

# StaResGRU-CNN with CMedLMs: A Stacked Residual GRU-CNN with Pre-trained Biomedical Language Models for Predictive Intelligence

Pin Ni<sup>1</sup>, Gangmin Li<sup>2</sup>, Patrick C. K. Hung<sup>3</sup>, Victor Chang<sup>4,5</sup>

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## Abstract

As a task that requires strong professional experience as support, predictive biomedical intelligence cannot be separated from the support of a large amount of external domain knowledge. By using transfer learning to obtain sufficient prior experience from massive biomedical text data, it is essential to promote the performance of specific downstream predictive and decision-making task models. This is an efficient and convenient method, but it has not been fully developed for Chinese Natural Language Processing (NLP) in the biomedical field. This study proposes a Stacked Residual Gated Recurrent Unit-Convolutional Neural Networks (StaResGRU-CNN) combined with the pre-trained language models (PLMs) for predictive tasks based on biomedical texts. By exploring related paradigms in biomedical NLP based on external expert knowledge transfer learning and comparing some Chinese and English language models. We found some key points that have not been developed or have practical applicability difficulties in the Chinese biomedicine field. Therefore, we also propose a Chinese bioMedical Language Model series (CMedLMs) with a detailed downstream tasks evaluation. By using transfer learning, language models are introduced with prior knowledge to improve the performance of downstream tasks and solve

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<sup>1</sup>School of Engineering, University College London, London, UK

<sup>2</sup>School of Computer Science and Technology, University of Bedfordshire, Luton, UK

<sup>3</sup>Faculty of Business and Information Technology at Ontario Tech University, Canada

<sup>4</sup>Artificial Intelligence and Information Systems Research Group, School of Computing, Engineering and Digital Technologies, Teesside University, Middlesbrough, UK

<sup>5</sup>Corresponding Author

specific predictive NLP tasks related to the Chinese biomedical field to serve the predictive medical system better. Additionally, a free-form text Electronic Medical Record (EMR)-based Disease Diagnosis Prediction task is proposed, which is used in the evaluation of the analyzed language models together with Clinical Named Entity Recognition, Biomedical Text Classification tasks. Our experiments prove that the introduction of biomedical knowledge in the analyzed models significantly improves their performance in the predictive biomedical NLP tasks with different granularity. And our proposed model also achieved competitive performance in these predictive intelligence tasks.

*Keywords:* Natural Language Processing, Predictive Intelligence, Biomedical Text Mining, Named Entity Recognition, Text Classification, Transfer Learning, Pre-trained Language Model

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## 1. Introduction

About one-fifth of the world’s population speaks Chinese. Hundreds of millions of Chinese speakers’ medical information is contained in large and complex electronic medical data management systems. At present, in the situation of  
5 such a huge number of electronic medical data, it is imperative to implement convenient and effective means of processing these massive amounts of textual data. The processing part means using deep learning-based NLP, modeling complex medical text data through deep learning-based NLP to build a more robust medical prediction system to provide more accurate clinical suggestions.  
10 Therefore, it can become another new and effective auxiliary diagnosis method besides relying on expert experience.

Some of the most effective paradigms today are based on the newly emerging pre-trained language models. They were introduced with a large amount of prior knowledge to raise the performance of downstream NLP tasks (e.g., EMR-based  
15 healthcare decision reference). These new methods can compensate for the predicament of insufficient training data in supervised learning and enhance the ability to encode the semantics of context in texts adequately. The effectiveness

of these models that use prior knowledge to solve different tasks they have been demonstrated in many recent experiments on various mainstream NLP tasks [1, 2]. It is now widely recognized by professionals as a new frontier in the NLP field. However, pre-trained language models (trained by large-scale prior knowledge) and their downstream task models, specifically in the Chinese biomedical field, have not been studied yet. Consequently, the NLP tasks processing Chinese biomedical data are often narrowed by the lack of prior domain knowledge and training resources. Compared with similar tasks using other languages (e.g., English), it is often not possible to reach a comparable performance in practical business scenarios, thus limiting the deployment in real-world medical Human-Computer Interaction (HCI) scenarios.

Many studies confirm that most of the selection of downstream task models have a limited impact on the performance of specific tasks [3, 4, 5, 6, 7]. At the same time, several studies [8, 9, 10] have begun to explore the introduction of external knowledge in language representation models. However, due to the late start in the usage of Chinese E-health technologies and the privacy problems related to storing and processing medical data. These all have played a certain role in limiting the development of Chinese biomedical language models. In addition, the introduction of Chinese biomedical field knowledge into pre-trained models poses a number of challenges, the first being that trainable resources, such as medical data, are difficult to access, and knowledge in specific professional fields is often abstract and diverse, making it difficult to comprehensively and deeply cover. Despite the terminology specifications, the expression of medical knowledge is still complicated and diverse in actual business (e.g., abbreviations, polysemy, free-form writing). Entities may have completely different definitions in different contexts. This, combined with frequent mixtures of Chinese and English terminologies, increases the difficulty for the model to process complete sentences correctly. Finally, the inaccuracy of Chinese word segmentation often leads to unsatisfactory actual results.

For the reasons detailed above, NLP in the Chinese biomedical field is currently incomparable to its English counterpart. There is a large amount of

open medical text data, corpus (JNLPBA, NCBI, BC2GM, etc.) and related  
50 research competitions (e.g., i2b2, SemEval, TREC Medical/CDS) [11] that deal  
with NLP tasks in English in the biomedical field. For example, the 2020 and  
2019 studies [1, 12] on biomedical pre-trained language models were the pio-  
neers in the English field. And the evaluation of downstream tasks [13, 14]  
has recently begun to be adopted, proving the value of this emerging research  
55 field. Pre-trained language models, which have absorbed a lot of the Chinese  
biomedical domain knowledge, can benefit the related Chinese NLP tasks. A  
Chinese medical record can be served as the context representation of medical  
terms and be used to train a model to enhance its capability in executing down-  
stream prediction-related NLP tasks. This also provides strong support for the  
60 construction of medical predictive intelligent systems.

In this study, we designed a Stacked Residual Gated Recurrent Unit Convo-  
lutional Neural Networks (StaResGRU-CNN) combined with the pre-trained  
SOTA language models for prediction tasks based on biomedical texts and  
achieved competitive performance in these tasks. We also introduce CMed-  
65 Language Models (CMedLMs), a series of domain-specific, pre-trained language  
models for downstream tasks with Chinese biomedical textual data. The series  
is made up of 3 major pre-trained language models (BERT, Word2Vec, GloVe)  
trained with a large, real Chinese biomedical corpus. We use them (CMed-  
BERT, CMed-Word2Vec, and CMed-Glove) with their downstream models (in-  
70 cluding our proposed) to perform three text-based prediction tasks with different  
granularity (Clinical Named Entity Recognition [a term fragment boundary and  
category prediction task], Biomedical Text Classification [label prediction task],  
and Free-form Text EMR-based Disease Diagnosis Prediction) in detailed and  
extensive comparative experiments (including ablation experiments). In addi-  
75 tion, we also discuss some practical difficulties with EMR-based clinical diag-  
noses. This research is also currently the first comprehensive work of pre-trained  
biomedical models with extensive experimental evaluations to the best of our  
knowledge. This contributes to medical predictive intelligence tasks related to  
biomedical NLP.

## 80 **2. Related Works**

### *2.1. Predictive Intelligence*

Predictive intelligence is very good at dealing with known knowns and can fill the gap between know unknowns well. This is usually done through a large amount of historical data or prior knowledge as the training samples so that the  
85 model can learn the information carried in these massive data to solve specific predictive tasks [15, 16, 17, 18, 19]. These predictive tasks also play many roles in the field of natural language processing [20, 21, 22, 23, 24]. Most predictive NLP tasks can be transformed into discrete data-oriented classification tasks. Therefore, the label prediction of text sequences at different granularities can be  
90 clearly defined as multi-class classification, multi-label classification, or sequence labeling tasks (e.g., Named Entity Recognition, a term fragment boundary and category prediction task).

And the machine cannot predict unprecedented things. Therefore, in many cases, the machine has a high probability of making a misjudgment in the  
95 prediction of unknown data. And through large-scale transfer learning (e.g., pre-training language model) or incremental learning of known knowledge from external sources, it ameliorates the weaknesses of the correct results inferred by the wrong decision-making process or similar situations. This can also enhance the decision-making accuracy and robustness of predictive intelligence to  
100 a certain extent.

### *2.2. Deep Learning-based NLP*

Deep learning technologies derived from neural network models are the most researched machine learning entities in the contemporary academic field. Many studies proved the effectiveness of these models and led to a change of views  
105 in the entire researcher community. Among them, the most representative of the deep learning models, including Convolutional Neural Network (CNN) and Recurrent Neural Network (RNN), are commonly used as models in developing natural language processing strategies. These are also widely used in many

major NLP tasks: sequential tagging, classification, text generation, etc. Studies confirmed the effectiveness of deep learning paradigms for sequence labeling tasks. Tomori et al. [25] proposed and trained a DNN+R model (a method that refers to real-world data to improve Named Entity Recognition (NER) specific to a domain.) and found that it performed much better on NER tasks than other simpler DNN models. Lample et al. [26] proposed two neural network architectures: a bidirectional LSTMs, with Conditional Random Fields (CRF), while another network constructs and segments labels, obtaining the best NER performance results ever reported in standard evaluation settings, even if compared to models that make use of use external resources, such as gazetteers. Bharadwaj et al. [27] added a layer of phoneme features to Lample et al.'s LSTM and achieved an even better performance in a monolingual setting using supervision.

Deep learning also challenges traditional methods in classification tasks. Venkataraman et al.[28] used LSTM-RNNs classifying unstructured medical descriptions, reaching accuracy and F1 score higher than those of decision trees [29] and random forests [30]. Mironczuk et al. [31] quantitatively analyzed the literature on text classification in springer, Elsevier, ACM, and IEEE repositories, studied what the most impacting elements in the performance of text classification tasks are. They found that many works relied on the generation of embeddings to provide richer semantic representations for classifiers [32, 33, 34, 35]. The authors also conducted a detailed literature review of machine learning type text classification methods, including neural networks. At the same time, deep learning model strategies are also constantly being updated iteratively. Du et al. [36] proposed recurrent BLS (R-BLS) and gated BLS (G-BLS), two novel text classification learning methods derived from a flat neural network known as Broad Learning System (BLS). These two methods can simultaneously learn from two sets of inputs, making them more accurate than LSTM. Thanks to the noniterative learning of BLS, the training process is faster than that of LSTM. Kim et al. [37] used a capsule network architecture for text classification tasks, proving how it provides more advantages than CNNs. At the same time, it also

140 proved that its accuracy is better than that of SA-LSTM [38], VA LSTM [39]  
and DCNN [40] on seven benchmark datasets.

### 2.3. Pre-trained Language Models

Pre-trained Language Models have been proven to improve the performance  
of NLP models based on deep learning [38, 41, 42, 43] on different benchmark  
145 datasets. Traditional vector representations with varying granularities (e.g.,  
Word2Vec [44] and GloVe [45]) tend to be uncontextualized and encapsulate all  
meaning within a single vector. However, some of the latest and most advanced  
models, like ELMo [41] and BERT [46], consider the context in which they  
operate and can consequently achieve better performance.

150 BERT [46] is a language model designed to pre-trained deep bidirectional  
representations from the unannotated text by collectively turning both the left  
and the right context in every layer. As a result, a pre-trained BERT model  
can be fine-tuned using only one additional output layer to create state-of-the-  
art (SOTA) models for a multitude of tasks, such as question-and-answering,  
155 language inference and named entity recognition, without any substantial task-  
specific architecture modifications [47].

## 3. Methodology

This research proposes the Stacked Residual Gated Recurrent Unit-Convolutional  
Neural Networks (StaResGRU-CNN). This method is inspired by the model  
160 structure of Recurrent Convolutional Neural Networks (RCNN) [48]. Compared  
with the previous method, this method has some improvements in multiple  
tasks. It can be divided into three aspects:

- Compared with Recurrent Neural Networks (RNN) as a model for text  
context information modeling, Gated Recurrent Unit (GRU) can handle  
165 long-distance dependencies better. Furthermore, compared with RNN and  
Long Short Term Memory (LSTM), it has a more simplified structure and  
fewer parameters, so the computing efficiency of each layer has a certain  
improvement.

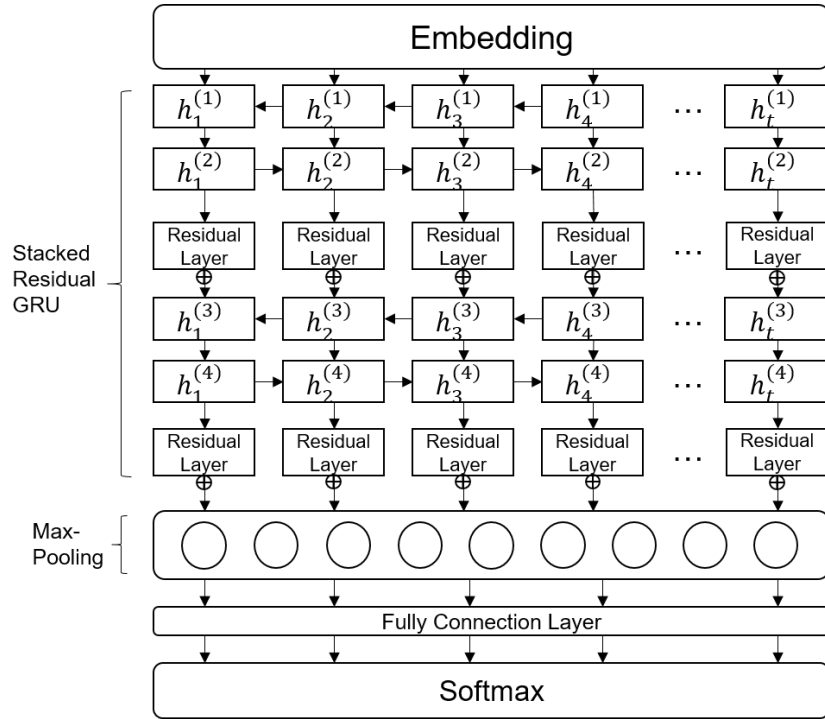


Figure 1: StaResGRU-CNN Structure

- This method uses Stacked GRU as the basis of feature modeling to represent features by constructing deeper networks.
- The Residual Connection is also introduced in Stacked GRU to center the layer gradients and the propagation error.

This model inherits the structural characteristics of RCNN: it makes full use of the advantages of RNN and CNN. Similar to the structure of RCNN, this model mainly creates a four-layer Stacked GRU (Dual Bidirectional GRU) with Residual Connection and combines Max-Pooling in CNN. The model can determine which features are critical in tasks related to classification to capture the key components in the text. Its specific structure is shown in Fig. 1.

The specific process can be divided into the following five steps:

- Use Stacked GRU to obtain contextual information.



- Add a Residual Layer after each BiGRU to speed up the convergence rate.
- Mapping the vectors to lower dimensions.
- At each position in the hidden size vector, take the maximum value of the all-time series to obtain the final feature vector (Max-Pool).
- 185 • Softmax classification.

Therefore, the proposed model can be expressed in the following parts:

### 3.1. Stacked Residual GRU

As a variant of RNN, GRU uses the current input  $x_t$  and the hidden state  $h_{t-1}$  passed down from the previous node. This hidden state contains information about the previous node. By combining  $x_t$  and  $h_{t-1}$ , GRU will get the output of the current hidden node  $y_t$  and the hidden state  $h_t$  passed to the next node. In the GRU, the gate state is obtained through the state  $h_{t-1}$  transmitted from the previous node and the input  $x_t$  of the current node. Among them,  $r$  represents the reset gate, and  $z$  represents the update gate.  $\sigma$  is the sigmoid function, through which the data can be transformed into a value in the range of  $[0, 1]$  to act as a gate signal.

$$r_t = \sigma(W_r \cdot [h_{t-1}, x_t]) \quad (1)$$

$$z_t = \sigma(W_z \cdot [h_{t-1}, x_t]) \quad (2)$$

After obtaining the gate signal, first to use the reset gate to get the data  $r_t \cdot h_{t-1}$  after “reset”, then concatenate  $h_{t-1}$  with the input  $x_t$ , and then scale the data to the range of  $[-1, 1]$  through  $\tanh$  activation function, that is:

$$\tilde{h}_t = \tanh(W \cdot [r_t \cdot h_{t-1}, x_t]) \quad (3)$$

200 The  $h'$  here mainly contains the current input  $x^t$  data and specifically adds  $h'$  to the current hidden state, which can also be considered as “Memorized the state of the present moment.”

Another key process is to “renew” the memory. This stage includes two sub-steps: forgetting and remembering. The updated expression is as follows:

$$h_t = (1 - z) \odot h_{t-1} + z \odot h' \quad (4)$$

205 This step is to forget the information of some dimensions in the passed  $h_{t-1}$ , and add the information of some dimensions input by the current node.

The gate signal  $z$  has a range of  $[0, 1]$ . The closer to 1, the more data is “remembered”, and the closer to 0 the more “forgotten”.  $(1 - z) \odot h_{t-1}$  represents the selective “forgetting” of the original hidden state.  $z \odot h'$  means  
210 to selectively “memorize” the  $h'$  containing the current node information.

In our model, we stack multiple layers of bidirectional GRU (BiGRU) together, where the hidden representation  $h_t^{(l)}$  of the previous layer is used as the input of the next layer, and  $l$  is the layer. Therefore, the hidden state of time  $t$  in the  $l$  layer can be expressed as:

$$\overleftarrow{h}_t^{(l)} = \overleftarrow{GRU} \left( x_t, \overleftarrow{h}_{t-1}^{(l)} \right) + x_t \quad (5)$$

$$\overrightarrow{h}_t^{(l)} = \overrightarrow{GRU} \left( x_t, \overrightarrow{h}_{t-1}^{(l)} \right) + x_t \quad (6)$$

### 215 3.1.1. Residual Connection Layer

When multiple layers of neurons are stacked, the neural network will degenerate due to the low convergence speed of training errors. However, the residual network can solve this problem. Therefore, inspired by ResNet [49], we add Residual Connection Layer at the end of each BiGRU. This method accelerates  
220 convergence by transferring residual information. Inspired by Toderici et al. /citetoderici2017full,  $h_t^{(o)}$  represents output, and  $W$  and  $U$  represent convolutional linear transformation. i.e., they are composites of Toeplitz matrices with padding and stride transformations.

$$h_t = (1 - z_t) \odot h_{t-1} + z_t \odot \tanh(Wx_t + U(r_t \odot h_{t-1})) + \alpha_h W_h h_{t-1} \quad (7)$$

$$h_t^o = h_t + \alpha_x W_{ox} x_t \quad (8)$$

In addition, each Residual Connection Layer will not add any additional  
 225 parameters that need to be learned, so it will not increase the complexity of the  
 model.

### 3.2. Max-pooling, Fully Connection Layer and Softmax

#### 3.2.1. Max-pooling

The overall structure of the StaResGRU-CNN mainly uses Stacked GRU to  
 230 replace the convolutional layer in CNN to obtain the semantic representation of  
 the context and combines the Max-pooling layer in CNN. Through this layer, a  
 fixed-length vector can be obtained. And obtain the latent semantic information  
 that best represents the meaning of the text.

$$y^{(2)} = \max_{i=1}^n y_i^{(1)} \quad (9)$$

#### 3.2.2. Fully Connection Layer

$$y^{(3)} = W y^{(2)} + b \quad (10)$$

#### 235 3.2.3. Softmax

Finally classify through Softmax.

$$p_i = \frac{\exp(y_i^{(3)})}{\sum_{k=1}^n \exp(y_k^{(3)})} \quad (11)$$

## 4. Tasks Description

### 4.1. Pre-trained Language Model

The combination of various language models to enhance the effect in NLP  
 downstream tasks has proven to be effective [50]. Researchers have lately been

240 applying prior external knowledge in specific fields to run downstream tasks, ef-  
fectively improving the adaptability and accuracy of these results. Since the cur-  
rent research development in the field of Chinese biomedical language models is  
almost none, the research also focuses on introducing Chinese biomedical knowl-  
edge into language representation models. Through this potential paradigm, it  
245 will attempt to improve downstream tasks related to Chinese biomedical NLP.  
Therefore, inspired by the idea in [50], we divide the pre-trained language model  
into two categories according to the characterization type: Word Embedding  
(Word2Vec, GloVe) and Seq2Seq (BERT).

#### 4.2. *Fine-Tuning the Pre-trained Language Models*

250 A language representation model is greatly influenced by the scale and qual-  
ity of the training data in downstream training tasks. Most of the existing pre-  
trained language models use commonly available data, such as online encyclo-  
pedias, Q&A discussion groups, and forums as sources [51, 46, 52]. For another,  
biomedical texts contain a large number of specific expressions (such as “Radical  
255 thyroidectomy for thyroid carcinoma”) and proper nouns (e.g., “Electronic Med-  
ical Record Basic Dataset Specification of P.R.China”), which are understand-  
able by professional medical practitioners only. Consequently, language models  
that are pre-trained using wide-domain sources have more limited performance  
in specific downstream tasks belonging to the biomedical field. Especially im-  
260 portant when dealing with Chinese biomedical texts, it is necessary to consider  
the number of training samples available, the word segmentation accuracy, the  
vocabulary, and the expressions’ diversity, as well as the coding uniformity of  
the characters (e.g., double-byte, single-byte, special symbols, GBK encoding),  
the expertise level of the authors, the uniformity of the text format specification  
265 and the quality of the dataset (noise content ratio), among other constraints.  
On a semantic level, understanding the meaning of sentences is more difficult  
in Chinese than in English [53]. Therefore, a pre-trained model, trained with  
specialized medical data in Chinese, will be used for solving three main biomed-  
ical NLP fine-grained prediction-related tasks (Clinical NER, Biomedical Text

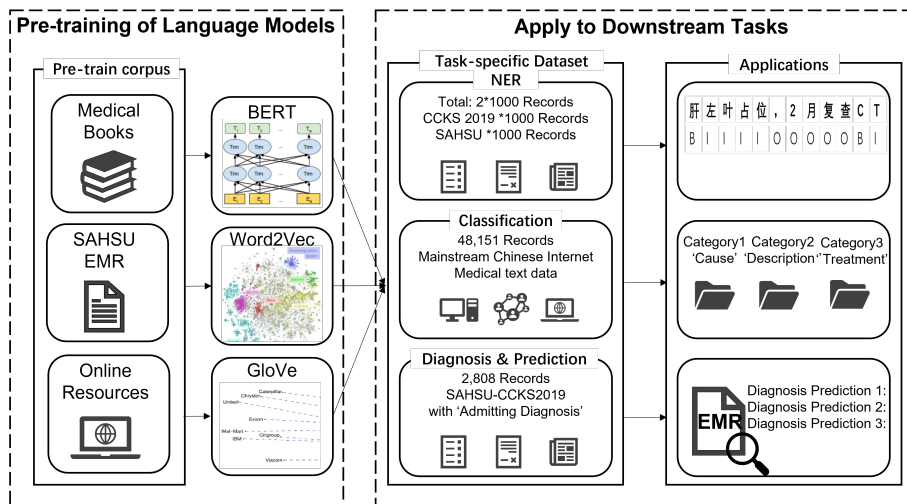


Figure 2: Overview of the overall structure of Chinese Medical Language Models (CMedLMs)

270 Classification, and Free-form Text EMR-based Disease Diagnosis Prediction). Both crowdsourced and actual Chinese EMR datasets are used in the experiments to evaluate the performance of the pre-trained language models on the various downstream tasks (Fig. 2).

#### 4.2.1. Clinical Named Entity Recognition (Clinical NER)

275 Clinical NER, an essential task in biomedical text mining, includes the identification of a large amount of domain-specific nouns and can be transformed into NLP extraction and classification tasks [54, 55]. Specifically, in the biomedical field, its task can be described as: “For a given set of EMR text documents, identify and extract all medical nouns, then classify them into one of some pre-  
280 defined categories (e.g., diseases, treatments, examinations).” Many researchers are currently focusing on a type of pipeline that combines LSTM and CRF. Others focus on this type of incremental pipeline [56, 57] instead. And other SOTA methods adopt pre-trained language models to obtain words or even characters representations [58, 59, 60]. However, in these models, biomedical-specific  
285 knowledge is not usually included as prior knowledge, thus limiting their effectiveness. Meanwhile, this task can be regarded as a fine-grained predictive task

at the next level to a certain extent. This prediction task aims to enable the model to recognize the boundaries of term fragments in the text sequence and which category the fragments within a certain byte range belong to.

#### 290 4.2.2. *Biomedical Text Classification*

Biomedical Text Classification is one of the main tasks of Biomedical NLP. Its goal is to infer a label (or a collection of labels) for a given text (be it a sentence, a document, etc.). Its role in the biomedical field is to label texts based on their specific area of interest. Classification is an indispensable core  
295 step in information retrieval, leading to automatic sorting of electronic medical records, hospital outpatient guiding robots, doctor-patient dialogue intention identification, Disease Diagnosis Prediction and more. Moreover, it is also a fine-grained category prediction task based on prior knowledge/expert experience. Therefore, as one of the most critical downstream tasks in the NLP field [61,  
300 62, 11], classification can be used as a task to evaluate the performance of pre-trained models. We use biomedical data captured from the four mainstream Chinese online medical knowledge encyclopedias (Tab. 2) in order to test the performance of the multi-class classification task. We will finally compare these results with those of the original models we used have used before applying any  
305 changes.

#### 4.2.3. *Free-form Text EMR-based Disease Diagnosis Prediction*

Outpatient diagnostic records contain a detailed history of the progression and treatment of a patient’s illness. When visiting outpatients, doctors make some initial judgments on likely diseases based on patients’ chief complaints,  
310 past medical history, and medical conditions. This information is of great help in possible later stages to accelerate diagnosis processes.

Free-form Text EMR-based Disease Diagnosis Prediction is a contextualized action derived from the classification task. However, this task has higher requirements than ordinary classification tasks: for example, it has a larger number of  
315 disease diagnosis labels (Super Multi-class Classification). There are also many

cases where a single medical record can diagnose multiple diseases (Multi-label Classification). In our study, the diagnosis of a patient with an illness is inferred from two pieces of data: a similar diagnosis found in the EMR dataset and information specific to the patient, such as the content of the patient’s complaint, the history of the illness, on-site checkups, etc.

By training the model on the contents of EMRs and using preliminary diagnostic information (labels), the task can be transformed into super multi-class and multi-label classification (each disease diagnosis being a label) with EMR text mining. Therefore, we model the HPI (History of Present Illness) records in the EMRs and use the information from the corresponding “initial diagnosis”, or “admitting diagnosis”, as label sets to train and test the model and make diagnostic predictions for a given disease record; then, using multiple deep learning models, we analyzed the contents of a medical record to predict the most likely disease given the symptoms. This will benefit the medical community as a way to provide doctors with a predictive reference for diagnosis through expert experience (a large amount of potential knowledge stored in biomedical text data, including electronic medical records, medical books, encyclopedias, etc.).

## 5. Experiments

### 5.1. Experimental Environment

The machine where we deployed our CMed-BERT pre-trained model a TPU v3-8 (128 GiB VRAM), with 4 vCPU and 15 GB of RAM. The CMed-Word2Vec and CMed-GloVe models and their downstream tasks are trained with dual NVIDIA 1080Ti GPUs (with 11 GB VRAM for each), an Intel Xeon CPU E5-2678 v3 and 64GB of RAM.

### 5.2. Description of Pre-train Corpora and Downstream Tasks’ Datasets

#### 5.2.1. Description of Pre-train Corpora

We have collected a large amount of Chinese biomedical literature and real-world electronic medical record data (both in Chinese and English) for pre-

345 training our language models. These are mainly taken from 3 sources: Chinese online biomedical encyclopedias, EMR datasets provided by the Second Affiliated Hospital of Soochow University (SAHSU, the large version), and Chinese biomedical books. The specific quantities, categories, and other relevant information can be found in Tab. 1.

Table 1: Description of Pre-trained Corpora

Corpus Source	Corpus Description	Size (Chinese Characters)
Medical Books	We used 13 books as a corpus, including <i>Manual For ICU Attending Doctor</i> , <i>Reading X-ray Guide</i> , <i>CT Diagnostics</i> , <i>Immunology</i> , <i>Pathology</i> , <i>Clinical Drug Therapy</i> , <i>Psychiatry</i> , <i>Clinical Electrocardiogram Detailed Analysis and Diagnosis</i> , <i>Tumor</i> , <i>Surgery</i> , <i>Hyperemia</i> , <i>Gynaecology</i> and other books of disciplines.	4,384,503 (4M)
SAHSU <sup>5</sup>	The electronic medical records of the Second Affiliated Hospital of Soochow University, including 5,090 electronic medical records from the 3 departments of General Surgery, Intervention and Oncology from the last 2 years.	2,002,202 (2M)
Online Resources	From the 4 mainstream Chinese websites in the medical field named "39 Health" <sup>1</sup> , "XunYiWenYao" <sup>2</sup> , "Feihua Health" <sup>3</sup> , "NetEase Health" <sup>4</sup> to capture the text data about medical encyclopedias such as disease symptoms, drugs, medical term explanations, medical cases, treatment plans, etc.	29,092,216 (29M)

<sup>1</sup> www.39.net, <sup>2</sup> www.xywy.com, <sup>3</sup> www.fh21.com.cn, <sup>4</sup> jiankang.163.com, <sup>5</sup> The large version of SAHSU electronic medical records dataset, separated from the full version of the SAHSU dataset.

### 350 5.2.2. Description of Downstream Tasks' Datasets

We have selected specific datasets for different tasks, which are all mainly composed of EMRs and online open medical text data. Details are listed in Tab. 2.

Table 2: Description of Downstream Tasks' Datasets

Task Name	Dataset Description	Size (Records)
Clinical Named Entity Recognition	1,000 randomly selected labelled Electronic Medical Records from CCKS 2019 and SAHSU <sup>1</sup> respectively for testing Clinical Named Entity Recognition task	2 × 1,000 records
Biomedical Classification	The dataset is taken from 4 mainstream Chinese online medical encyclopedias and Q&A websites (Refer to the "Online Resources" section of the table above), for a total of 48,151 records. These typically include 6 sections: "Cause", "Description", "Diagnosis", "Prevention", "Symptom", "Treatment". These sections are used as the basis for multi-class classification.	48,151 records
Free-form Text EMR-based Disease Diagnosis & Prediction	An EMR-based Disease Diagnosis Prediction dataset with "Admitting Diagnosis" labels integrated by SAHSU <sup>1</sup> and CCKS 2019 after data cleaning. (Named SAHSU-CCKS)	2,808 records

<sup>1</sup> The small version of SAHSU electronic medical records dataset, separated from the full version of the SAHSU dataset



### 5.3. Pre-training Seq2Seq Language Models Process

355 BERT is a huge Seq2Seq type language model; Its training process is longer and more complicated than that of Word Embedding type models. When pre-training CMed-BERT, due to the huge memory consumption of the BERT and the limited memory of the TPU (TPU v3-8 with 128 GB of memory), the training program can only be run when the batch size is adjusted to 32 and the  
360 maximum sequence length is adjusted to 384. Pre-training included 120k steps and took 12 days, 20 hours, 11 minutes 10 seconds, with a final loss of 1.633, which is already a relatively ideal result.

The hyper-parameter settings for pre-training CMedLMs (CMed-BERT, CMed-Word2Vec and CMed-GloVe) and different types of downstream models can be  
365 found in Tab. 3-6.

In addition, the hyperparameter settings of our proposed model depend on the tasks involved and the datasets used. Therefore, we refer to and adopt the hyperparameter setting strategies commonly used in previous studies to set specific parameters for different tasks and datasets. The general parameter  
370 settings used in the different datasets of the three tasks in the experiment include the batch size is 64, epochs are 100, dropout is 0.5, the activation function in CNN is ReLu, and the final activation layer of the overall model using Softmax.

Table 3: List of Hyper-parameters Settings and Training Process Data Records for Pre-training CMed-BERT

<b>max_predictions_per_seq</b>	77
<b>max_sequence_length</b>	384
<b>learning_rate</b>	1e-4
<b>num_warmup_steps</b>	10,000
<b>batch_size</b>	32
<b>smoothed</b>	1.625
<b>num_train_steps</b>	120.00k
<b>time-consuming</b>	12d 20h 11m 10s
<b>final loss</b>	1.633

Table 4: List of Hyper-parameter Settings for Pre-training CMed-Word2Vec<sup>1</sup>

<b>sentences</b>	None	<b>workers</b>	3
<b>size</b>	100	<b>min_alpha</b>	0.0001
<b>alpha</b>	0.025	<b>sg (skip-gram)</b>	0 (disable, adopt CBOW)
<b>window</b>	5	<b>negative</b>	5 (negative sampling, 5 noise words)
<b>min_count</b>	5	<b>cbow_mean</b>	1 (enable)
<b>max_vocab_size</b>	None	<b>hashfxn</b>	hash
<b>sample</b>	1e-3	<b>iter</b>	5
<b>seed</b>	1	<b>null_word</b>	0
<b>trim_rule</b>	None (min_count)	<b>sorted_vocab</b>	1
<b>batch_words</b>	MAX_WORDS_IN_BATCH	<b>hs (hierarchica softmax)</b>	0 (negative sampling)

<sup>1</sup> The overall hyper-parameter setting of CMed-GloVe is consistent with CMed-Word2Vec.

Table 5: List of Hyper-parameter Settings for the Overall Models and LSTM/GRU Components

<b>batch_size</b>	64
<b>epochs</b>	100
<b>dropout</b>	0.4
<b>bilstm_units</b>	512
<b>dense_units</b>	512
<b>dense layers activation</b>	Softmax

Table 6: List of Hyper-parameter Settings in the CNNs Component

<b>filters</b>	64
<b>kernel_size</b>	3
<b>padding</b>	same
<b>activation</b>	ReLU

To compare the effects of different semantic segmentation (Chinese word segmentation) applied to biomedical texts, we designed two types of segmentation methods to operate on raw corpus: word-level and character-level segmentation. In CMed-Word2Vec and CMed-GloVe, a corpus of nearly 36 million characters was mapped to both word vectors and character vectors for training purposes, after going through the processes of word segmentation and character

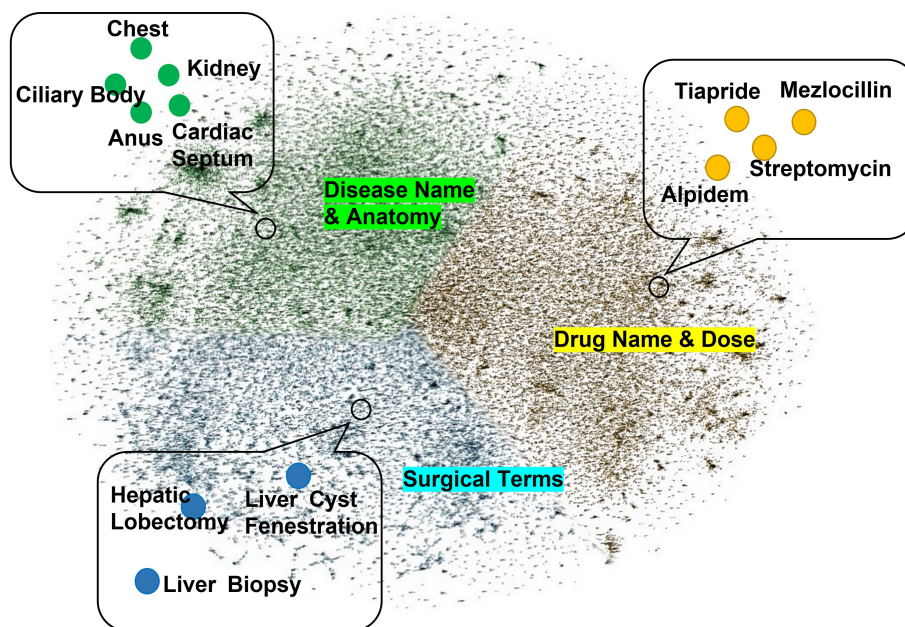


Figure 3: 2-D scatter graphs of CMed-Word2Vec (Word-Level)

segmentation, and finally generates a 50-dimensional vector for each word or  
 380 character. Consequently, we obtained a total of 4-word embedding models: 2  
 CMed-Word2Vec models (Word-Level and Character-Level) and 2 CMed-GloVe  
 models (Word-Level and Character-Level). Fig. 3 shows 2-D scatter graphs of  
 the word vectors (CMed-Word2Vec). Taking Fig. 3 as an example (approximate  
 range), the drug name and dose are mainly embedded in the yellow region. The  
 385 anatomy term and disease name are mainly concentrated in the green region;  
 the blue area mostly contains the vocabulary of surgical terms. These word  
 embeddings are trained from a large-scale biomedical corpus containing mixed  
 Chinese and English.

Additionally, we conduct detailed ablation studies to verify the actual perfor-  
 390 mance of the following three types of language models on different downstream  
 tasks: bare embedding, the original pre-trained language models (based on gen-  
 eral knowledge pre-training), the Chinese biomedical models (based on Chinese  
 biomedical domain knowledge pre-training). In these models, we use GloVe

pre-trained based on the official offline version of Wikipedia (Chinese) [63] and  
395 Word2Vec pre-trained on Chinese Wikipedia and Baidu encyclopedia<sup>6</sup> [64] as  
the word embedding for ablation experiments. At the same time, we also use  
“BERT-Base, Chinese” [46] provided by Google as the embedding of the original  
BERT model. For the bare embedding method in the ablation experiments, a  
random parameter initialization method is used to generate each token vector.

## 400 6. Results and Analysis

### 6.1. Clinical Named Entity Recognition

CCKS 2019 Task1 is an academic evaluation task for Chinese EMR Named  
Entity Recognition. The dataset published together with the task is also the  
largest and only open Chinese EMR medical entity recognition dataset glob-  
405 ally. Its records are organized in 6 categories: “Drugs”, “Anatomical Sites”,  
“Diseases and Diagnoses”, “Surgery”, “Laboratory Inspection”, and “Image Ex-  
aminations”. We randomly selected 1,000 complete samples and divided them  
into 3 datasets for training, validation, and testing with an 8:1:1 random split  
before training. In addition, we have also used the EMRs provided by the Sec-  
410 ond Affiliated Hospital of Soochow University, randomly selecting 1,000 sample  
records and splitting them into the same categories as above. To uniform the  
two datasets, we manually labeled the latter records to give each of the six cat-  
egories of the dataset from CCKS 2019 Task1. The annotation specification is  
also consistent with the details in CCKS 2019 Task1.

#### 415 6.1.1. CCKS 2019

On the CCKS 2019 dataset, the performance of CMed-BERT compared to  
vanilla BERT on the five downstream models has an average of F1-Score im-  
provement of 2.04% per model. The average of F1-Score of each downstream  
model reached 73.31%, whereas the official BERT has 71.27% and fine-tuned

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<sup>6</sup>baike.baidu.com

420 BERT 72.56%. In addition, compared to word embedding models like general GloVe, Word2Vec, and Bare Embedding, CMed-BERT performs better, with a higher average of F1-score of 18.98%, 16.82%, and 13.35%, respectively. Among these models, the best-performing one follows a CMed-BERT-StaResGRU-CNN-CRF pipeline; its F1-Score reached 76.32%, 1.33% higher  
425 than with a BERT-ResGRU-CNN-CRF pipeline (the best performing pipeline for BERT). The performance of CMed-Word2Vec (Word-Level & Character-Level) and CMed-GloVe (Word-Level & Character-Level) is less than that of CMed-BERT and BERT. The average F1-Scores of CMed-Word2Vec are 68.01% and 64.33% for its Word-Level and Character-Level variants, respectively. The  
430 difference between the two is 3.68%, which is higher than the difference between CMed-BERT and BERT (i.e., 2.04%). These performances are poorer than those of CMed-BERT and BERT, but better than those of CMed-GloVe Word-Level (56.10%) and Character-Level (55.94%).

### 6.1.2. SAHSU

435 Using the SAHSU dataset, the gap between the performance of similar language models in each downstream model is smaller than that using CCKS 2019. The average of F1-Score performance gap of models within the same class is always less than 1%. Precision, Recall, and F1-Score stats of the models, compared with those found using CCKS 2019, have shown better results (the overall  
440 average of F1-Score being 16% higher than with CCKS 2019). Compared with the general pre-training models, CMedLMs increased the performance of each downstream model by an average of 4.64%. Among them, the best-performing model is still CMed-BERT-ResGRU-CNN-CRF (improving upon the BERT-ResGRU-CNN-CRF pipeline by 2.21% and upon a fine-tuned BERT by 3.53%  
445 in their F1-scores), which demonstrates how CMed-BERT contributes to the performance on NER tasks.

Fig. 4 and Fig. 5 show how the F1-Scores of different pre-trained language models change during training and the difference in performance between these models. In summary, CMedLMs provide significant improvements in the perfor-

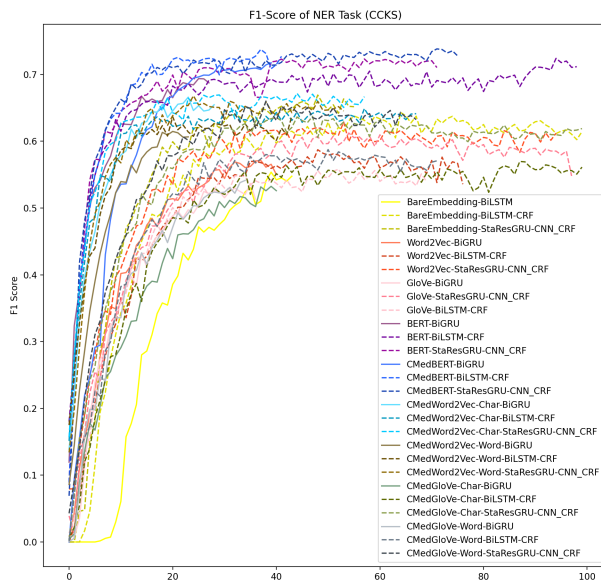


Figure 4: Performance of the top three pipelines under each type of embedding on the NER task (CCKS 2019)

450 mance of NER tasks. With the CCKS 2019 NER dataset, CMedLMs bring an additional 2.84% F1-Score improvement for each downstream model over general language models. On the SAHSU NER dataset, the performance showed a 4.64% increase. The best pipeline of CMed-BERT (which is CMed-BERT-ResGRU-CNN-CRF) shows improvements of 3.76% and 3.53% respectively on  
 455 the two datasets compared with fine-tuned BERT models (Tab. 7).

### 6.2. Biomedical Text Classification

The classification tests in this study use a dataset obtained and compiled from 4 mainstream Chinese biomedical Q&A and encyclopedia websites (see Tab. 2). This dataset can be split into 6 major categories. We tested a total of 45 pipelines based on 9 embeddings and a fine-tuned language model  
 460 to evaluate the different language models' performance. These pipelines are composed of the following deep learning models: CNN-LSTM, CNN, BiLSTM, StaResGRU-CNN, DPCNN [65, 66, 67, 68]. The data analyzed include the

Table 7: Results of the Clinical Named Entity Recognition Task

Embedding	Model	CCKS 2019					SAHSU						
		Params	P	R	F1	Time <sup>1</sup>	Loss <sup>2</sup>	Params	P	R	F1	Time <sup>1</sup>	Loss <sup>2</sup>
Bare Embedding	BiLSTM.CRF	3.17M	0.6267	0.6601	0.6408	28	4.62/845	3.14M	0.7804	0.8483	0.8129	28	2.87/874
	CNN.LSTM	1.34M	0.4789	0.5876	0.5277	2	0.08/0.17	1.31M	0.5907	0.7382	0.6562	2	0.06/0.18
	BiLSTM	2.66M	0.5559	0.6195	0.5849	3	0.08/0.14	14.7M	0.8181	0.8954	0.8543	3	0.06/0.13
	BiGRU	2.03M	0.5557	0.6083	0.5801	3	0.08/0.15	2.00M	0.7658	0.8622	0.8111	3	0.02/0.12
	StaResGRU-CNN_CRF	3.54M	0.6547	0.6794	0.6645	37	17.97/741	2.51M	0.8137	0.8770	0.8442	37	8.30/822
BERT (Original)	Fine-Tuning	-	0.7084	0.7540	0.7256	-	-	-	0.8375	0.8290	0.8511	-	-
BERT (official)	BiLSTM.CRF	15.2M	0.6897	0.7716	0.7282	54	1.80/736	15.2M	0.8297	0.8824	0.8549	54	2.01/955
	CNN.LSTM	17.8M	0.6033	0.6910	0.6421	24	0.08/0.10	1.78M	0.7518	0.8454	0.7953	15	0.03/0.07
	BiLSTM	14.7M	0.6852	0.7640	0.7214	28	0.02/0.11	14.7M	0.8181	0.8954	0.8543	19	0.01/0.08
	BiGRU	11.0M	0.7047	0.7437	0.7221	27	0.02/0.09	11.0M	0.8375	0.9037	0.8689	18	0.02/0.06
	StaResGRU-CNN_CRF	21.5M	0.7214	0.7820	0.7499	63	0.99/930	21.5M	0.8369	0.8944	0.8643	63	2.24/979
Word2Vec (General)	BiLSTM.CRF	3.45M	0.5582	0.6493	0.5981	28	11.37/793	3.45M	0.7912	0.8427	0.8159	28	2.09/969
	CNN.LSTM	1.22M	0.4588	0.5502	0.4984	2	0.09/0.19	1.23M	0.6145	0.7558	0.6772	2	0.04/0.16
	BiLSTM	2.93M	0.4772	0.5290	0.5005	4	0.08/0.17	2.94M	0.6742	0.7345	0.7021	3	0.06/0.12
	BiGRU	2.20M	0.5699	0.5777	0.5725	3	0.06/0.14	2.20M	0.7214	0.7872	0.7521	3	0.04/0.12
	StaResGRU-CNN_CRF	3.72M	0.6217	0.6929	0.6551	38	1.39/913	3.72M	0.8039	0.8659	0.8334	38	1.04/979
GloVe (General)	BiLSTM.CRF	3.04M	0.5740	0.6069	0.5886	28	5.68/711	3.04M	0.6906	0.7391	0.7116	28	5.02/811
	CNN.LSTM	1.20M	0.4432	0.4903	0.4641	2	0.10/0.23	1.21M	0.5598	0.6503	0.5984	2	0.07/0.14
	BiLSTM	2.52M	0.4959	0.5038	0.4980	3	0.07/0.20	2.53M	0.5939	0.6568	0.6210	3	0.07/0.13
	BiGRU	1.90M	0.5400	0.5840	0.5600	3	0.07/0.18	1.90M	0.6134	0.6688	0.6279	3	0.08/0.11
	StaResGRU-CNN_CRF	3.41M	0.6055	0.6087	0.6056	37	6.97/906	3.41M	0.7251	0.7586	0.7384	38	7.66/950
CMed-BERT	BiLSTM.CRF	15.2M	0.7201	0.7874	0.7516	54	1.70/796	15.2M	0.8331	0.8935	0.8618	54	0.78/1050
	CNN.LSTM	17.8M	0.6481	0.7248	0.6839	18	0.06/0.11	1.78M	0.7546	0.8472	0.7975	15	0.01/0.09
	BiLSTM	14.7M	0.7095	0.7536	0.7303	22	0.02/0.11	14.7M	0.8274	0.8991	0.8612	22	0.01/0.07
	BiGRU	11.0M	0.7125	0.7635	0.7367	20	0.02/0.09	11.0M	0.8407	0.9056	0.8716	18	0.02/0.08
	StaResGRU-CNN_CRF	21.5M	0.7240	0.8072	<b>0.7632</b>	63	2.21/899	21.5M	0.8669	0.9074	<b>0.8864</b>	63	1.06/951
CMed-Word2Vec (Char-Level)	BiLSTM.CRF	3.04M	0.6646	0.7515	0.7043	28	1.97/930	3.04M	0.7909	0.8575	0.8227	28	1.05/969
	CNN.LSTM	1.21M	0.5390	0.6484	0.5869	2	0.09/0.16	1.22M	0.6775	0.7956	0.7284	2	0.04/0.13
	BiLSTM	2.52M	0.6435	0.7060	0.6731	3	0.03/0.15	2.53M	0.7919	0.8566	0.8224	3	0.01/0.17
	BiGRU	1.90M	0.6725	0.7609	0.7133	3	0.04/0.13	1.90M	0.8186	0.8760	0.8459	3	0.01/0.14
	StaResGRU-CNN_CRF	3.41M	0.6937	0.7555	0.7229	38	1.15/1036	3.41M	0.8116	0.8816	0.8448	38	3.42/1100
CMed-Word2Vec (Word-Level)	BiLSTM.CRF	3.04M	0.6549	0.7213	0.6859	28	1.04/843	3.04M	0.7939	0.8585	0.8248	28	2.68/912
	CNN.LSTM	1.21M	0.4877	0.5907	0.5340	2	0.07/0.16	1.21M	0.6633	0.7863	0.7182	2	0.04/0.12
	BiLSTM	2.52M	0.6045	0.6664	0.6330	3	0.04/0.14	2.53M	0.7742	0.8464	0.8083	3	0.02/0.17
	BiGRU	1.90M	0.6071	0.6686	0.6349	3	0.03/0.14	1.90M	0.7773	0.8529	0.8125	3	0.02/0.12
	StaResGRU-CNN_CRF	3.41M	0.6980	0.7636	0.7287	38	2.81/866	3.41M	0.8535	0.8881	0.8701	37	2.02/871
CMed-GloVe (Char-Level)	BiLSTM.CRF	2.84M	0.6223	0.6727	0.6462	28	0.88/941	2.84M	0.7786	0.8353	0.8057	28	3.08/987
	CNN.LSTM	1.20M	0.4193	0.5011	0.4554	2	0.11/0.17	1.20M	0.6470	0.7660	0.7004	2	0.04/0.14
	BiLSTM	2.32M	0.4857	0.5259	0.5046	3	0.08/0.17	2.32M	0.6881	0.7660	0.7231	2	0.04/0.12
	BiGRU	1.74M	0.5152	0.5727	0.5415	3	0.07/0.16	1.74M	0.7180	0.8076	0.7595	3	0.04/0.10
	StaResGRU-CNN_CRF	3.26M	0.6293	0.6907	0.6577	37	1.20/874	3.26M	0.8098	0.8631	0.8355	38	1.48/895
CMed-GloVe (Word-Level)	BiLSTM.CRF	2.84M	0.5965	0.6285	0.6113	28	2.08/730	2.84M	0.7885	0.8353	0.8111	28	1.62/990
	CNN.LSTM	1.20M	0.4151	0.4849	0.4465	2	0.10/0.18	1.20M	0.6375	0.7613	0.6925	2	0.04/0.19
	BiLSTM	2.32M	0.4772	0.5290	0.5005	3	0.09/0.18	2.32M	0.6935	0.7539	0.7208	3	0.04/0.09
	BiGRU	1.74M	0.5689	0.5849	0.5757	3	0.07/0.14	1.74M	0.7287	0.7937	0.7573	3	0.04/0.08
	StaResGRU-CNN_CRF	3.26M	0.6310	0.7001	0.6632	38	2.63/827	3.26M	0.8166	0.8603	0.8373	38	4.92/995

<sup>1</sup> Time (s/epochs), <sup>2</sup> Loss/Valid Loss

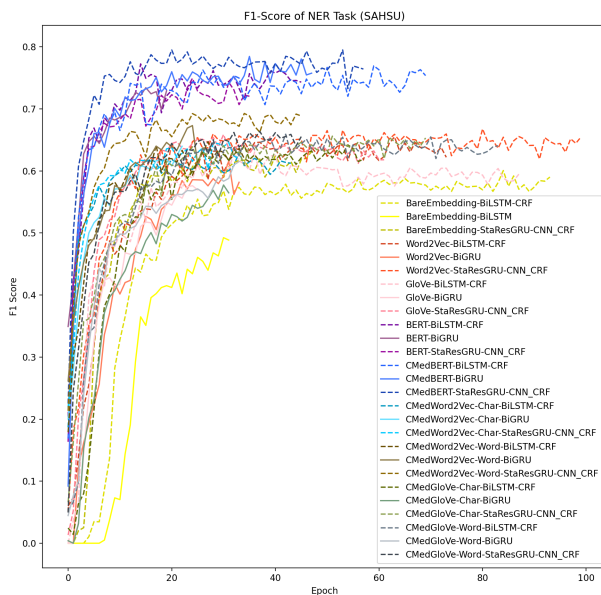


Figure 5: Performance of the top three pipelines under each type of embedding on the NER task (SAHSU)

number of trainable parameters, the time spent for each epoch, the F1-Score, and the final epoch’s loss and validation set loss (more details in Tab. 8).

The experimental results show that the performance of the task-specific model is ideal in multi-class classification tasks, reaching an F1-Score of more than 90%. And the average of the F1-Scores of the models based on CMed-BERT reached 95.42%, which is 0.23% higher than the average of the F1-Scores of the BERT-based ones and also higher than fine-tuned BERT (95.28%). In addition, it can be seen that the effect of the models based on CMed-Word2Vec and CMed-GloVe on multi-class classification tasks is not much different than that of the models based on CMed-BERT and BERT. However, both the quantity of parameters and the epoch time is significantly lower than the BERT-based pipelines. Therefore, CMed-Word2Vec and CMed-GloVe have higher comprehensive competitiveness in classification tasks than CMed-BERT and BERT. At the same time, CMed-Word2Vec (char & word levels) and CMed-GloVe (char & word levels) show better performances than general Word2Vec and GloVe (with



Table 8: The Performance of Chinese Biomedical Text Classification

Embedding	Model	Performance						Embedding	Performance					
		Params	P	R	F1	Time <sup>1</sup>	Loss <sup>2</sup>		Params	P	R	F1	Time <sup>1</sup>	Loss <sup>2</sup>
GloVe (General)	CNN-LSTM	0.06M	0.9387	0.9383	0.9383	12	0.11/0.20	Word2Vec (General)	0.07M	0.9464	0.9461	0.9460	12	0.11/0.18
	CNN	0.07M	0.9333	0.9306	0.9304	8	0.04/0.25		0.13M	0.9392	0.9390	0.9389	8	0.02/0.26
	BiLSTM	2.52M	0.9272	0.9268	0.9265	89	0.20/0.23		2.93M	0.9472	0.9470	0.9469	95	0.06/0.20
	StaResGRU-CNN	3.16M	0.9550	0.9541	0.9542	110	0.11/0.16		3.20M	0.9537	0.9528	0.9528	110	0.08/0.17
	DPCNN	2.03M	0.8288	0.6830	0.6450	97	0.02/0.81		2.10M	0.8706	0.7267	0.7413	100	0.02/0.86
BERT (official)	CNN-LSTM	0.35M	0.9575	0.9573	0.9572	587	0.10/0.14	CMed-BERT	0.35M	0.9603	0.9598	0.9599	573	0.10/0.14
	CNN	1.97M	0.9513	0.9491	0.9494	512	0.05/0.16		1.97M	0.9520	0.9510	0.9509	660	0.04/0.30
	BiLSTM	14.7M	0.9581	0.9579	0.9578	807	0.08/0.14		14.7M	0.9559	0.9555	0.9555	796	0.07/0.14
	StaResGRU-CNN	17.31M	0.9615	0.9612	0.9612	1030	0.09/0.15		17.30M	0.9639	0.9616	<b>0.9619</b>	1118	0.09/0.15
	DPCNN	4.26M	0.9408	0.9332	0.9339	1466	0.08/0.20		4.26M	0.9467	0.9431	0.9432	1522	0.09/0.24
CMed-Word2Vec (Char-Level)	CNN-LSTM	0.06M	0.9398	0.9383	0.9386	13	0.06/0.24	CMed-Word2Vec (Word-Level)	0.06M	0.9433	0.9431	0.9431	12	0.08/0.21
	CNN	0.07M	0.9119	0.9107	0.9105	9	0.04/0.39		0.07M	0.9303	0.9299	0.9299	9	0.04/0.28
	BiLSTM	2.52M	0.9431	0.9423	0.9424	80	0.02/0.27		2.52M	0.9391	0.9387	0.9385	81	0.01/0.29
	StaResGRU-CNN	3.16M	0.9566	0.9561	0.9562	101	0.09/0.19		3.16M	0.9580	0.9580	0.9579	100	0.07/0.17
	DPCNN	2.03M	0.9019	0.8814	0.8826	92	0.01/0.21		2.03M	0.9380	0.9339	0.9342	93	0.01/0.37
CMed-GloVe (Char-Level)	CNN-LSTM	0.05M	0.9484	0.9477	0.9476	16	0.14/0.20	CMed-GloVe (Word-Level)	0.06M	0.9425	0.9421	0.9421	18	0.12/0.19
	CNN	0.04M	0.9321	0.9321	0.9320	16	0.04/0.26		0.04M	0.9297	0.9296	0.9296	16	0.05/0.23
	BiLSTM	2.31M	0.9420	0.9420	0.9419	62	0.24/0.18		2.31M	0.9428	0.9422	0.9422	63	0.05/0.24
	StaResGRU-CNN	3.14M	0.9545	0.9536	0.9538	82	0.14/0.17		3.14M	0.9542	0.9537	0.9537	82	0.13/0.16
	DPCNN	1.99M	0.9279	0.9235	0.9232	64	0.06/0.44		1.99M	0.8889	0.8218	0.8248	60	0.02/0.51
Bare Embedding	CNN-LSTM	0.47M	0.9229	0.9210	0.9211	13	0.08/0.29	BERT (Original) Fine-Tuning	-	0.9335	0.9728	0.9528	-	-
	CNN	0.48M	0.9434	0.9430	0.9429	8	0.01/0.21		-	-	-	-	-	
	BiLSTM	2.93M	0.9430	0.9425	0.9425	88	0.07/0.25		-	-	-	-	-	
	StaResGRU-CNN	3.58M	0.9502	0.9496	0.9496	91	0.08/0.19		-	-	-	-	-	
	DPCNN	2.44M	0.9127	0.9084	0.9070	64	0.01/0.27		-	-	-	-	-	

<sup>1</sup> Time (s/epochs), <sup>2</sup> Loss/Valid Loss

an increase of 2.08%, 3.55% and 6.08%, 3.96%, respectively). These results also  
480 prove that language models pre-trained based on domain knowledge can better  
solve NLP downstream tasks, including classification.

### 6.3. Free-form Text EMR-based Disease Diagnosis Prediction

In the experiments of the Free-form Text EMR-based Disease Diagnosis Pre-  
prediction task, EMR data provided by the Second Affiliated Hospital of Soochow  
485 University and CCKS 2019 Task1 were both used for evaluation. We finally  
merged these two datasets into a new free-form text EMR-based Disease Di-  
agnosis Prediction dataset named SAHSU-CCKS, which contains 2,808 records  
with 44 types of disease diagnosis labels (Tab. 9).

Experiments assess the performance of 86 pipelines that are respectively  
490 based on the permutation and combination of 1 language model fine-tuning, 1  
Bare Embedding, 8 language models, and 10 mainstream deep learning models

with the same parameters (64 for batch size, 100 epochs, the sequence length of 512, 10 for early stopping and 0.4 dropout rate, see Tab. 5 & 6). The results are shown in Tab. 9.

495 The performance of CMed-BERT on diagnosis prediction tasks is generally higher than that of BERT. However, there are two exceptions, namely BiGRU and CNN-LSTM, based on CMed-BERT and yet perform slightly worse than their BERT counterparts. CMed-BERT achieved an average of F1-Score of 62.77%, almost 4% higher than BERT’s 58.84%. In the diagnosis prediction  
500 tasks, however, the best-performing models are not the same as for other tasks. In this latter case, the top 3 models are CMed-GloVe (Word-Level)-StaResGRU-CNN (76.60%), CMed-GloVe (Char-Level)-StaResGRU-CNN (74.50%) and CMed-Word2Vec (Char-Level)-StaResGRU-CNN (74.27%). For comparison, CMed-BERT-StaResGRU-CNN (73.48%) and BERT-StaResGRU-CNN (70.28%) only  
505 reached 73.48% and 70.28%, respectively. This shows how CMed-Word2Vec and CMed-GloVe are more performant in prediction tasks. From this densely distributed figure (Fig. 6), it is clear that these models showed a smaller F1-score gap during training in the prediction/classification task than in the NER task. Additionally, the CMedLMs model (with an average of F1-score of 57.2  
510 6% per model) has a higher competitive performance on this mixed task than general language models (with an average of the F1-scores of 52.52% per model) and Bare Embedding (with an average of F1-score of 46.06% per model). This also reflects the importance of Chinese Biomedical domain knowledge in related Biomedical NLP tasks.

## 515 7. Analysis and Discussion

### 7.1. Analysis

This study thoroughly evaluated the effect of pre-trained language models in various biomedical field tasks through sub-tasks such as Clinical NER, Biomedical Text Classification, Free-form Text EMR-based Disease Diagnosis  
520 Prediction. Upon analyzing the results, the best performing models in each

Table 9: Free-form Text EMR-based Disease Diagnosis Prediction Results of Comparison

Models		Performance						Performance						
Embedding	Model	Params	P	R	F1	Time <sup>1</sup>	Loss <sup>2</sup>	Embedding	Performance					
		Params	P	R	F1	Time <sup>1</sup>	Loss <sup>2</sup>		Params	P	R	F1	Time <sup>1</sup>	Loss <sup>2</sup>
GloVe (General)	CNN-LSTM	0.06M	0.2012	0.2412	0.2013	1	1.44/2.13	Word2Vec (General)	0.07M	0.2247	0.2645	0.2315	1	1.26/2.07
	CNN	0.07M	0.5540	0.5523	0.5293	1	0.22/1.43		0.13M	0.6319	0.6021	0.5950	1	0.07/1.03
	BiGRU	1.93M	0.4818	0.4845	0.4648	5	0.10/1.93		2.23M	0.4260	0.4135	0.4002	5	0.08/2.17
	CNN-GRU	0.05M	0.4419	0.4037	0.4040	1	0.45/1.95		0.06M	0.4941	0.4543	0.4407	1	0.59/1.75
	BiLSTM	2.56M	0.3631	0.3592	0.3448	6	0.22/2.62		2.96M	0.3852	0.3908	0.3666	6	0.42/2.39
	Dropout-BiGRU	0.16M	0.5619	0.5557	0.5309	3	0.87/1.54		0.2M	0.5996	0.6007	0.5792	3	0.75/1.33
	Dropout-AVRNN	0.17M	0.4746	0.4963	0.4691	3	0.95/1.30		0.20M	0.6193	0.6101	0.5920	3	0.76/1.16
	AVRNN	0.26M	0.6704	0.6803	0.6674	3	0.51/1.43		0.30M	0.5826	0.5966	0.5677	3	0.74/1.20
	AVCNN	0.82M	0.6769	0.5995	0.6054	2	0.50/1.23		1.12M	0.6651	0.6361	0.6259	2	0.44/1.08
	StaResGRU-CNN	3.14M	0.6316	0.6217	0.6113	7	0.80/1.20		3.18M	0.7174	0.6500	0.6457	7	0.82/1.19
BERT (official)	CNN-LSTM	0.35M	0.4287	0.3762	0.3823	38	0.48/1.80	CMed-BERT	0.35M	0.5731	0.5273	0.5285	39	0.30/1.69
	CNN	1.97M	0.5544	0.5300	0.5103	37	0.09/1.26		1.97M	0.5921	0.5562	0.5448	37	0.06/2.26
	BiGRU	11.0M	0.6091	0.5918	0.5741	49	0.03/1.31		11.0M	0.5971	0.5829	0.5631	47	0.04/1.38
	CNN-GRU	0.33M	0.6296	0.5835	0.5791	43	0.13/1.21		0.33M	0.6073	0.5802	0.5745	41	0.14/1.68
	BiLSTM	14.7M	0.6006	0.5696	0.5657	53	0.13/1.46		14.7M	0.6359	0.6259	0.6136	59	0.05/1.61
	Dropout-BiGRU	1.31M	0.6561	0.6506	0.6310	39	0.32/1.56		1.31M	0.7063	0.6826	0.6730	41	0.20/1.35
	Dropout-AVRNN	1.17M	0.6862	0.6585	0.6417	39	0.58/1.11		1.33M	0.6996	0.6861	0.6745	49	0.33/1.47
	AVRNN	1.33M	0.6610	0.6701	0.6488	46	0.17/1.21		1.33M	0.6976	0.7158	0.6911	44	0.14/1.15
	AVCNN	9.74M	0.6706	0.6605	0.6486	51	0.24/1.11		9.74M	0.6998	0.6971	0.6800	40	0.06/1.69
	StaResGRU-CNN	16.28M	0.7389	0.7114	0.7028	68	0.23/1.24		16.42M	0.7577	0.7534	0.7348	68	0.28/1.20
CMed-Word2Vec (Char-Level)	CNN-LSTM	0.55M	0.3164	0.3402	0.3159	1	0.54/1.77	CMed-Word2Vec (Word-Level)	0.06M	0.3793	0.3989	0.3684	1	0.65/1.77
	CNN	0.07M	0.5888	0.6029	0.5722	1	0.04/1.77		0.07M	0.6639	0.6298	0.6289	1	0.06/1.20
	BiGRU	1.93M	0.4465	0.4673	0.4267	5	0.11/2.89		8.14M	0.4663	0.4835	0.4577	5	0.11/2.16
	CNN-GRU	2.56M	0.4566	0.4420	0.4365	1	0.45/2.32		0.05M	0.5765	0.5212	0.5268	1	0.29/1.77
	BiLSTM	2.56M	0.4685	0.4883	0.4568	5	0.15/2.07		2.56M	0.4186	0.4621	0.4236	5	0.15/2.17
	Dropout-BiGRU	10.16M	0.6691	0.6649	0.6448	3	0.53/1.38		0.16M	0.6852	0.6789	0.6628	3	0.61/1.39
	Dropout-AVRNN	0.17M	0.7132	0.6939	0.6903	3	0.78/1.01		0.17M	0.7629	0.7365	0.7278	3	0.60/1.02
	AVRNN	0.26M	0.7457	0.7011	0.6989	4	0.38/1.42		0.26M	0.7187	0.7242	0.7040	4	0.16/1.52
	AVCNN	0.82M	0.3787	0.5036	0.4077	2	1.46/1.72		0.82M	0.5989	0.6583	0.6147	2	1.11/1.32
	StaResGRU-CNN	11.14M	0.7854	0.7473	0.7427	7	0.67/0.95		11.14M	0.7700	0.7280	0.7252	8	0.60/0.87
CMed-GloVe (Char-Level)	CNN-LSTM	0.06M	0.2944	0.2923	0.2797	1	1.08/1.59	CMed-GloVe (Word-Level)	0.06M	0.3564	0.3335	0.3197	1	1.01/1.62
	CNN	0.04M	0.6278	0.6170	0.6052	1	0.14/1.08		0.04M	0.6423	0.6268	0.6174	1	0.05/1.62
	BiGRU	1.77M	0.5138	0.5083	0.4883	5	0.04/1.88		3.10M	0.4520	0.4710	0.4432	5	0.04/3.03
	CNN-GRU	0.04M	0.5240	0.5203	0.5017	1	0.29/1.26		0.05M	0.4512	0.4721	0.4369	1	0.22/1.55
	BiLSTM	2.35M	0.4182	0.4007	0.3950	5	0.08/2.42		2.35M	0.3874	0.3845	0.3662	5	0.08/3.31
	Dropout-BiGRU	0.14M	0.7091	0.7088	0.6896	3	0.37/1.35		0.16M	0.6852	0.6789	0.6628	3	0.36/1.27
	Dropout-AVRNN	0.15M	0.5434	0.5496	0.5275	3	1.06/1.19		0.15M	0.6533	0.6396	0.6156	3	0.67/1.17
	AVRNN	0.25M	0.6643	0.6639	0.6540	3	0.40/1.03		0.25M	0.6690	0.6491	0.6354	4	0.54/1.17
	AVCNN	0.67M	0.7114	0.6942	0.6816	2	0.55/1.56		0.67M	0.7392	0.7014	0.6903	2	0.70/0.86
	StaResGRU-CNN	3.12M	0.7809	0.7542	0.7450	7	0.40/1.08		3.14M	0.8019	0.7647	<b>0.7660</b>	7	0.88/1.29
Bare Embedding	CNN-LSTM	0.21M	0.3260	0.3065	0.2931	1	1.129/1.89	BERT (Original) Fine-Tuning	-	0.6429	0.6207	0.6316	-	-
	CNN	0.22M	0.5000	0.4979	0.4719	1	1.11/1.45							
	BiGRU	2.08M	0.5100	0.5247	0.5000	5	0.20/2.37							
	CNN-GRU	0.20M	0.1705	0.2049	0.1720	1	1.25/2.22							
	BiLSTM	2.70M	0.3334	0.3436	0.3205	6	0.76/2.41							
	Dropout-BiGRU	0.31M	0.4934	0.4947	0.4812	3	0.78/1.54							
	Dropout-AVRNN	0.32M	0.6251	0.6123	0.6019	3	0.49/1.76							
	AVRNN	0.41M	0.5405	0.5478	0.5347	3	0.52/2.13							
	AVCNN	0.97M	0.6940	0.6497	0.6463	2	0.49/1.05							
	StaResGRU-CNN	3.29M	0.5968	0.5924	0.5845	9	0.56/1.34							

<sup>1</sup> Time (s/epochs), <sup>2</sup> Loss/Valid Loss

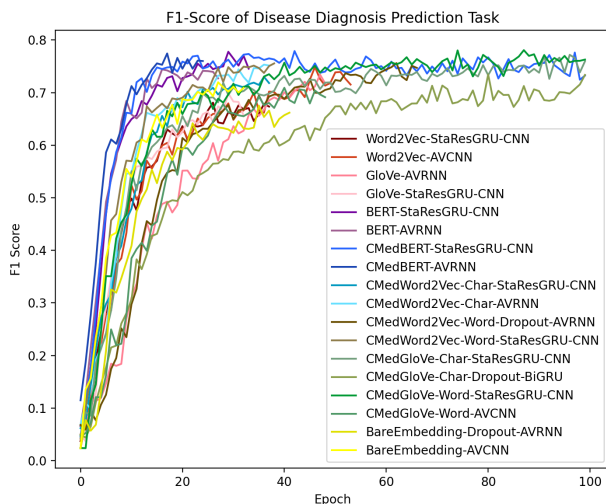


Figure 6: Performance of the top 2 models in each language model on the Free-form Text EMR-based Disease Diagnosis Prediction task

task are as follows: CMed-BERT-ResGRU-CNN-CRF (NER task, with CCKS 2019 dataset: F1 of 76.32%; with SAHSU dataset: F1 of 88.64%), CMed- BERT-StaResGRU-CNN (Classification task, F1: 96.19%), CMed-GloVe (Word-Level)-StaResGRU-CNN (Disease Diagnosis Prediction task, F1: 76.60%). In these 525 parallel comparative experiments combining different language models, the effectiveness of the proposed StaResGRU-CNN model has been verified.

Comparing the average of the F1-scores of CMed-BERT with other bare embedding’s pipelines shows that CMed-BERT’s is consistently higher. Following are the performance gains in comparison with average F1-scores of bare embedding’s pipelines: NER (CCKS: +13.35%, SAHSU: +5.99%), Classification (+2.16%) and Disease Diagnosis Prediction (+16.71%). The pipelines based on CMed-Word2Vec and CMed-GloVe have a similar performance with CMed-BERT and BERT in the Biomedical Classification and Disease Diagnosis Prediction tasks, but the number of parameters is smaller and each epoch takes a 530 shorter time, thus providing higher efficiency. Finally, these models do not rely heavily on powerful hardware (e.g., GPU, TPU), making them more easily deployable than CMed-BERT and BERT. In addition, CMedLMs perform higher

on average than general language models by 3.74% (2.84%, CCKS 2019 NER; 4.64%, SAHSU NER), 2.38% and 4.73% on the first three evaluation tasks, respectively. These gaps can also be observed as “stratification” in the training process visualization (Fig. 4-6). These performance improvements for multiple tasks help analyze large-scale datasets when deployed in online/streamed biomedical NLP tasks processing systems.

### 7.2. The role of *StaResGRU-CNN* and *CMedLMs* in predictive intelligence tasks

The proposed method is used as a deep learning model for decision-making tasks with different granularities and can be used for various predictive tasks related to discrete variables (e.g., prediction/classification attribute labels). As an integrated application based on the above tasks, predictive medical intelligence can achieve greater practical goals (e.g., prediction and decision-making tasks in the medical field) by integrating these complex prediction and decision-making tasks. According to the granularity level of decision/prediction/classification in their tasks, these goals can be transformed into specific applications (e.g., token boundary decision and type classification in clinical Named Entity Recognition) according to the granularity level of decision/prediction/classification contained in their tasks. Therefore, in different predictive intelligence tasks, the proposed model can exert different actual effects in different scenarios or domains according to the characteristics of the inputted dataset.

In addition, simple learning of latent patterns in specific tasks from data-driven models can gradually evolve into learning a large amount of prior experience to realize multiple complex prediction tasks. This exciting change will greatly promote the effective use of valuable but not yet annotated data. At the same time, these language models that “absorb” the “wisdom” stored in the large-scale corpus can be directly customized or combined with downstream task models to achieve ideal performance in multi-type prediction and decision tasks better. Therefore, the pre-trained language models also play an important role in predictive intelligence tasks.

## 8. Conclusion

This study proposed a Stacked Residual Gated Recurrent Unit-Convolutional Neural Networks (StaResGRU-CNN) combined with the pre-trained SOTA language models for prediction tasks based on biomedical texts. Our proposed  
570 stacked model increases the depth of the network. This makes the model have better nonlinear expression capabilities, can learn more complex transformations, and can fit more diverse feature inputs. At the same time, it makes the model have more powerful expression ability and feature learning layer by layer.  
575 And it can also perform long-term time series prediction and avoid overfitting. And the residual layer solves the degradation problem of the deep neural network well and makes the model converge faster. All of these features contribute to the model achieving the ideal results in the above-mentioned biomedical text-related predictive tasks.

The work also explores some issues that have not yet been solved and  
580 presents practical difficulties in the field of Chinese biomedicine. It proposes and validates the first pre-trained language model series in the Chinese biomedical field in response to those unsolved issues. It also proposes a novel free-form text EMRs-based Disease Diagnosis Prediction to support intelligent clinical  
585 assistants' design. These models are made according to 3 schemes (BERT, Word2Vec, Glove). Through transfer learning, a language model can assimilate a large amount of biomedical knowledge in Chinese to generate word representations that are more suitable for the biomedical field and support downstream prediction tasks. And extensive comparative experiments presented have also  
590 proved their effectiveness.

In conclusion, it was proved that bringing biomedical domain knowledge into general language models improves their performance in biomedicine-related tasks. Together with the tested medical tasks, the proposed StaResGRU-CNN model and the presented set of language models provide a framework for building  
595 smarter and more accurate automated clinical assistants and moving towards more efficient and humane HCI-oriented medical services.

## 9. Limitation and Future Work

The models proposed in this study suffer from several resources and implementation issues, mainly: limited diversity of the medical data available, limitations in computing power (hardware limitations), models' inability to identify polysemy, and take advantage of abbreviations and implicit semantics. In the future, we will solve the problems mentioned above accordingly.

We will also incorporate the Autoregressive-based language model, including the GPT type (e.g., GPT-2, GPT-3), into a broader evaluation. A more detailed investigation will also be conducted on the progress of embedding-based and transformer-based language models in the fields of biomedicine and medical psychology. The relevant language models that have been pre-trained in biomedical and medical psychology domain knowledge will be applied to more complex or comprehensive tasks (e.g., Lifelong Machine Learning, dialogue system).

Besides, the variety and content of medical data are continuously updated as we expand our knowledge on emerging diseases (e.g., COVID-19). How to continuously and efficiently enable Chinese biomedical language models to learn comprehensively and deeply is the direction that future research needs to explore. Future explorative research needs to consider strategies to let Chinese biomedical language models learn in a continuous, efficient, comprehensive and deep fashion. This will also provide greater contributions to human-computer interaction-oriented medical predictive intelligence.

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