An interpretable DIC risk prediction model based on convolutional neural networks with time series data

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Introduction
“Disseminated intravascular coagulation (DIC) is an acquired syndrome characterized by the intravascular activation of coagulation with loss of localization and arising from different causes. It can originate from and cause damage to the microvasculature, which if sufficiently severe, can produce organ dysfunction” (defined by the International Society on Thrombosis and Haemostasis, ISTH) [1]. DIC is often regarded as a serious, life-threatening and complex clinical condition [2, 3], which is elicited by malignancies, serious infections, trauma, obstetric diseases, liver diseases, etc. [4]. Mortality is remarkable to increase in patients who develop DIC, and the risk of death is doubled in critically ill patients [5].

The diagnostic criteria, the DIC score (by ISTH scoring system) is widely used in clinical practice [6], similar scoring algorithms have been developed and widely evaluated in various countries, like the Japanese Ministry of Health and Welfare (JMHW) and Japanese Association for Acute Medicine (JAAM) [7]. However, no single clinical or

Abstract
Disseminated intravascular coagulation (DIC) is a complex, life-threatening syndrome associated with the end-stage of different coagulation disorders. Early prediction of the risk of DIC development is an urgent clinical need to reduce adverse outcomes. However, effective approaches and models to identify early DIC are still lacking. In this study, a novel interpretable deep learning based time series is used to predict the risk of DIC. The study cohort included ICU patients from a 4300-bed academic hospital between January 1, 2019, and January 1, 2022. Experimental results show that our model achieves excellent performance (AUC: 0.986, Accuracy: 95.7%, and F1:0.935). Gradient-weighted Class Activation Mapping (Grad-CAM) was used to explain how predictive models identified patients with DIC. The decision basis of the model was displayed in the form of a heat map. The model can be used to identify high-risk patients with DIC early, which will help in the early intervention of DIC patients and improve the treatment effect.

Keywords: Disseminated intravascular coagulation, Prediction, Machine learning
laboratory test has adequate sensitivity and specificity to confirm or reject a diagnosis of DIC [3]. Because of the poor prognosis of DIC, it is necessary to identify its potential risk factors. The diagnosis and treatment of DIC are therefore important and an early diagnosis of DIC as pre-DIC may help improve patient survival. Therefore, it is clinically important to identify high-risk patients with DIC promptly and perform the appropriate intervention.

Recently, artificial intelligence has been widely applied to the prediction of various clinical events and including DIC. For example, Yoon et al. [8] exploited several machine learning approaches including logistic regression, linear regression, ridge regression, random forest, and gradient boosting machine to diagnose DIC and prove that machine learning (ML) could optimize the use of clinical parameters for DIC diagnosis. Hasegawa et al. [9] used ML techniques to evaluate predictive accuracies of ML (support vector machine, random forest, and neural network) and conventional approaches (logistic regression) for the progression of coagulopathy in septic patients. It is unearthed in our study that a convolutional neural network (CNN) can provide robust long-term forecasting results in the time-series analysis due to its capability of essential feature learning, distortion invariance, and temporal dependence learning [10].

However, applying CNN to the prediction of DIC based on the densely collected clinical data, especially with the visual interpretation of reasons underlying the prediction results has been scarcely investigated. In this study, we developed CNN to predict the risk of DIC in ICU patients using readily available data from electronic health record (EHR). In addition, Gradient-weighted Class Activation Mapping (Grad-CAM) [11] technique was used to improve the interpretability of the model and to obtain a heat map of the input features.

Materials and methods
Data sources
The study cohort included ICU patients from West China Hospital of Sichuan University between January 1, 2019, and January 1, 2022. West China Hospital is a 4300-bed academic hospital in Southwest China and one of the largest hospitals in China. All patient data were obtained from the EHR of the hospital.

Data selection
As patients with DIC were the target cohort of this study, we included all the patients who had more than 18 years old and had at least one ICU stay. The diagnosis of DIC (D65) was defined according to the International Classification of Diseases-Tenth Revision (ICD-10) code. Patients with multiple ICU admissions, a hospital stay of ≤1 day, or missing data by more than 30% [12] was excluded. The patient selection process was shown in Fig. 1.

Feature matrix construction
We extracted 136 features to predict future ICD based on the EHR, including laboratory test values, demographic characteristics, and clinical events. SQL Server database software and python data preprocessing packages [13–17] were used to sort out the patient time series data matrix. According to the time since the patient entered
the ICU, the maximum length of the time series is 953 time steps and the matrix is 953 * 136 [18] (Fig. 2). The data were randomly divided into a training dataset, validation dataset and test dataset in a ratio of 7:2:1.

**Missing data and filling**
In time series analysis, missing data is a very common problem in time series [19]. Considering the limitations of traditional missing data imputation methods and the reality of missing data in this study, we adopted the forward imputation method [20] and random forest imputation [21].

**Analysis platform**
The current general-purpose deep learning framework PyTorch is used to build predictive models. Every aspect of PyTorch is a normal Python program under the full control of the user [22].

The predictive model was built on a personal desktop computers (operating system: windows 11; central processing unit: 12th Gen Intel(R) Core(TM) i7-12700F; random access memory 32 G; graphics processing unit: NVDIA GeForce RTX3060Ti).
Artificial intelligence models

XGBoost model

XGBoost (Extreme Gradient Boosting) is a scalable machine learning system for tree boosting [21]. It is adept at handling classification and regression tasks. Optimizing the value of the objective function is the core of the algorithm. XGBoost has the advantages of full-scene scalability, speed and performance [23]. Based on the python toolkit (XGBoost Documentation- XGBoost 1.6.1 documentation), we built the XGBoost model. The two-dimensional time series matrix is processed into one-dimensional data into the input model for classification and recognition, where the parameters are set to n_estimators = 50; max_depth = 5; learning_rate = 0.01.
**LSTM model**

Long short-term memory neural network (LSTM) was developed by Hochreiter and Schmidhuber [24]. It can capture long and short dependencies in time series and is not affected by gradient disappearance [25]. LSTM also has feedback loops, but moreover, it uses a gating mechanism to delete or add information to the model state, and controls model state update and change through the ‘forgetting gate’, ‘input gate’ and ‘output gate’ [26]. It is suitable for processing and predicting events with time series data [25]. We build a Pytorch-based LSTM time series model. The model consists of two layers of LSTMs, each of which consists of 128 hidden units. The binary cross-entropy was used as a loss function and the Adam optimizer was used together with a learning rate of 0.01 (Fig. 3).

**CNN model**

CNN consists of three main neural layers, namely convolutional layers, pooling layers, and fully connected layers that can be stacked according to their functions. CNN make use of knowledge about specific input types rather than focusing on the entire problem domain. This facilitates to set up of simpler network architectures [27]. The advantage of CNN is that it minimizes the number of parameters, which greatly improves the performance of the algorithm [28].

In this study, the CNN model adopts the convolution kernel size of 3 * 1 (Fig. 4), only abstracts the features in time series, and retains the feature map consistent with the model input features. This will help to improve the interpretability of models using Grad-CAM technology [10], as well as ensure that the resulting feature maps are consistent with the input features. The maximum pooling layer is used to effectively reduce the size of the parameter matrix and adjust the number of channels and convolution kernel size in the last convolution layer. The 1 * 1 convolution kernel [29] is used for dimensionality reduction and aggregating across channels so that the model gets a feature map with the number of features * 1 dimension before entering the fully connected layer. It can be regarded as a feature of all indicators of the patient. Then the classification result
was obtained by inputting the final fully connected layer. The binary cross-entropy was used as a loss function and the Adam optimizer was used together with a learning rate of 0.01. The parameters are shown in Table 1.

**Model visualization**

Gradient-weighted Class Activation Mapping (Grad-CAM) is a visual interpretation technique for decisions from CNN-based models, making them more transparent [10]. It generates location maps using back-propagated gradients of specified class prediction scores to highlight important decision regions of the input matrix. Each feature was fed into the CNN model to generate a predicted score for a class, and the score was back-propagated to the convolutional layer of the model to assign importance values to each input feature. In our study, Grad-CAM uses the gradient information flowing into the last convolutional layer (136 * 1) of the CNN to assign the importance of each feature (neuron) for the decision of interest. Using Grad-CAM, explain how predictive models identify patients with DIC, i.e., determine which features are more likely to trigger patients to develop DIC. The decision-making basis of the model is displayed in the form of a heat map.

### Table 1 The CNN parameters

| Layer                                      | Filters | Size | Stride | Output          |
|--------------------------------------------|---------|------|--------|-----------------|
| Conv1(ReLU) + BatchNorm + ReLu            | 16      | (3,1)| (2,1)  | 16*476*136      |
| Conv2(ReLU) + BatchNorm + ReLu            | 32      | (3,1)| (2,1)  | 32*237*136      |
| Conv3(ReLU) + BatchNorm + ReLu            | 64      | (3,1)| (2,1)  | 64*118*136      |
| Maxpool                                   |         | (118,1)|      | 64*1*136        |
| Conv4(ReLU)                               | 1       | (1,1)| (1,1)  | 1*1*136         |
| Fully-connected layer                     | –       | –    | –      | 136             |
| Output layer                              | –       | –    | –      | 2               |
The term $L_{\text{grad-CAM}}^{C}[\mathbb{R}^{u \times v}]$ of width $u$ and height $v$ was used to distinguish between DIC and Non-DIC patients. The score gradient was first calculated for class $c$ and $y^c$ (before SoftMax), with respect to feature maps $A^k$ in the final convolutional layer. These gradients were global average pooled to obtain neuron importance weights $a^c_k$:

$$a^c_k = \frac{1}{z} \sum_i \sum_j \frac{\partial y^c}{\partial A_{ij}},$$

representing the importance of a feature map $k$ in a target class $c$. A weighted combination of forwarding activation maps was then performed, followed by a ReLU, to obtain the final heat map:

$$L_{\text{grad-CAM}}^C = \text{ReLU} \left( \sum_k a^c_k A^k \right).$$

In a deep network, heat maps can be used to visualize any area that contributes to classification results, thereby increasing interpretability, as was the case in this study.

**Statistics**

Categorical variables are presented as counts and percentages, and continuous variables are presented as mean and standard deviation (SD). Comparisons between groups were performed by 2-tailed $t$-test for continuous variables and chi-square test for categorical variables. All statistical analyses were performed in the python package SciPy (SciPy) [30]. The statistical significance was considered as $P<0.05$.

**Results**

**Patient characteristics**

The cohort included 6631 ICU patients, of whom 1539 patients (23.2%) developed DIC. There were more males than females in this cohort (DIC: 60.0% male vs 40.0% female; Non-DIC: 60.2% male vs 39.8% female). The mean age of DIC patients and Non-DIC patients was 52.6 and 51.3 years old, and BMI was 21.88 and 22.79, respectively. There was no statistical significance ($P>0.05$). The basic demographic characteristics of the cohort was shown in Table 2.

| Variables (mean ± SD)  | DIC          | Non-DIC      | $P$        |
|------------------------|--------------|--------------|------------|
| Sex                    |              |              | >0.05*     |
| Male                   | 923 (60.0%)  | 3069 (60.2%) |            |
| Female                 | 616 (40.0%)  | 2023 (39.8%) |            |
| Age (years)            | 52.60 ± 21.24| 51.35 ± 23.25| >0.05      |
| BMI                    | 21.88 ± 4.49 | 22.79 ± 4.35 | >0.05      |
| Surgery                | 842          | 4443         | <0.001     |
| Ventilator use         | 684          | 718          | <0.001     |
| ICU stay               | 10.76 (13.20)| 5.77 (11.33) | <0.001     |

*Chi-square test
Model performance

For the CNN model, the Loss value decreases gradually with epoch and stabilizes at 35 epochs, and the accuracy reaches 95% on both the training and validation sets (Fig. 5). Figure 6 shows the area under the receiver operating characteristic (AUROC) curves for these predictive models. Among the three models, the CNN model showed the best area under the curve (AUC) (0.986), accuracy (95.7%) and F1 (0.935), which was statistically significant with XGBoost ($P < 0.01$) (Table 3).

Model interpretation

To understand the contribution of features to the model predictions, Grad-CAM was used to interpret the CNN predictions, as shown in Fig. 7. Figure 7a showed the 136 features of the input model (Additional file 1); Figure 7b showed the activation features on all samples in the CNN model. Grad-CAM analysis identified that the top ten features for DIC prediction were CK (creatine kinase), GLU (glucose), AST (aspartate aminotransferase), NRBC-rate (nucleated red blood cells rate), NRBC, IG-rate (immature granulocyte rate), ALP (Alpha-fetoprotein), β-HB (β hydroxybutyric acid), BPC-impedance (blood platelet count), IG (immature granulocyte). The higher the value of Grad-CAM, the higher the risk of model output (increased risk of DIC).

Figure 8 showed an example of real-time sequential prediction using the CNN model on different patients (chronic kidney disease, liver abscess, sepsis, type 2 diabetes ketosis). With data from each time point after a patient enters the ICU, the model provides a real-time assessment of the risk and uncertainty of future DIC episodes. This demonstrates that the model can detect DIC up to 12 h in advance, which is important for clinicians to take preventive action before an event occurs.

Discussion and conclusions

DIC represents the end-stage of different coagulation disorders. It is a complex syndrome involving the dysfunction of multiple physiological systems and processes. The characteristics of the multiple coagulopathies described may differ considerably depending on the pathophysiology and time in the disease course.

In our study, DL and ML algorithms were used to perform early prediction of DIC. The patient’s temporal data during ICU is processed into a two-dimensional matrix, and a convolutional network is used to convolve the temporal sequences on each dimensional
This can also be seen as combining features from different temporal points or convolving the receptive field of the kernel to perform feature abstraction over the temporal sequence. In addition, the data size and model complexity in our study are not high, and both RNN and CNN networks can obtain good classification performance for such a size study. The results show that the development of models to identify patients

| Model     | XGBoost | LSTM    | CNN     | P (XGBoost vs. LSTM) | P (XGBoost vs. CNN) | P (CNN vs. LSTM) |
|-----------|---------|---------|---------|----------------------|---------------------|------------------|
| AUC       | 0.851 (0.035) | 0.983 (0.022) | 0.986 (0.018) | < 0.001 | < 0.001 | > 0.05 |
| Accuracy  | 82.03% (1.63%) | 95.13% (0.69%) | 95.68% (0.71%) | < 0.001 | < 0.001 | > 0.05 |
| F1-score  | 0.771 (0.058) | 0.915 (0.061) | 0.935 (0.044) | < 0.001 | < 0.001 | 0.0197 |

- **TBil**
- **DBil**
- **ALT**
- **I Bil**
- **TP**
- **Alb**
- **GLB**
- **Alb/GLB**
- **Cre**
- **UA**
- **AST/ALT**
- **GLU**
- **AST**
- **ALP**
- **CK**
- **GOT**
- **LDH**
- **HBDH**
- **TG**
- **Urea**
- **CHOL**
- **Ca**
- **Mg**
- **P**
- **IDL**
- **LDL**
- **Na**
- **K**
- **C1**
- **CO2-CP**
- **AG**
- **CysC**
- **β-HB**
- **GFR**
- **IG**
- **IG-rate**
- **NRBC**
- **NRBC-rate**
- **BPC-impedance**
- **VLC**
- **Micro-rate**
- **RBC**
- **HGB**
- **Hct**
- **MCV**
- **MCH**
- **MCHC**
- **RDW-CV**
- **RDW-SD**
- **PLT**
- **WBC**
- **NEUT-rate**
- **LY-rate**
- **Mono-rate**
- **EOS-rate**
- **BASO-rate**
- **Protocell**
- **Nsg**
- **Lym**
- **Mono**
- **Eos**
- **Baso**
- **PLT-F**
- **PT**
- **APTT**
- **APIT-rate**
- **IT**
- **IT-rate**
- **FIB**
- **AT-II A**
- **FDP**
- **D-Dimer**
- **Plg-calculus**
- **D-Dimer/LFEU**
- **HCO**
- **PH**
- **Pco2**
- **Pco2**
- **LD**
- **s-creatinine**
- **Hb**
- **s-creatinine**
- **Sp02**
- **CaO2**
- **Hb**
- **MethB**
- **BIL**
- **Ca2+**
- **BEB**
- **BE-efc**
- **BB**
- **MCHC**
- **Hct**
- **OC**
- **BE**
- **CRP**
- **IL-6**
- **PCT**
- **CK-MB**
- **MYO**
- **NT-proBNP**
- **CTnT**
- **Pct**
- **MPV**
- **P-LCR**
- **PDCW**
- **PAO2**
- **SpO2**
- **P50**
- **SB**
- **AIFP**
- **CAI-9**
- **CEA**
- **LMWH**
- **C3**
- **C4**
- **vWF**
- **vWF-Ag**
- **IL-5**
- **IL-12p70**
- **TNF-α**
- **IL-17**
- **IL-1b**
- **INF-α**
- **IL-8**
- **IL-2**
- **IL-10**
- **INF-γ**
- **IL-4**
- **male**
- **age**
- **BMI**
- **Ventilator use**
- **Surgery**
- **APACHE**

**Fig. 7** Input feature and heat map
who are at high risk of developing DIC early in ICU patients is clinically important to predict the prognosis. The results might be explained by the time window for the anticoagulant therapy [31], since the use of anticoagulation at an early stage may be most effective [32, 33]. Early diagnosis of DIC is important for the restoration of coagulation abnormalities and patient survival [34]. Thus, the prediction of coagulopathy development is clinically important for the proper selection of patients and anticoagulation time window.

In order to facilitate clinical application and help clinicians to understand, CNN models are visualized. Combined with Grad-CAM technology, the important features that affect decision-making are displayed in the heat maps [35]. The CNN model not only explains the decision-making process of deep learning models but also provides visualization of the feature selection process.

Since DIC is an acquired syndrome, various underlying causes may influence the clinical manifestations of DIC and may produce different accents on the laboratory findings [36, 37, 38].
A group-level activation heat map was obtained by Grad-CAM, and some differences in activators of DIC induced by different diseases could be found (Fig. 8). Although the findings demonstrate good performance and accuracy of the CNN prediction model, it still needs multi-centre validation before it can be used in clinical practice.

However, our study also has some limitations. First, this model was developed at a single center, which reduces effectiveness and may require retraining when applying the model to other hospitals. Secondly, the results of different DIC risk predictions are often difficult to compare due to their different data sources, inconsistent data inclusion criteria, and differences in data types. In addition, the study was retrospective and requires further validation in prospective clinical studies. In future studies, more variables such as medications [38] and protein sequences [39] will be used in early prediction models for DIC.

In the study, we propose a CNN Grad-CAM model for the early prediction of DIC. The model uses Grad-CAM technology to visualize and interpret the prediction results. It provides a faithful visual explanation of the decisions of the DIC prediction model. Further studies should conduct external validation of the model to ensure its suitability for clinical application.

**Supplementary Information**
The online version contains supplementary material available at https://doi.org/10.1186/s12859-022-05004-2.

**Additional file 1.** Related acronyms and abbreviations.

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**Author contributions**
HY, and JL contributed equally. JL, HY, and JL conceptualized the study. JL, HY, JL, SL, and MZ carried out the collection and analysis of the literature and data, and drafted the manuscript. Both HY and JL acted as first authors for this study. All authors reviewed and approved the final version of the manuscript.

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**Availability of data and materials**
The data that support the findings of this study are available from the corresponding author upon reasonable request (Dlj8@163.com).

**Declarations**

**Ethics approval and consent to participate**
The research was approved by the Medical Ethics Committee of West China Hospital Sichuan University (2021-1100). All procedures were performed in accordance with the relevant guidelines and regulations in Ethics Approval and Consent to participate. Written informed consent was obtained from each participant.

**Consent for publication**
Not applicable.

**Competing interests**
The authors declare that they have no conflict of interest.

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**References**
1. Taylor FB Jr. Scientific Subcommittee on Disseminated Intravascular Coagulation (DIC) of the International Society on Thrombosis and Haemostasis (ISTH). Towards definition, clinical and laboratory criteria, and a scoring system for disseminated intravascular coagulation. Thromb Haemost. 2001;86:1527–30.
2. Gando S, Levi M, Toh CH. Disseminated intravascular coagulation. Nat Rev Dis Primers. 2016;2(1):1–16.

3. Levi M. Diagnosis and treatment of disseminated intravascular coagulation. Int J Lab Hematol. 2014;36(3):228–36.

4. Squizzato A, Hunt BJ, Kinasewitz GT, Wada H, Ten Cate H, Thachil J, Di Nisio M, et al. Supportive management strategies for disseminated intravascular coagulation. Thromb Haemost. 2016;116(3):896–904.

5. Costello RA, Nehring SM. Disseminated intravascular coagulation. Treasure Island: StatPearls Publishing; 2017.

6. Taylor FB Jr, Toh CH, Hoots KW, Wada H, Levi M. Towards definition, clinical and laboratory criteria, and a scoring system for disseminated intravascular coagulation. Thromb Haemost. 2001;86(1):1327–30.

7. Gando S, Iba T, Eguchi Y, Ohtomo Y, Okamoto K, Kosuki K, Japanese Association for Acute Medicine. Disseminated Intravascular Coagulation (JAAM DIC) Study Group. A multicenter, prospective validation of disseminated intravascular coagulation diagnostic criteria for critically ill patients: comparing current criteria. Crit Care Med. 2006;34(3):625–31.

8. Yoon JG, Heo J, Kim M, Park YJ, Choi MH, Song J, Tsyo Y, et al. Machine learning-based diagnosis for disseminated intravascular coagulation (DIC): development, external validation, and comparison to scoring systems. PLoS ONE. 2018;13(5):e0195861.

9. Zou L, Yeung A, Li C, Wei GX, Chen KW, Kinser PA, Ren Z, et al. Effects of meditative movements on major depressive disorder: a systematic review and meta-analysis of randomized controlled trials. J Clin Med. 2018;7(8):195.

10. Nabi KN, Tahmid MT, Rafi A, Kader ME, Haider MA. Forecasting COVID-19 cases: a comparative analysis between recurrent and convolutional neural networks. Results Phys. 2021;24:104137.

11. Selvaraju RR, Cogswell M, Das A, Vedantam R, Parikh D, Batra D. Grad-cam: visual explanations from deep networks via gradient-based localization. In: Proceedings of the IEEE international conference on computer vision, 2017, p. 618–626.

12. Lin K, Hu Y, Kong G. Predicting in-hospital mortality of patients with acute kidney injury in the ICU using random forest model. Int J Med Inform. 2019;125:55–61.

13. Mistry R, Misner S. Introducing Microsoft SQL server 2014. Redmond: Microsoft Press; 2014.

14. Van Der Walt S, Colbert SC, Varoquaux G. The NumPy array: a structure for efficient numerical computation. Comput Sci Eng. 2011;13(2):22–30.

15. McKinney W. pandas: a foundational Python library for data analysis and statistics. Python High Perform Sci Comput. 2011;14(9):1–9.

16. Pedregosa F, Varoquaux G, Gramfort A, Michel V, Thirion B, Grisel O, et al. Scikit-learn: machine learning in Python. J Mach Learn Res. 2011;12:2825–30.

17. Hunter JD. Matplotlib: a 2D graphics environment. Comput Sci Eng. 2007;9(03):90–5.

18. Gamboa JCB. Deep learning for time-series analysis. arXiv preprint, 2017; arXiv:1701.01887.

19. Torres J, Hadjout D, Sebaa A, Martinez-Artas F, Troncoso A. Deep learning for time series forecasting: a survey. Big Data. 2021;9(1):3–21.

20. Weerakody FB, Wong KW, Wang G, Ela W. A review of irregular time series data handling with gated recurrent neural networks. Neurocomputing. 2021;441:161–78.

21. Deng W, Guo Y, Liu J, Li Y, Liu D, Zhu L. A missing power data filling method based on improved random forest algorithm. Chin J Electr Eng. 2019;5(4):33–9.

22. Paszke A, Gross S, Massa F, Lerer A, Bradbury J, Chanan G, et al. Pytorch: an imperative style, high-performance deep learning library. In: Advances in neural information processing systems, 2019; p. 32.

23. Liu J, Wu J, Liu S, Li M, Hu L, Li K. Predicting mortality of patients with acute kidney injury in the ICU using XGBoost model. PLoS ONE. 2021;16(2):e0246306.

24. Graves A. Long short-term memory. In: Supervised sequence labelling with recurrent neural networks. Studies in Computational Intelligence. Vol 385. Berlin: Heidelberg, Springer, 2012. p. 37–45.

25. Petrozzioello A, Jordanov I, Papageorghiou TA, Redman WC, Georgieva A. Deep learning for continuous electronic fetal monitoring in labor. In: 2018 40th annual international conference of the IEEE engineering in medicine and biology society (EMBC), 2018; p. 5866–5869.

26. Shi X, Chen Z, Wang H, Yeung DY, Wong WK, et al. Convolutional LSTM network: a machine learning approach for precipitation nowcasting. arXiv preprint, 2015; arXiv:1506.04214.

27. O’Shea K, Nash R. An introduction to convolutional neural networks. arXiv preprint 2015; arXiv:1511.08458.

28. Li P, Liang F. An assessment and analysis model of psychological health of college students based on convolutional neural networks. Neurocomputing. 2021;441:161–78.

29. Lin M, Chen Q, Yan S. Network in network. arXiv preprint, 2013; arXiv:1312.4400.

30. Papageorgiou C, Jourdi G, Adjambri E, Walborn A, Patel P, et al. Disseminated intravascular coagulation: an update on pathogenesis, diagnosis, and therapeutic strategies. Clin Appl Thromb Hemost. 2018;24(9_suppl):85–285.

31. van der Poll T. Recombinant human soluble thrombomodulin in patients with sepsis-associated coagulopathy: another negative sepsis trial. JAMA. 2019;321(20):1978–80.

32. Yamakawa K, Umemura Y, Murao S, Hayakawa M, Fujimi S. Optimal timing and early intervention with anti-coagulant therapy for sepsis-induced disseminated intravascular coagulation. Clin Appl Thromb Hemost. 2019;25:10760296119835055.

33. Hasegawa D, Nishida O. Individualized recombinant human thrombomodulin (ART-123) administration in sepsis patients based on predicted phenotypes. Crit Care. 2019;23(1):1–2.

34. Papageorgiou C, Jourdi G, Adjambri E, Walborn A, Patel P, et al. Disseminated intravascular coagulation: an update on pathogenesis, diagnosis, and therapeutic strategies. Clin Appl Thromb Hemost. 2018;24(9_suppl):85–285.

35. Li Y, Yang H, Li J, Chen D, Du M. EEG-based intention recognition with deep recurrent-convolution neural network: performance and channel selection by Grad-CAM. Neurocomputing. 2020;415:225–33.

36. Levi M. Disseminated intravascular coagulation in cancer: an update. In: Seminars in thrombosis and hemostasis. Thieme Medical Publishers; 2019; vol. 45, no. 04, p. 342–347.
37. Levi M. Pathogenesis and management of peripartum coagulopathic calamities (disseminated intravascular coagulation and amniotic fluid embolism). Thromb Res. 2013;131:S32–4.
38. Zhao BW, Hu L, You ZH, Wang L, Su XR. Hingrl: predicting drug–disease associations with graph representation learning on heterogeneous information networks. Brief Bioinform. 2022;23(1):bbab515.
39. Hu L, Wang X, Huang YA, Hu P, You ZH. A survey on computational models for predicting protein–protein interactions. Brief Bioinform. 2021;22(5):bbab636.

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