Data and text mining

Chemical-protein Interaction Extraction via Gaussian Probability Distribution and External Biomedical Knowledge

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Abstract

Motivation: The biomedical literature contains a wealth of chemical-protein interactions (CPIs). Automatically extracting CPIs described in biomedical literature is essential for drug discovery, precision medicine, as well as basic biomedical research. However, the existing methods do not consider the impact of overlapping relations on CPI extraction. This leads to the extraction of sentences with overlapping relations becoming the bottleneck of CPI extraction.

Results: In this paper, we propose a novel neural network-based approach to improve the CPI extraction performance of sentences with overlapping relations. Specifically, the approach first employs BERT to generate high-quality contextual representations of the title sequence, instance sequence, and knowledge sequence. Then, the Gaussian probability distribution is introduced to capture the local structure of the instance. Meanwhile, the attention mechanism is applied to fuse the title information and biomedical knowledge, respectively. Finally, the related representations are concatenated and fed into the softmax function to extract CPIs. We evaluate our proposed model on the CHEMPROT corpus. Our proposed model is superior in performance as compared with other state-of-the-art models. The experimental results show that the Gaussian probability distribution and external knowledge are complementary to each other. Integrating them can effectively improve the CPI extraction performance. Furthermore, the Gaussian probability distribution can significantly improve the extraction performance of sentences with overlapping relations in biomedical relation extraction tasks.

Availability: Data and code are available at https://github.com/CongSun-dlut/CPI_extraction.

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

Knowledge of chemical-protein interactions (CPIs) is essential for drug discovery, precision medicine, as well as basic biomedical research (Krallinger et al., 2017). Currently, PubMed has included approximately 30 million articles and continues to grow at a rate of more than one million articles per year. Extensive valuable CPI knowledge is hidden in biomedical texts, and how to accurately and automatically extract these interactions is increasingly attracting interest. Therefore, the automatic extraction of CPIs from biomedical literature is becoming a crucial task in biomedical natural language processing (NLP) tasks. Recently, the BioCreative VI task organizers released a CHEMPROT corpus, which is the first corpus for CPI extraction (Krallinger et al., 2017).

Most existing CPI extraction methods can be roughly categorized into two classes: statistical machine learning-based methods and neural
CPR:5

Fig. 1. An example sentence which has six overlapping relations. Chemical and protein entities are labeled green and blue, respectively. This example shows how a sentence with overlapping relations generates instances.

To date, research on CPI extraction is still at an early stage, and the performance has much room to improve. As shown in Figure 1, one sentence with overlapping relations will generate multiple identical instances based on different target entity pairs. For these identical instances, we refer to them as overlapping instances. Correspondingly, we refer to the sentences that have only one pair of target entities as normal instances. Both the above-mentioned statistical machine learning-based methods and neural network-based methods do not consider the impact of overlapping instances. However, there are a large number of overlapping instances in the CHEMPROT corpus, and the extraction of these instances has become the bottleneck of CPI extraction. Existing methods usually use position features (e.g., relative distance embeddings) to indicate the position of each token in the instance, which can help the model learn different latent information for overlapping instances to some extent. Nevertheless, because the word/token sequence of the instance is usually exploit elaborate kernel functions or explicit feature engineering to extract CPIs. For example, (Takanobu et al., 2018) introduced a linguistic pattern-aware dependency tree kernel to extract CPIs, and their method obtains an F-score of 61.41%. (Liang et al., 2019) constructed chemical-protein relation (CPR) pairs and triplets and exploited sophisticated features to implement CPI extraction. Their method achieves an F-score of 56.71%. In general, the performance of these methods depends heavily on the designed kernel function and chosen feature set, which is an empirical and skill-dependent work. Compared with statistical machine learning-based methods, neural network-based methods can automatically learn latent features and have become a dominant method for CPI extraction. For example, (Corbett and Boyle, 2019) introduced transfer learning and specialized word embeddings to extract CPIs, and their method obtains an F-score of 61.41%. (Peng et al., 2018) proposed a method integrating a support vector machine (SVM) (Cortes and Vapnik, 1995), a convolutional neural network (CNN) (Kim, 2014) and a recurrent neural network (RNN) to extract CPIs. Their system achieves an F-score of 64.10%. (Sun et al., 2019) proposed an end2end neural network-based model called ELMo representations (Peters et al., 2018) into the stacked bidirectional long short-term memory (Bi-LSTM) (Hochreiter and Schmidhuber, 1997). Their method obtains an F-score of 69.44%. Despite the success of these neural networks, some disadvantages remain. First, the pre-trained word embeddings (Mikolov et al., 2013; Pennington et al., 2014; Joulin et al., 2017) can only learn a context-independent representation for each word (Peters et al., 2018). Second, CNNs and RNNs perform distinctly worse than the self-attention on word sense disambiguation (Tang et al., 2018). Recently, (Devlin et al., 2019) proposed a language representation model called BERT, which stands for bidirectional encoder representations from Transformers (Vaswani et al., 2017). Compared with the previous neural network-based models, BERT eschews the disadvantages of CNNs and RNNs and addresses the drawbacks of pre-trained word embeddings. (Peng et al., 2019) made a comprehensive comparison of various pre-trained BERTs and introduced the biomedical language understanding evaluation (BLUE) benchmark to facilitate research in the biomedical domain. In their experiments, BERTs pretrained on PubMed abstracts achieved a start-of-the-art performance of CPI extraction, and the F-scores of BERTBASE and BERTLARGE reach 72.5% and 74.4%, respectively. Overall, neural network-based methods can automatically learn latent features from vast amounts of unlabeled biomedical texts, thereby achieving start-of-the-art performances of CPI extraction.

Our work focuses on improving the CPI extraction performance of overlapping instances and starts from the following two aspects. On the one hand, it is more reasonable that the relation extraction model should focus on the target entity and its adjacent words than on treating each token in the instance equally. Although the attention mechanism can use word embeddings to calculate the weights, it cannot distinguish the importance of the same word at different positions in the instance. Take the sentence in Figure 1 as an example. The importance of these three ‘agonist’ in different instances is different, but the attention mechanism cannot distinguish them. Therefore, we introduce the Gaussian probability distribution to enhance the weights of the target entity and its adjacent words. On the other hand, the CHEMPROT corpus is a corpus composed of abstracts from PubMed. The title information and the knowledge from the biomedical knowledge base may have a positive impact on CPI extraction. For example, in the abstract file of the CHEMPROT corpus, the title “Loperamide modulates but does not block the corticotropin-releasing hormone-induced ACTH response in patients with Addison’s disease” contains vital information on the entities ‘loperamide’ and ‘ACTH’. This information may be helpful for correctly predicting the interaction between these two entities. Moreover, the Therapeutic Target Database (TTD) (Li et al., 2017) is a knowledge...
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2 Methods

2.1 CPI Extraction

CPI extraction is a task for detecting whether a specified CPR type between the target chemical-protein pair within a sentence or document and if so, classifying the CPR type. The CHEMPROT corpus contains five types (i.e., CPR:3, CPR:4, CPR:5, CPR:9 and False) used for evaluation purposes.

In this paper, we propose a novel neural network-based approach to improve the CPI extraction performance of overlapping instances. Specifically, the approach first employs BERT to generate high-quality contextual representations of the title sequence, instance sequence, and knowledge sequence, respectively. Then the Gaussian probability distribution is introduced to enhance the weights of the target entity and its adjacent words in the instance sequence. Meanwhile, the attention mechanism is applied to fuse the title information and biomedical knowledge. Finally, the related representations are concatenated and fed into the softmax function to extract CPIs. The contributions of our study are three-fold:

- We propose a novel neural network-based approach to improve the CPI extraction performance of overlapping instances. The experimental results show that our proposed model can improve the extraction performance of overlapping instances while maintaining the performance of normal instances.
- We introduce the Gaussian probability distribution and external knowledge into our proposed model to improve CPI extraction. Through extensive experiments on the CHEMPROT corpus, we demonstrate that the Gaussian probability distribution and external knowledge are helpful for CPI extraction, and they are highly complementary to each other.
- To the best of our knowledge, this is the first study that introduces the Gaussian probability distribution into biomedical relation extraction tasks. Through extensive experiments on the CHEMPROT and DDIExtraction 2013 corpora, we demonstrate that the Gaussian probability distribution can effectively improve the extraction performance of overlapping instances.

2.2 Gaussian Probability Distribution Operation

In the CHEMPROT dataset, we found that there are a total of 19,460, 11,820 and 16,943 instances in the training set, development set and test set, respectively. However, of these instances, only 915, 517 and 811 instances are normal instances, and the others are all overlapping instances. These overlapping instances have the same sentence structure, which makes it difficult for existing methods to accurately extract their CPR types. Therefore, we introduce the Gaussian probability distribution to enhance the weights of the target entity and its adjacent words, so that the model can learn the local structure of the instance. The Gaussian probability density function is:

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x - \mu)^2}{2\sigma^2}\right)$$  \hspace{1cm} (5)

The Gaussian cumulative distribution function is:

$$F(x) = \int_{-\infty}^{x} f(x) \, dx$$  \hspace{1cm} (6)

The Gaussian probability distribution function is:

$$P(x) = F(x) - F(x - \mu)$$  \hspace{1cm} (7)

where \(x\) is a real number, \(\mu\) is the mean of the distribution, \(\sigma\) is the standard deviation, and \(w\) is the token window. In the experiments, we set the token window to 5.
window to \( w = 1 \) to represent the distance of each token itself, and set the optimal values of \( \mu \) and \( \delta \) to 0 and 3, respectively.

Figure 3 illustrates the Gaussian probability distribution operation process for tokens in the instance. We first numbered the tokens according to the two target entities in the instance, thus obtaining two token relative distance lists (\( x_1 \) and \( x_2 \) in Figure 3). Then we used the Gaussian probability distribution function to calculate the probability of each token in the instance. Afterwards, these token probabilities were performed element-wise multiplication with the token representations. Finally, we obtained the first and second target-entity-aware representations, respectively. The formula is as follows:

\[
R_{\text{tar}1} = \sum_{i=1}^{N} P(x_1)u_i \quad (8)
\]

\[
R_{\text{tar}2} = \sum_{i=1}^{N} P(x_2)u_i \quad (9)
\]

where \( N \) is the sequence length, \( x_1 \) and \( x_2 \) are token numbers, and \( R_{\text{tar}1} \) and \( R_{\text{tar}2} \) denote the first and second target-entity-aware representations, respectively.

2.2.3 External Knowledge Acquisition

In this study, we used the title information and biomedical knowledge to improve the performance of CPI extraction. For the title information acquisition, we first employed BERT to generate high-quality contextual representations of the title sequence. Then we applied the attention mechanism to calculate the query of the title sequence and the key-value pairs of the instance sequence, thereby incorporating the title information into our proposed model. The title fusion attention is defined as follows:

\[
t_i = QT_t u_i \quad (10)
\]

\[
\alpha_i = \frac{\exp(t_i)}{\sum_{n} \exp(t_n)} \quad (11)
\]

\[
R_{\text{title}} = \sum_{i}^{N} \alpha_i u_i \quad (12)
\]

where \( N \) is the sequence length, \( QT_t \) is the representations of the title sequence, \( u_i \) is the representation of the \( i \)-th token, and \( R_{\text{title}} \) denotes the fused title representations.
Figure 4 illustrates the process for obtaining the biomedical knowledge sequence. We first obtained the CPR tags from TTD based on the target chemical and protein entities of the instances, which we denote by $K$. To improve the quality of $K$, we only obtained the tags of the ‘CPR:4’, ‘CPR:5’ and ‘CPR:6’ types and eliminated the ambiguous CPR tags. Then, we extended $K$ by including tokens in the shortest dependency path (SDP) from the target chemical and protein entities. Thus, we used $K$ as the knowledge sequence. More details on the knowledge sequence acquisition are provided in Supplementary Material: Knowledge Sequence Acquisition. Afterwards, we also employed BERT to generate high-quality contextual representations of the knowledge sequence. Finally, the attention mechanism is applied to calculate the query of $K$ and the key-value pairs of the instance sequence. The knowledge fusion attention is defined as follows:

$$k_i = Q_i u_i$$  \hspace{1cm} (13)$$

$$\alpha_k = \exp(k_i)$$  \hspace{1cm} (14)$$

$$R^{know} = \sum_{k=1}^{N} \alpha_k u_i$$  \hspace{1cm} (15)$$

where $N$ is the sequence length, $Q_i$ is the representations of the knowledge sequence, $u_i$ is the representation of the $i$-th token, and $R^{know}$ denotes the fused knowledge representations.

### 3 Experiments and Discussion

#### 3.1 Dataset and Experimental Settings

In this study, to make a fair comparison with other methods, we used the BLUE CHEMPROT dataset provided by Peng et al. (2019) to evaluate our proposed model. More detailed descriptions of the CHEMPROT dataset are provided in Supplementary Material: CHEMPROT Dataset. The only difference between our instance with Peng’s is that we replaced the corresponding chemical and gene mentions with '@CHEMPROT' and '@GENES', respectively. For example, as shown in Figure 1, the fourth instance is processed as "PEA was a potent and full agonist at each species of @CHEMICALS, whereas @GENES was a full agonist for the rodent TAAR1s but was a partial agonist at h-rChTAAR1." in Peng’s instance, but the instance is more reasonable to be processed into our instance "PEA was a potent and full agonist at each species of @CHEMICALS, whereas @CHEMICALS was a full agonist for the rodent TAAR1 but was a partial agonist at h-rChTAAR1." The statistics of evaluated CPR types in the CHEMPROT dataset are illustrated in Table 1.

| Set          | CPR:3 | CPR:4 | CPR:5 | CPR:6 | CPR:9 | False |
|--------------|-------|-------|-------|-------|-------|-------|
| Training set | 768   | 2,251 | 173   | 235   | 727   | 15,306|
| Development set | 550   | 1,094 | 116   | 199   | 457   | 9,404 |
| Test set     | 665   | 1,661 | 195   | 293   | 644   | 13,485|
| Total        | 1,983 | 5,009 | 484   | 727   | 1,828 | 38,195|

#### 3.2 Experimental Results

In this section, we first compared our approach with other state-of-the-art methods on the CHEMPROT corpus. Table 2 shows the experimental results of different methods in detail. The first two methods are based on statistical machine learning. These methods exploited a tree kernel function or feature engineering to construct a classifier to implement CPI extraction. However, the performance of these two methods is not satisfactory. This indicates that it is difficult to effectively achieve CPI extraction on the CHEMPROT corpus using statistical machine learning-based methods. In addition to the first two methods, the others are all neural network-based methods. It can be observed from Table 2 that neural network-based methods generally achieve better performance than statistical machine learning-based methods. In these neural network-based methods, the first four methods utilized ensemble methods to obtain better performance. However, the individual model (e.g., CNNs or RNNs) still has much room for improvement. Lu et al. (2019) attempted to improve the performance by using a granular attention mechanism to...
enhance the RNN model. \cite{Zhang2019} exploited the multi-head attention mechanism and ELMo representations to improve CPI extraction. \cite{Sun2018} introduced the entity attention mechanism and ELMo representations into the stacked Bi-LSTM to improve the performance of CPI extraction. These three methods are all single models and obtain competitive performance on CPI extraction. Recently, BERT raised the F-score to a new level, which demonstrates the success of the language representation model. Our approach exploited BERT to generate high-quality contextual representations and introduced the Gaussian probability distribution and external knowledge to enhance the extraction ability of the model. Our proposed model obtains an F-score of 76.03\%, which is currently the best performance. These experimental results demonstrate that our proposed model can effectively improve the performance of CPI extraction.

Then, we compared the performance of each evaluated CPR type. Compared with other models, our proposed model achieves the highest F-scores on the ‘CPR:3’, ‘CPR:4’, ‘CPR:5’ and ‘CPR:9’ types, respectively. This experimental result demonstrates the effectiveness of our proposed model. On the other hand, it can be observed that the extraction performance of different CPR types varies significantly. We can see all methods achieve relatively high performance on the ‘CPR:3’, \{CPR:4, \ldots, CPR:6\}, ‘CPR:9’ types. The reason may be that these four CPR types have obvious recognition words (e.g., ‘activator’, ‘inhibitor’, ‘agonist’ and ‘antagonist’) in the instance, so it is easier for the model to extract these types of chemical-protein interactions. In contrast, all methods have relatively low F-scores on the ‘CPR:9’ type. This suggests that it is the most challenging to accurately extract the ‘CPR:9’ type chemical-protein interactions on the CHEMPROT corpus. According to our observations, the ‘CPR:9’ type has no obvious recognition words in the instance. Moreover, from Table 2, we can see that the training set for the ‘CPR:9’ type only contains 727 instances. Therefore, the worse extraction performance on the ‘CPR:9’ type may be caused by an insufficient number of the ‘CPR:9’ instances in the training set. Despite this, our proposed model is still superior to other models on the extraction of the ‘CPR:9’ type. This demonstrates the effectiveness of our proposed model from another aspect.

In conclusion, the experimental results show that our proposed model is superior in performance compared with other state-of-the-art methods used for CPI extraction. Due to space limitations, the error analysis of our proposed model is provided in Supplementary Material: Error Analysis.

### 3.3 Extraction of Overlapping and Normal Instances

In this section, we explored the impact of our proposed model on overlapping instances and normal instances. Table 3 shows the statistics for the instances in the CHEMPROT dataset. There are 19,460, 11,820 and 16,943 instances in the training set, development set and test set, of which 18,545, 11,303 and 16,132 instances are overlapping instances. However, the existing methods do not consider the impact of these instances on CPI extraction. This leads to the extraction of overlapping instances becoming the bottleneck for CPI extraction. Unlike the previous works, our proposed approach is designed to focus on these overlapping instances by introducing the Gaussian probability distribution and external knowledge. We performed comparative experiments to explore the reason for the CPI performance improvement of our proposed model. In the comparative experiments, we first used overlapping instances and normal instances in the test set as input, and then compared the performance of BERT with the performance of our proposed model (the input of our proposed model also contains the title sequence and knowledge sequence). As shown in Table 4, BERT obtains F-scores of 73.62\% and 83.28\% in the extraction of overlapping instances and normal instances, respectively. Correspondingly, our proposed model achieves F-scores of 75.40\% and 82.84\%, respectively. These experimental results show that our proposed model can improve the CPI performance of overlapping instances while maintaining the performance of normal instances.

### Table 2. Performance comparison on the CHEMPROT dataset.

| Method               | F-score on each CPR type (%) | Overall performance (%) |
|----------------------|-----------------------------|-------------------------|
|                      | CPR:3 | CPR:4 | CPR:5 | CPR:6 | CPR:9 | Precision | Recall | F-score |
| **Machine learning-based methods** |       |       |       |       |       |           |        |         |
| Wartkio et al. (2018)| -     | -     | -     | -     | -     | 27.32     | 55.14  | 36.54   |
| Li et al. (2019)    | 49.80 | 66.50 | 56.49 | 69.64 | 28.74 | 63.52     | 51.21  | 56.71   |
| Corbett and Boyle (2016)| -     | -     | -     | -     | -     | 56.10     | 67.84  | 61.41   |
| Mehryary et al. (2018)| -     | -     | -     | -     | -     | 59.05     | 67.76  | 63.10   |
| Peng et al. (2018)  | -     | -     | -     | -     | -     | 72.66     | 57.35  | 64.10   |
| Liu and Kang (2018) | -     | -     | -     | -     | -     | 74.8      | 56.0   | 64.1    |
| Li et al. (2019)    | -     | -     | -     | -     | -     | 65.44     | 64.84  | 65.14   |
| Zhang et al. (2019a)| 59.4  | 71.8  | 65.7  | 72.5  | 50.1  | 70.6      | 61.8   | 65.9    |
| Sun et al. (2019)   | 64.69 | 75.26 | 68.14 | 79.26 | 55.71 | 67.04     | 72.01  | 69.44   |
| BERT (Peng et al. 2019)| -     | -     | -     | -     | -     | 74.5      | 70.6   | 72.5    |
| Our proposed model  | **72.27** | **80.92** | **71.66** | **78.28** | **66.77** | **76.82** | **75.25** | **76.03** |

### Table 3. Statistics for the instances in the CHEMPROT dataset.

| Set                  | Overlapping | Normal | All  |
|----------------------|-------------|--------|------|
| Training set         | 18,545      | 915    | 19,460 |
| Development set      | 11,303      | 517    | 11,820|
| Test set             | 16,132      | 811    | 16,943|
| Total                | 45,980      | 2,243  | 48,223|

### Table 4. Overlapping and normal instance extraction on the test set.

| Model                | Instances | Precision(%) | Recall(%) | F-score(%) |
|----------------------|-----------|--------------|-----------|------------|
| BERT (local)         | overlapping | 74.57     | 72.69     | 73.62     |
|                       | normal    | 81.61     | 85.02     | 83.28     |
|                       | all       | 75.19     | 73.71     | 74.45     |
| Our proposed model   | overlapping | 76.30    | 74.52     | 75.40     |
|                       | normal    | 82.41     | 83.28     | 82.84     |
|                       | all       | 76.82     | 75.25     | 76.03     |

Notes. ‘Local’ denotes the BERT runs locally.
3.4 Ablation Study

In this section, to explore the contribution of each component to overall performance, we performed an ablation study over our proposed model on the CHEMPROT test set. The experimental results are presented in Table 5. We first explored the impact brought by the Gaussian probability distribution. This experimental result demonstrates that the Gaussian probability distribution operation is critical in obtaining state-of-the-art performance. Next, we evaluated the impact of external knowledge (i.e., the title information and biomedical knowledge). When the title sequence or knowledge sequence is removed, the F-score of the model decreases by 1.49% and 1.46%, respectively. However, when both the title sequence and knowledge sequence are both removed, the F-score of the model drops only 0.78%. These experimental results indicate that both the title information and biomedical knowledge contribute to our proposed model, and the two external knowledge are complementary. Finally, we validated the effects of Gaussian probability distribution and external knowledge. When removing the Gaussian probability distribution and external knowledge, our proposed model degenerates into the BERT model, and the performance drops to 74.45% in F-score. These experimental results demonstrate that the Gaussian probability distribution and external knowledge are helpful for CPI extraction, and they are also highly complementary to each other.

| model | Precision(%) | Recall(%) | F-score(%) |
|-------|--------------|-----------|------------|
| Our proposed model | 76.82 | 75.25 | 76.03 |
| – Gaussian | 77.73 | 73.08 | 75.33 |
| – title | 75.35 | 73.74 | 74.54 |
| – knowledge | 75.69 | 73.48 | 74.57 |
| – title & knowledge | 77.13 | 73.45 | 75.25 |
| – Gaussian & title & knowledge | 75.39 | 73.71 | 74.45 |

Notes: ‘–’ denotes removing the corresponding component.

3.5 Impact of Gaussian Probability Distribution on Biomedical Relation Extraction

In this study, we introduced the Gaussian probability distribution into biomedical relation extraction tasks. When removing the external knowledge, our proposed model degenerates into a ‘BERT+Gaussian’ model. To explore the impact of Gaussian probability distribution on biomedical relation extraction tasks, we further evaluated the ‘BERT+Gaussian’ model on the CHEMPROT and DDIExtraction 2013 corpora. DDIExtraction 2013 corpus is a manually annotated drug-drug interaction (DDI) corpus based on the DrugBank database and MEDLINE abstracts. This corpus contains four DDI types for evaluation purposes, namely 'Advice', 'Effect', 'Mechanism' and 'Int'. We also formulate DDI extraction into a multi-class classification problem, and the evaluation metrics of DDI are consistent with CPI, which are precision, recall and F1-score. In the experiments, to fairly compare with existing methods, we also used the BLUE DDIExtraction 2013 dataset provided by Peng et al. (2019) to evaluate the model. Table 6 illustrates the statistics for the instances in the DDIExtraction 2013 dataset. More detailed descriptions of the DDIExtraction 2013 dataset are provided in Supplementary Material: DDIExtraction 2013 Dataset.

Table 6. Statistics for the instances in the DDIExtraction 2013 dataset.

| Set | Overlapping | Normal | All |
|-----|-------------|--------|-----|
| Training set | 17,584 | 1,195 | 18,779 |
| Development set | 6,850 | 394 | 7,244 |
| Test set | 5,426 | 335 | 5,761 |
| Total | 29,860 | 1,924 | 31,784 |

Table 7. Performance comparison on the DDIExtraction 2013 dataset.

| Method | Precision(%) | Recall(%) | F-score(%) |
|--------|--------------|-----------|------------|
| [Zhang et al. 2017] | 74.1 | 71.8 | 72.9 |
| BERT [Peng et al. 2019] | 81.1 | 75.3 | 78.1 |
| BERT+Gaussian | 83.28 | 79.88 | 81.54 |

Notes. BERT is pre-trained on PubMed and provided by Peng et al. (2019). 'Local' denotes the BERT runs locally.
4 Conclusion

In this paper, we propose a novel neural network-based approach to improve the performance of CPI extraction by introducing the Gaussian probability distribution and external knowledge. We evaluate our proposed model on the CHEMPROT corpus. It is encouraging to see that the performance of our proposed model outperforms other state-of-the-art models, reaching an F-score of 76.03%. The experimental results show that the Gaussian probability distribution and external knowledge are highly complementary to each other. Integrating them can effectively improve the CPI extraction performance. Furthermore, the Gaussian probability distribution can significantly improve the extraction performance of overlapping instances in biomedical relation extraction tasks.

Although our proposed approach exhibits promising performance for CPI extraction from biomedical literature, there is still some room to improve. In particular, our proposed approach does not obtain a high F-score on the 'CPR:9' type, likely because of insufficient training data. This indicates that our proposed approach depends on high-quality training data. In future work, we would like to explore the effectiveness of the semi-supervised or unsupervised approach in CPI extraction.

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