, including a CNN, a light gradient boost machine (LightGBM), and a convergence model called the sleepMI model. In addition, we demonstrated the potential of a clinical decision support system for MI screening during a diagnostic PSG study. The sleepMI model was developed and validated by a long-term sleep cohort study, the Sleep Heart Health Study (SHHS), provided by sleep-data.org [24].

2. Materials and methods

The proposed sleepMI algorithm for automatic screening of MI from nocturnal ECG findings from PSG data comprises three main parts: the PSG database, nocturnal ECG dataset, and sleepMI model. A multi-center cohort PSG database was used to select the study population for the development and validation of the model (Fig. 1A). Nocturnal ECG signals were extracted from the PSG data of the study population to build an ECG dataset (Fig. 1B). A sleepMI model for automatic screening of MI was designed and optimized, and a detailed description of each component is presented (Fig. 1C).

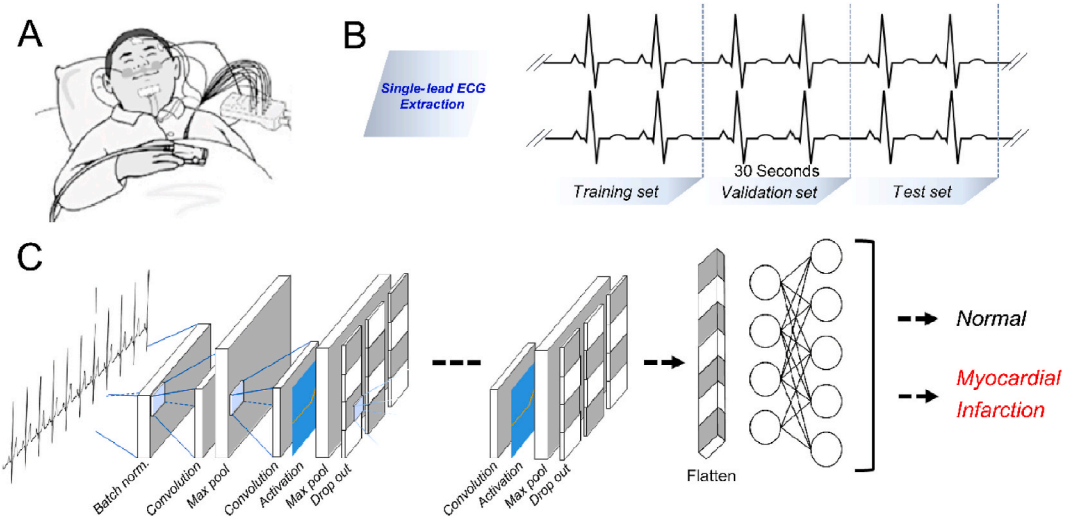

Fig. 1. Graphical representation of the proposed sleepMI algorithm for automatic screening of MI from nocturnal ECG signals. (**A**) PSG study, (**B**) nocturnal ECG datasets, and (**C**) the proposed SleepMI model.

2.1. PSG study

We used a multi-center PSG cohort study, the SHHS, implemented by the National Heart Lung and Blood Institute, to determine the cardiovascular and other consequences of sleep-disordered breathing [25]. The initial purpose of the SHHS was to test whether sleep-related breathing is associated with an increased risk of coronary heart disease, stroke, all-cause mortality, and hypertension. In the baseline study, 6,441 males and females aged ≥40 years were enrolled from November 1, 1995, to January 31, 1998, to participate in SHHS visit 1. SHHS visit 2 was conducted from January 2001 to June 2003, and the second PSG was conducted on 3,295 participants.

In this study, our study sample size was 2,691 participants, which consisted of 2,331 healthy and 360 MI groups. Our inclusion criteria were those who underwent PSG at visit 2 of SHHS. To obtain a more robust performance of the proposed sleepMI model, we did not apply any exclusion criteria to select certain participants.

2.2. Nocturnal ECG datasets

A nocturnal ECG signal was recorded using a lead II transducer at 250 samples/s and a high-pass filter at 0.15 Hz during diagnostic PSG (Computmedics P-series). A bandpass filter (5–11 Hz) was applied to the nocturnal ECG signals to remove undesired noise for data preprocessing. After preprocessing, filtered nocturnal ECG signals were segmented at 30-s intervals with no overlap, and a sleep specialist matched the sleep annotations. To build the AI datasets, we extracted the nocturnal ECG segments as a balanced distribution, with all normal segments from the healthy group and MI segments from the MI groups. Finally, we obtained 1,436,824 events, of which 747,746 were normal and 689,078 were MI (Table 1).

2.3. Proposed SleepMI algorithm

The proposed sleepMI model was designed to discriminate MI events using the morphological characteristics and temporal patterns of nocturnal ECG signals. The sleepMI model was implemented by converging a deep CNN and light gradient boost machine (LightGBM), which can extract high-dimensional feature maps and patterns of a nocturnal single-lead ECG. In addition, the sleepMI model was optimized to be applicable in the nocturnal PSG for automatic and in-hospital MI screening using real-world data. To optimize the sleepMI model, batch normalization [26], dropout [27], and a rectified linear unit (ReLU) [28] were appropriately set and used through trial and error. A detailed description (Fig. 2) of the AI techniques used in the sleepMI model is given below.

2.3.1. Deep CNN model

1D convolution layer: It is appropriate for analyzing time series, and is simpler and faster than two-dimensional convolutions. The deep CNN section was designed by a four-layer CNN structure consisting of conv1d_1 (size 50x1, filters 100), conv1d_2 (size 50x1, filters 80), conv1d_3 (size 20x1, filters 60), and conv1d_4 (size 20x1, filters 40), as presented in Fig. 2. The 1D convolution is represented as follows Equation (1):

$$x_k = b_k + \sum_{i=1}^{N} w_k \times y_i \tag{1}$$

where x_k is the k-th feature map, b_k is the bias of the k-th feature map, w_k is the k-th convolutional kernel from all features of the k-th feature map, and y_i represents the i-th feature map.

1D max-pooling layer: pooling reduces the dimensions of the intermediate feature maps. If a 1D kernel is used in the pooling operation, this is called 1D pooling. All pooling layers use maximum pooling (size 2 x 1).

Batch normalization: Before training the generated sleepMI model, batch normalization was applied (size 7,500 x 1) to the nocturnal ECG signal, as shown in Equation (2):

$$x_b = \alpha \cdot \left(\frac{x_i - \mu}{\sqrt{\sigma^2 + \varepsilon}} \right) + \beta \tag{2}$$

where ε is a small random noise, μ is the mini-batch mean, σ is the mini-batch variance, α is the scale parameter, and β is the shift parameter. Both α and β are trainable and updated epochwise.

Dropout: This technique is used to reduce overfitting and prevent complex adaptations to training data in which random nodes in a network are excluded.

Table 1
ECG dataset distribution according to the training, validation, and test sets.

Data sets	Normal	MI	Total
Training set	298,916	275,813	574,729
Validation set	74,957	68,726	143,683
Test set	373,873	344,539	718,412
Total	747,746	689,078	1,436,824

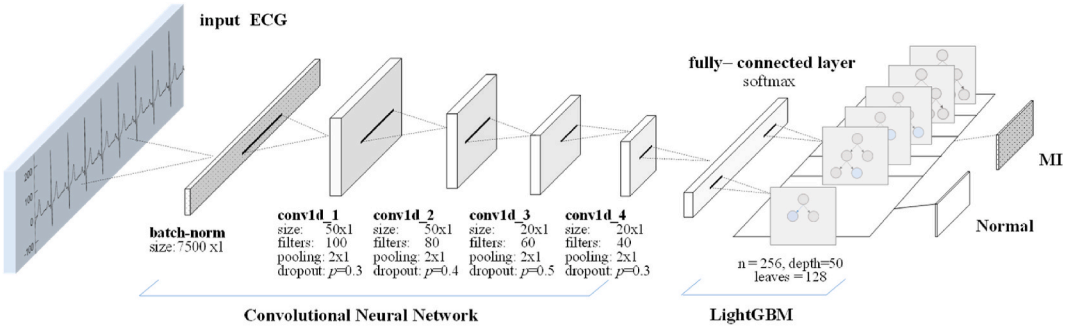

Fig. 2. Architecture of the proposed sleepMI model for automatic screening of MI from nocturnal single-lead ECG signals.

ReLU: This is used as the activation function of each layer of the sleepMI model and can be represented as follows Equation (3):

$$f(x) = \max(0, wx + b) \tag{3}$$

where x is the feature map, w is the weight, and b is the bias. ReLU delivers robust training performance and consistent gradients, facilitating gradient-based learning [28].

2.3.2. LightGBM model

LightGBM is one of the most popular gradient-boosting decision tree algorithms [29]. This is an ensemble learning method because it learns additively while adding weak learners, and the loss function decreases gradually. LightGBM is an updated version of XGBoost that implements gradient-based one-sided sampling for effective learning and exclusive feature bundling for fast learning [30]. We tuned and optimized the hyperparameters of LightGBM as follows: the number of estimators, maximum depth, number of leaves, minimal amount of data in one leaf, subsampling (n_estimators = 256, max_depth = 50, num_leaves = 128, min_child_samples = 60, subsample = 0.8), and the other parameters were used as the default settings.

2.4. Implementation

The implementation environment of the proposed sleepMI model, including the software and hardware specifications, is as follows: The software environment comprised a Keras library running with a TensorFlow backend [31], and the hardware comprised a workstation with an Intel CPU (i9-9900X @3.5 GHz) and an NVIDIA GPU (GeForce RTX 3090).

2.5. Evaluation indexes

Evaluation measures were calculated for the model training and testing phases to assess the sleepMI model developed for MI screening. We employed accuracy, precision, recall, and F1-score to evaluate the performance of the proposed sleepMI model. These are defined as follows Equation (4−7):

$$\text{Accuracy} = (\text{TP} + \text{TN})/(\text{TP} + \text{TN} + \text{FP} + \text{FN}), \tag{4}$$

$$\text{Precision} = \text{TP}/(\text{TP} + \text{FP}), \tag{5}$$

$$\text{Recall} = \text{TP}/(\text{TP} + \text{FN}), \tag{6}$$

where TP, FP, TN, and FN denote true positives, false positives, true negatives, and false negatives, respectively, and represent the number of events.

$$F_1 = \sum_i 2 \cdot w_i \frac{precision_i \cdot recall_i}{precision_i + recall_i}, \tag{7}$$

where i is the class index, $w_i = n_i/N$ is the proportion of samples in class i, n_i is the number of samples in the ith class, and N is the total number of samples.

3. Results

We performed several experiments to examine the comparative and robust performance of the proposed sleepMI model. We obtained some meaningful results from the baseline characteristics of the study population (Table 2). The sex distribution of the study population was 45.2% males and 54.8% females. In contrast, the demographic data showed that the proportion of males in the MI group increased by almost 3:1. Regarding age, the proportion of older patients was higher in the MI group, with one in five patients

aged more than 70 years. Finally, systolic blood pressure was significantly higher in the MI group than in the control group.

For comparison, we implemented simple deep CNN, LightGBM, and SleepMI models, as presented in Table 3. For the test set, all models showed very high performance with F1 scores of 99.26%, 86.17%, and 99.36% for CNN, LightGBM, and SleepMI, respectively. Our experimental results showed that the DL-based model exhibited better performance than the ML-based model. Among the DL-based models, the proposed SleepMI model showed a more robust and slightly better performance in all evaluation phases, such as training, validation, and testing.

Receiver operating characteristic (ROC) curves of the proposed sleepMI algorithm for automatic screening of MI using a nocturnal ECG signal are presented in Fig. 3. It is very difficult to distinguish the performances of the DL-based methods using ROC curves; therefore, we zoomed up the section in Fig. 3.

We used confusion matrices to illustrate the discordance between the proposed sleepMI model predictions and the cardiologist's diagnosis. The three confusion matrices, i.e., the training set (Fig. 4A), validation set (Fig. 4B), and test set (Fig. 4C), exhibited a similar pattern. In particular, the confusion matrices of the validation and test sets demonstrated stable or almost the same prediction.

4. Discussion

In this study, we proposed a sleepMI model for the automatic screening of MI based on nocturnal ECG signals using a hybrid neural network. The sleepMI model was designed using a hybrid architecture of the deep CNN and LightGBM models for robust and stable screening of MI from nocturnal ECGs. The proposed method was trained, validated, and tested using a multi-center sleep cohort from the SHHS database. We observed outstanding performance, with a mean accuracy of 99.387%, for the automatic screening of MI using nocturnal single-lead ECG. These results are comparable with those of previous studies that used daytime ECG signals (Table 4).

Several conventional studies have proposed methods for automatically detecting MI using ECG signals, as listed in Table 4. All the listed studies used daytime ECG signals for MI detection; therefore, it may not be appropriate to directly compare the performances of these studies with that of our study. However, we reviewed and analyzed recent studies to obtain insights and determine the state-of-the-art approach in this field. Acharya et al. [23] proposed a traditional ML-based method for detecting MI using ECGs, in which they extracted various features such as DWT, DCT, and EMD from the input ECG signals. Subsequently, dimension reduction was performed on the final seven discriminative features to apply the KNN classifier to detect MI. Tripathy et al. [32] studied a novel approach for MI detection based on a combination of ML and DL techniques using diverse feature maps from the temporal, spatial, and statistical domains. Liu et al. [33] demonstrated a hybrid model based on CNN and RNN structures for MI detection using standard 12-lead ECGs. Jahmunah et al. [34] developed DL models based on CNN and GaborCNN models for the multiclass classification of four classes: normal, MI, coronary artery disease, and congestive heart failure. All these studies proposed novel features, hybrid AI models, and multiclass classification and achieved good performance. However, none of these studies used daytime ECG signals not nocturnal ECG, to screen MI events automatically.

Recently, many alternative methods that can be applied to diverse cases of MI detection have been developed. Cao et al. [22] proposed and designed a lightweight DL model for real-time MI detection. Tadesse et al. [36] focused on MI detection and its occurrence time using a multi-lead ECG-based DeepMI model. Xiong et al. [37] introduced a novel method for MI localization from a multi-lead ECG signal based on the DenseNet model. These studies considered MI detection, real-time implementation, event

Table 2
Demographic and anthropometric characteristics of the study population.

Measures	Total	Normal	MI	*P*-value
Participants (*N*)	2,691 (100.0)	2,331 (86.6)	360 (13.4)	
Sex				
Male	1,217 (45.2)	995 (42.7)	222 (61.7)	<0.001
Female	1,474 (54.8)	1.336 (57.3)	138 (38.3)	
BMI (kg/m^2)	27.87 ± 5.02	27.83 ± 5.09	28.14 ± 4.53	*NS*
Age (years)				
39–49	541 (20.1)	528 (22.7)	13 (3.6)	<0.001
50–59	625 (23.2)	588 (25.2)	37 (10.3)	
60–69	476 (17.7)	409 (17.5)	67 (18.6)	
>69	1,049 (39.0)	806 (34.6)	243 (67.5)	
Waist circumference (cm)				*NS*
Male	99.33 ± 10.98	99.01 ± 11.18	100.63 ± 10.00	
Female	91.44 ± 14.51	90.74 ± 14.23	97.72 ± 15.48	
Neck circumference (cm)				*NS*
Male	40.25 ± 3.16	40.23 ± 3.24	40.34 ± 2.78	
Female	34.92 ± 2.93	34.84 ± 2.91	35.63 ± 3.04	
Total cholesterol (mg/dl)	205.61 ± 38.70	205.64 ± 38.65	205.45 ± 39.02	*NS*
Triglycerides (mg/dl)	154.69 ± 106.72	153.47 ± 106.42	161.92 ± 108.40	*NS*
BP (mmHg)				
Systolic	127.02 ± 18.54	125.86 ± 17.81	134.32 ± 21.28	<0.001
Diastolic	73.38 ± 11.37	73.96 ± 11.20	69.72 ± 11.76	
Sleep efficiency (h)	6.1 ± 0.9	5.9 ± 0.9	5.7 ± 1.2	*NS*

Note: N: Number, BMI: Body mass index, AHI: Apnea–hypopnea index, *NS*: Not significant (*p*-value >0.01).

Table 3
Performance of the proposed SleepMI algorithm for MI screening.

Models	Data sets	Events	Precision	Recall	F1-score
CNN	Training set	Normal	0.99772	0.99761	0.99766
		MI	0.99740	0.99751	0.99746
	Validation set	Normal	0.99420	0.99209	0.99314
		MI	0.99149	0.99376	0.99263
	Test set	Normal	0.99445	0.99194	0.99320
		MI	0.99127	0.99399	0.99263
LightGBM	Training set	Normal	0.92478	0.92279	0.92378
		MI	0.91614	0.91829	0.91721
	Validation set	Normal	0.86702	0.88278	0.87483
		MI	0.87120	0.85413	0.86258
	Test set	Normal	0.86656	0.88430	0.87534
		MI	0.87150	0.85213	0.86171
SleepMI	Training set	Normal	0.99969	0.99970	0.99969
		MI	0.99967	0.99966	0.99967
	Validation set	Normal	0.99323	0.99456	0.99390
		MI	0.99413	0.99270	0.99341
	Test set	Normal	0.99358	0.99465	0.99411
		MI	0.99418	0.99302	0.99360

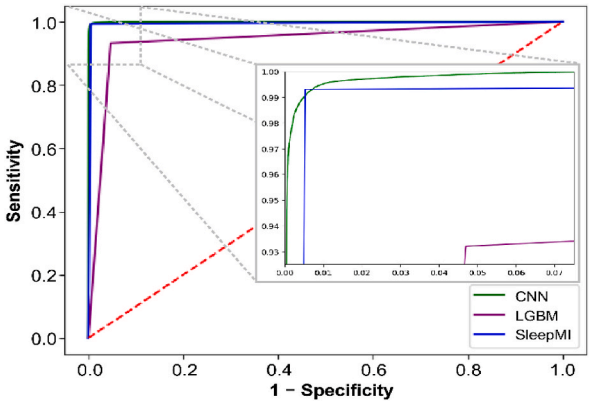

Fig. 3. Comparison of the area under the ROC curve (AUC) of the sleepMI algorithm.

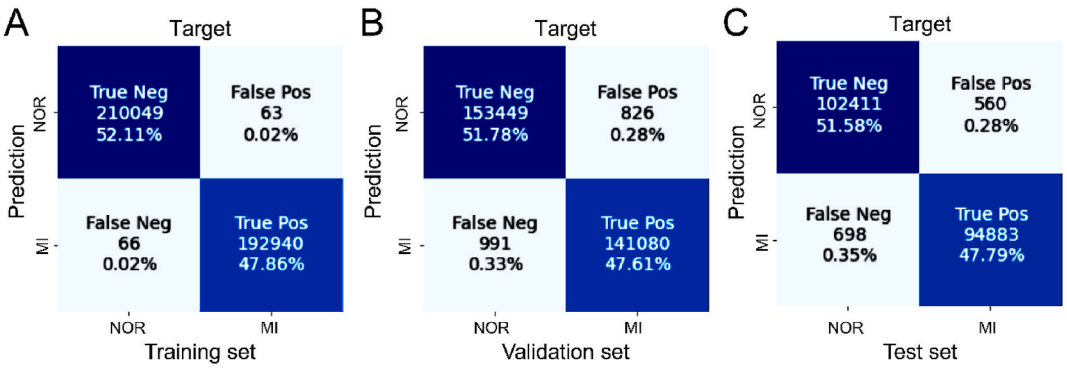

Fig. 4. Confusion matrices. Confusion matrix of the sleepMI model for automatic screening of MI in (A) the training set, (B) validation set, and (C) test set.

occurrence time, and event localization. In contrast, we proposed a robust and lightweight AI model for MI screening during sleep. The proposed sleepMI model constructed hybrid network architecture employed deep CNN and LightGBM, it can detect MI segments with a duration of 30s with robust performances using nocturnal ECG.

An important finding of our study was that the proposed sleepMI model could screen patients with MI during nocturnal PSG. In addition, the proposed method can extend conventional PSG, which focuses on sleep disorders, including sleep apnea, insomnia, and

Table 4
Performance comparison with other studies.

Study	Year	Method	Acc.	Sens.	Spec.
Acharya et al. [23]	2017	CNN	95.22	95.49	94.19
Dohare et al. [17]	2018	SVM	96.66	96.66	96.66
Tripathy et al. [32]	2019	DL-LSSVM	99.74	99.87	99.60
Liu et al. [33]	2019	MFB-CBRNN	93.08	94.42	86.29
Baloglu et al. [35]	2019	CNN	99.78	99.00	=
Kayikcioglu et al. [18]	2020	KNN	94.23	95.72	98.15
Han et al. [21]	2020	ML–ResNet	95.49	94.85	97.37
Cao et al. [22]	2021	ML-Net	96.65	94.30	97.72
Tadesse et al. [36]	2021	DeepMI	96.70	75.50	83.30
Our study	2023	SleepMI	99.38	99.0	99.0

other sleep movement disorders, to MI screening, which is one of the most common CVDs. With regard to AI technology, we demonstrated the combined architecture of the deep CNN and LightGBM models to achieve enhanced robustness of the model performance compared to conventional single-type models. In addition, the proposed sleepMI model can be used as an end-to-end system for PSG studies. Furthermore, there is an increase in model stability for the precise screening of MI, which is rarely observed in conventional classification methods. In biomedical engineering, single-or multi-lead ECGs are the main source signals for detecting or classifying MI, as listed in Table 4. All these studies used ECGs measured during the day; however, we used nocturnal ECG to screen for MI in this study. This can be a new opportunity for a more comprehensive and compact diagnosis or treatment by sleep researchers, clinicians, and physicians. From a clinical perspective, the proposed sleepMI model can provide a more robust performance for MI detection during diagnostic and monitoring PSG studies. Thus, the proposed sleepMI model can serve as an alternative extension of PSG. Using this method, sleep technicians can provide more insightful annotations and make more accurate clinical decisions.

However, this study has some limitations. Currently, the proposed sleepMI model focuses only on automatic screening of MI, even though CVD includes many diseases. In future studies, we plan to include as many patients with CVDs as possible. We did not perform subject-based screening; our results were based on segment-based training, testing, or validation. Our model consists of a deep CNN and LightGBM, which only consider single-lead ECGs during PSG; we did not use other physiological and phenotypic information provided by PSG. In the future, we will extend our single input to multiple inputs, including bio-signals and demographic data of the participants. In addition, the proposed method will apply a wearable single-lead ECG signal that can monitor or screen MI not only during the day but also during the nocturnal period.

5. Conclusion

We developed a sleepMI model for automatically screening MI that can be extended to a full nocturnal PSG study. The proposed sleepMI comprised a convergence model of a deep CNN and LightGBM for precise and robust screening of MI from a normal short-term ECG. The proposed model showed a possibility with a mean accuracy of 99.38% for MI screening based on nocturnal short-term ECG signals. Our results support the use of the sleepMI algorithm as a helpful tool for MI screening in diagnostic PSG studies. In future studies, we plan to develop an AI model based on nocturnal ECG signals that cover more diverse CVDs during sleep.

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Data availability statement

https://sleepdata.org/datasets/shhs. All data were approved by the National Sleep Research Resource (NSRR) for the specific purpose of this study.

CRediT authorship contribution statement

Youngtae Kim: Visualization, Validation, Software, Data curation. **Hoon Jo:** Writing – original draft, Investigation, Formal analysis. **Tae Gwan Jang:** Writing – review & editing, Writing – original draft, Formal analysis, Data curation. **So Yeon Park:** Writing – review & editing, Writing – original draft, Software, Formal analysis, Data curation. **Ha Young Park:** Project administration, Investigation. **Sung Pil Cho:** Software, Resources, Funding acquisition. **Junghwan Park:** Software, Resources, Funding acquisition. **Sang-Ha Kim:** Validation, Resources, Methodology, Funding acquisition. **Erdenebayar Urtnasan:** Writing – review & editing, Writing – original draft, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Conceptualization.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Erdenebayar Urtnasan reports financial support was provided by the National Research Foundation of Korea (NRF) funded by the Ministry of Education (MOE). If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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