Abstract

The biomedical scientific literature comprises a crucial, sometimes life-saving, natural language resource whose size is accelerating over time. The information in this resource tends to follow a style of discourse that is intended to provide scientific explanations for various pieces of evidence derived from experimental findings. Studying the rhetorical structure of the narrative discourse could enable more powerful information extraction methods to automatically construct models of scientific argument from full-text papers. In this paper, we apply richly contextualized deep representation learning to the analysis of scientific discourse structures as a clause-tagging task. We improve the current state-of-the-art clause-level sequence tagging over text clauses for a set of discourse types (e.g., "hypothesis", "result", "implication", etc.) on scientific paragraphs. Our model uses contextualized embeddings, word-to-clause encoder, and clause-level sequence tagging models and achieves F1 performance of 0.784.

1 Introduction

Primary experimental articles (i.e., papers that describe original experimental work) provide the crucial raw material for all other scientific publications (books, reviews, theoretical studies, etc.). The task of extracting information from biomedical articles for use by scientists has been a goal for computational linguistics for some time (Hobbs, 2002), where the focus is typically placed on identifying relevant entities, relations, and events from text to populate a database that could be queried to inform users of the reported scientific knowledge.

These conventional methods do not take into account the fact that scientific work involves attempting to provide explanations for evidence derived from experiments and is therefore driven principally by authors attempting to convince expert readers that their claims are the “correct” explanations for the experimental evidence. Thus, an important aspect of building machines capable of understanding scientific texts is that it must first recognize different rhetorical components of scientific discourse. We must then be able to distinguish the observations made in experiments from their implications and distinguish between claims supported by evidence and hypotheses put forward to prompt further research. It is this goal, of being able to distinguish between the different types of rhetorical statements, that motivates our work.

Dasigi et al. (2017) studied the problem of identifying the discourse type of each clause in a biomedical experiment paragraph and composed a dataset for it. However, the dataset was quite...
small which hindered the performance and thus the usefulness of such a tool. We compose a larger dataset expanding the original data from Dasigi et al. (2017), annotating discourse type of each clause in biomedical literature. We adopt the discourse type taxonomy for biomedical papers proposed by De Waard and Maat (2012). The taxonomy contains eight types including goal, fact, result, hypothesis, method, problem, implication and none. The definition of each type can be found in Table 1; Figure 1 shows an example paragraph of clauses labeled with discourse types.

We formulate it as a clause-level sequence tagging problem, and extend the deep-structured model proposed by Dasigi et al. (2017) to conduct discourse tagging, and compare to feature-based structured learning models, such as Conditional Random Field (CRF) (Lafferty et al., 2001) and Support Vector Machine (SVM) (Hearst, 1998) that most of the prior works used. We study the effectiveness of contextualized word embeddings v.s. static word embeddings, compare different ways to summarize word representations into clause representations using attention mechanisms. We also explore different sequence taggers on top of the clause representations.

We summarize our contributions as follows:

- We expand the scientific discourse tagging dataset created by Dasigi et al. (2017).
- We develop a state-of-the-art model for scientific discourse tagging by extending the model proposed by Dasigi et al. (2017).
- Ablation study and analysis are conducted to compare the effect of different embeddings, various word-to-clause summarizing mechanisms, as well as various sequence tagging strategies to understand how to build better systems for scientific discourse tagging.

2 Related Work

Feature-based Scientific Discourse Tagging.

There has been a significant amount of work aimed at understanding the scientific discourse types. Teufel and Moens (1999) and Teufel and Moens (2002) described argumentative zoning, which groups sentences into a few rhetorical zones highlighted by important clauses such as “in this paper we develop a method for”. Hirohata et al. (2008) used CRF with handcrafted features to classify sentences in abstracts into 4 categories: objective, methods, results, and conclusions. Liakata (2010) defined “zone of conceptualization” which classifies sentences into 11 categories in scientific papers and Liakata et al. (2012) used CRF and LibSVM to identify these “zone of conceptualization”. Guo et al. (2010) used Naive Bayes and SVM to compare three schemas described above. Most recently, Cox et al. (2017) used the same schema as we used in this work (De Waard and Maat, 2012) by exploring a variety of methods for balancing classes before applying classification algorithms.

All of these studies perform the task using handcrafted features, which suffers from problems such as text specific, time-consuming and lower performance than the deep learning approach.

Deep Learning for Scientific Discourse Tagging.

Neural sequence labeling approach using bidirectional LSTM (Hochreiter and Schmidhuber, 1997) and CRF has been prevailing for classic word-level sequence tagging problems such as named entity recognition (NER) and part of speech tagging (POS) (Huang et al., 2015; Ma and Hovy, 2016; Chiu and Nichols, 2016). Since the clause-level sequence tagging problem has one additional dimension of input comparing to word-level sequence tagging problems, Dasigi et al. (2017) used an RNN-Attention to encode word-level representations to clause-level representations before tagging each clause using an LSTM.

3 Dataset

We expand the scientific discourse corpus developed by Dasigi et al. (2017) by applying the same clause parsing and annotation pipeline described by Dasigi et al. (2017). This dataset is derived from the Pathway Logic (Eker et al., 2002) and INTACT databases (Orchard et al., 2013). Texts from all sections of each of those papers were preprocessed by parsing each sentence to generate a sequence of main and subordinate clauses using Stanford Parser (Socher et al., 2013). Domain experts were asked to label each of those clauses using the 7-label taxonomy proposed by De Waard and Maat (2012). We apply sequential methods to sequences of clauses in individual paragraphs.

Overall, as Appendix Figure 5 and Figure 6 show, our dataset has a total of 634 paragraphs and 6124 clauses. We randomly split 570 para-
graphs as the training and validation set and the rest as the test set. Each paragraph contains up to 30 clauses and the number of word per clause has a mean of 17.7 and a standard deviation of 12.5. The total vocabulary size is 8563, which is still a small dataset for an NLP task. However, we note the difficulties of obtaining such dataset.

4 Approach

Model Overview We develop a deep structured model extending Dasigi et al. (2017), which consists of a word embedding layer (contextualized or static), an attention layer that summarizes word embeddings into clause embeddings, and a BiLSTM-CRF sequence tagger on top of the clause embeddings for discourse type tagging. Figure 2 gives an overview of the architecture.

Embeddings Static embeddings such as GloVe (Pennington et al., 2014) and recent contextualized embedding methods such as BERT (Devlin et al., 2018) have been widely used. Comparing to static embedding methods, contextualized word embedding produces different word vectors for the same word under different contexts and thus can provide richer representations to each word.

In this work, we explore pre-trained BioBERT (Lee et al., 2019) embedding. We also train BioGloVe, a GloVe (Pennington et al., 2014) embedding on biomedical articles for comparison.

Clause Representations via Attention We observe that only keywords such as “show” and “indicate” are essential to determine the discourse types. Attention is an appropriate mechanism for emphasizing certain inputs and ignoring others. We adopt Dasigi et al. (2017)’s method of using an attention mechanism to summarize word representations to clause representations. We further propose a new variation of attention mechanism using LSTM to provide contextualization of the words in the clause. Specifically, we first encode the words using an LSTM to get contextualized hidden vectors $h_i$, and use them to learn attentions for each word by introducing another trainable vector $S$ of the same dimension of $h_i$. We apply the attention to summarizing the word embeddings into a clause embedding. The dashed circle in Figure 2 illustrates our LSTM-Attention based clause encoder.

Clause-level Sequence Tagging We observe that the discourse labels have a clear transition of logic flow (e.g., result usually followed by implication, and method usually followed by hypothesis). Therefore, we hypothesize that a CRF sequence tagging module can efficiently capture these transition and enhance the performances. Therefore, we extend (Dasigi et al., 2017)’s LSTM sequence tagging to BiLSTM-CRF sequence tagging to label discourse types for each clause in a paragraph.

5 Experiments

Baseline Models. In addition to Dasigi et al. (2017)’s model trained on our expanded dataset, we also compare with feature based CRF 3 and

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3 https://github.com/edvisees/sciDT

3 CRFsuite package (Okazaki, 2007)
Architecture CV F1
Baselines
SVM 0.697
CRF 0.713
Dasigi et al. (2017) 0.746

Varying Embeddings
BioW2V (Dasigi et al. (2017)) 0.746
BioGloVe 0.772
BioBERT (Best Model) 0.784

Varying Attention Context Encoder
No Attention 0.666
No Context 0.777
RNN 0.778
LSTM (Best Model) 0.784

Varying Sequence Tagger
CRF 0.768
LSTM 0.771
BiLSTM 0.780
BiLSTM+CRF (Best Model) 0.784

Table 2: Main results including baseline models and ablations of our model.

SVM\(^4\) with unigram, bigram and trigram words in the previous, current and next clauses as features.

**Ablation Study.** We perform ablation studies to compare the model performance by varying the types of embedding, clause encoder, and sequence tagger. We compare static BioGloVe embedding and contextualized BioBERT embedding for the embedding methods. Then we compare no attention (max pooling instead), attention without context, or simple RNN-Attention proposed by Dasigi et al. (2017), against our LSTM-Attention. Finally, we compare sequence taggers implemented by CRF alone, LSTM, bidirectional LSTM or BiLSTM-CRF.

**5.1 Model Performances**

Table 2 compares the best performances of the baseline models and our different models with embeddings, attention context, and sequence tagger variations. We also report all of the tested model performance in Appendix Table 5. As we explained in the Dataset section, due to the small size of our dataset, we use 5-fold cross-validation weighted F1 score which is weighted by support (the number of true instances for each label), as our main metric to compare model performance. Our best model is with BioBERT embedding, LSTM-Attention mechanism as word-to-clause encoding and a BiLSTM-CRF as the sequence tagger achieves cross-validation F1 of 0.784. We also re-run Dasigi et al. (2017)'s best model and obtained 0.746 mean of 5-fold cross-validation F1 score. Our best model’s cross-validation F1 score is significantly higher (per McNemar’s test, \(p < 10^{-5}\)). Accordingly, our best model significantly outperforms feature-based SVM and CRF models. We also conduct ablation study to understand the effect of different components of our model.

**Embedding** We observe that models with BioBERT embedding globally outperform models with BioGloVe embedding. This indicates word representations with contextualization improve the downstream tasks.

**Attention Context** Dasigi et al. (2017) observed that models with an attention-based word-to-clause encoder with context perform better than the one without context. We extended their model replacing simple RNN with LSTM. As Table 2 shows, the more strongly the attention mechanism is contextualized, the better the model performs.

**Sequence Tagger** As demonstrated by previous sequence tagging works, we observe that more complex sequence taggers such as BiLSTM-CRF perform the best. However, the improvements in BiLSTM-CRF over BiLSTM was not huge. However, CRF brings interpretability of the model as we will show in Section 5.3.

**5.2 Error Analysis**

We visualize the confusion matrix of our best model’s predictions on the test data in Figure 3a. The dark diagonals indicate that the model is capable of correctly predicting most of the labels. In-
Interestingly, the difficulty of predicting labels varies on the discourse types. The model predicts relatively better on labels such as method and result while it predicts problem and none poorly. The difference of difficulty comes from the nature that the number of the labels in the training set is unbalanced, as shown in Table 3.

5.3 CRF Transition Probability Visualization

Given the explainable nature of the CRF weights, we visualize the relation between the linear chain CRF weights of our best BioBERT model and the label transition probabilities in the test set in Figure 3b. We compute Pearson correlation between these two variables to be -0.63 ($p \approx 0$) as shown in Figure 4. This indicates that the CRF layer captures the discourse type transition probabilities in the training data.

6 Conclusion

We study a deep-structured sequence tagging approach for labeling the discourse types of the clauses in biomedical documents. Our model uses a contextualized word embedding to construct input features, then uses an attention mechanism to encode word-level representations to clause-level, and finally uses BiLSTM-CRF to tag discourse labels. The results show that overall the architectures with more contextualization on the embedding, the attention-based word-to-clause encoder, and the sequence tagger yields better performances.

Our system can help identify scientific discourse structures, which assists downstream information extraction tasks such as extracting scientific arguments from full-text papers.
References

Martín Abadi, Ashish Agarwal, Paul Barham, Eugene Brevdo, Zhifeng Chen, Craig Citro, Greg S. Corrado, Andy Davis, Jeffrey Dean, Matthieu Devin, Sanjay Ghemawat, Ian Goodfellow, Andrew Harp, Geoffrey Irving, Michael Isard, Yaqing Jia, Rafal Jozefowicz, Lukasz Kaiser, Manjunath Kudlur, Josh Levenberg, Dan Mané, Rajat Monga, Sherry Moore, Derek Murray, Chris Olah, Mike Schuster, Jonathon Shlens, Benoit Steiner, Ilya Sutskever, Kunal Talwar, Paul Tucker, Vincent Vanhoucke, Vijay Vasudevan, Fernando Viégas, Oriol Vinyals, Pete Warden, Martin Wattenberg, Martin Wicke, Yuan Yu, and Xiaoqiang Zheng. 2015. TensorFlow: Large-scale machine learning on heterogeneous systems. Software available from tensorflow.org.

Jason PC Chiu and Eric Nichols. 2016. Named entity recognition with bidirectional lstm-cnns. Transactions of the Association for Computational Linguistics, 4:357–370.

François Chollet et al. 2015. Keras. https://github.com/fchollet/keras.

Jessica Cox, Corey A Harper, and Anita de Waard. 2017. Optimized machine learning methods predict discourse segment type in biological research articles. In Semantics, Analytics, Visualization, pages 95–109. Springer.

Pradeep Dasigi, Gully APC Burns, Eduard Hovy, and Anita de Waard. 2017. Experiment segmentation in scientific discourse as clause-level structured prediction using recurrent neural networks. arXiv preprint arXiv:1702.05398.

Anita De Waard and Henk Pander Maat. 2012. Epistemic modality and knowledge attribution in scientific discourse: A taxonomy of types and overview of features. In Proceedings of the Workshop on Detecting Structure in Scholarly Discourse, pages 47–55. Association for Computational Linguistics.

Jacob Devlin, Ming-Wei Chang, Kenton Lee, and Kristina Toutanova. 2018. Bert: Pre-training of deep bidirectional transformers for language understanding. arXiv preprint arXiv:1810.04805.

S. Eker, M. Knapp, K. Laderoute, P. Lincoln, and C. Talcott. 2002. Pathway Logic: Executable Models of Biological Networks. In Fourth International Workshop on Rewriting Logic and Its Applications (WRLA 2002, volume 71 of Electronic Notes in Theoretical Computer Science. Elsevier.

Yufan Guo, Anna Korhonen, Maria Liakata, Ilona Slinis Karolinska, Lin Sun, and Ulla Steinu. 2010. Identifying the information structure of scientific abstracts: an investigation of three different schemes. In Proceedings of the 2010 Workshop on Biomedical Natural Language Processing, pages 99–107. Association for Computational Linguistics.

Marti A. Hearst. 1998. Support vector machines. IEEE Intelligent Systems, 13(4):18–28.

Kenji Hirohata, Naoki Okazaki, Sophia Ananiadou, and Mitsuji Ishizuka. 2008. Identifying sections in scientific abstracts using conditional random fields. In Proceedings of the Third International Joint Conference on Natural Language Processing: Volume-I.

Jerry R. Hobbs. 2002. Information extraction from biomedical text. Journal of biomedical informatics, 35(4):260–264.

Sepp Hochreiter and Jürgen Schmidhuber. 1997. Long short-term memory. Neural computation, 9(8):1735–1780.

Zhiheng Huang, Wei Xu, and Kai Yu. 2015. Bidirectional lstm-crf models for sequence tagging. arXiv preprint arXiv:1508.01991.

Diederik P Kingma and Jimmy Ba. 2014. Adam: A method for stochastic optimization. arXiv preprint arXiv:1412.6980.

John Lafferty, Andrew McCallum, and Fernando CN Pereira. 2001. Conditional random fields: Probabilistic models for segmenting and labeling sequence data. In ICML.

Jinhyuk Lee, Wonjin Yoon, Sungdong Kim, Donghyeon Kim, Sunkyu Kim, Chan Ho So, and Jaewoo Kang. 2019. Biobert: pre-trained biomedical language representation model for biomedical text mining. arXiv preprint arXiv:1901.08746.

Maria Liakata. 2010. Zones of conceptualisation in scientific papers: a window to negative and speculative statements. In Proceedings of the Workshop on Negation and Speculation in Natural Language Processing, pages 1–4. Association for Computational Linguistics.

Maria Liakata, Shyamasree Saha, Simon Dobnik, Colin Batchelor, and Dietrich Rebholz-Schuhmann. 2012. Automatic recognition of conceptualization zones in scientific articles and two life science applications. Bioinformatics, 28(7):991–1000.

Xuezhe Ma and Eduard Hovy. 2016. End-to-end sequence labeling via bi-directional lstm-cnns-crf. arXiv preprint arXiv:1603.01354.

Naoki Okazaki. 2007. Crfsuite: a fast implementation of conditional random fields (crfs).

Sandra Orchard, Mais Ammari, Bruno Aranda, Lionel Breuza, Leonardo Briganti, Fiona Broackes-Carter, Nancy H Campbell, Gayatri Chavali, Carol Chen, Noemi Del-Toro, et al. 2013. The mintact project: intact as a common curation platform for 11 molecular interaction databases. Nucleic acids research, 42(D1):D358–D363.
Jeffrey Pennington, Richard Socher, and Christopher Manning. 2014. Glove: Global vectors for word representation. In Proceedings of the 2014 conference on empirical methods in natural language processing (EMNLP), pages 1532–1543.

Richard Socher, John Bauer, Christopher D Manning, et al. 2013. Parsing with compositional vector grammars. In Proceedings of the 51st Annual Meeting of the Association for Computational Linguistics (Volume 1: Long Papers), volume 1, pages 455–465.

Simone Teufel and Marc Moens. 1999. Discourse-level argumentation in scientific articles: human and automatic annotation. Towards Standards and Tools for Discourse Tagging.

Simone Teufel and Marc Moens. 2002. Summarizing scientific articles: experiments with relevance and rhetorical status. Computational linguistics, 28(4):409–445.
A Supplemental Material

In this section, we provide details of the model design and training for better understanding Figure 2 and reproducing the results.

A.1 Static and Contextualized Embeddings

BioGloVe Static Embedding Our BioGloVe embedding is a $d$ dimensional GloVe embedding (Pennington et al., 2014) for each of the word in the INTACT abstract corpus (Orchard et al., 2013) that appeared 5 times or more. Each out of vocabulary word is represented by a random word vector. The pre-trained word embeddings are not fine-tuned during training.

BioBERT Contextualized Embedding We apply BioBERT (Lee et al., 2019) embedding fine-tuned on the PubMed and PubMed Central (PMC) databases and use the activation from the first Transformer layer which has $d_{BERT}$ dimensions for each word representation.

PCA for BioBERT Activation Dimension Reduction We perform Principle Component Analysis (PCA) dimension reduction on the activations generated from BioBERT to reduce the word embedding dimension from $d_{BERT}$ to $d$. We use PCA because a smaller size of discourse tagger saves computational resources and it is also more intuitive when comparing with $d$ dimensional BioGloVe.

In order to perform PCA, we also generate the BioBERT contextualized word embedding of a large subset of unlabeled INTACT abstracts (Orchard et al., 2013). The word embedding of the subset of abstracts are aligned to form a large matrix $B$ of shape $w_{abstract} \times d_{BERT}$ where $w_{abstract}$ is the number of words in the subset. This matrix $B$ is used to compute the covariance (principal component) matrix $C$ of shape $d_{BERT} \times d$. We use this $C$ matrix to perform transfer learning from the large unlabeled dataset and transform the $d_{BERT}$ dimensional BioBERT word embedding of our labeled dataset to $d$ dimensions.

Loading the embeddings The dimension of the input tensor $D$ is $c \times w \times d$ where $c$ is the largest number of clauses in each paragraph and $w$ is determined by $w = \frac{w_{mean} + 3 \times w_{std}}{2}$ where $w_{mean}$ is the mean length of the clauses across the training set and similarly $w_{std}$ is the standard deviation. The tensors are zero-padded along the clause and word dimensions if needed.

A.2 Clause Representations via Attention

Each of the word representations in the input tensor $D$ is first reduced from $d$ to $d_2$ dimensions. Then the word representations are projected from $d_2$ dimension to $p$ dimension. For attention without context, $p$ dimensional reduced word representations directly perform dot product with a $p$ dimensional vector to obtain attention scores without using RNN. For attention with context, a simple RNN or LSTM with unit size $h$ is used to compute attention scores. After obtaining the summarized matrix $D_{summ}$, we use LSTM or bidirectional LSTM with hidden state of size $H$ to tag the clauses.

LSTM-Attention We take the input tensors $D$ of shape $c \times w \times d$ and output a matrix $A$ of shape $c \times w$ which contains the attention weights of all the words in each clause. We first project each input word into a lower dimensional space using a projection matrix $P$ of shape $d \times p$.

$$D_l = \tanh(D \cdot P) \in \mathbb{R}^{c \times w \times d}$$

We score $D_l$ with context that is summarized by an LSTM. Specifically, we score each word in the $i$th clause in the context of other words in the same clause using an LSTM. The score for each word is a function of its $p$ dimensional representation $W_j$ and the previous words in the clause represented by the hidden states $(h_{l-1}^j)$ in the LSTM cell. The equations are the following:

$$D_l^i = D_l[i,:) \in \mathbb{R}^{w \times p}$$
$$W_j = D_l[j,:) \in \mathbb{R}^p$$
$$h_l^j = LSTM(W_j, h_{l-1}^j) \in \mathbb{R}^h$$
$$h' = [h_1^j h_2^j ... h_w^j] \in \mathbb{R}^{w \times h}$$
$$a^i = \text{softmax}(h' \cdot s) \in \mathbb{R}^w$$
$$A = [a^1 a^2 ... a^w] \in \mathbb{R}^{c \times w}$$

where $LSTM$ is an LSTM cell with the unit size of $h$. $s$ is a vector of length $h$.

Finally like Dasigi et al. (2017), a $c \times d$ shaped weighted sum $D_{summ}$ of the input tensor $D$ is computed, with the weights computed by the attention mechanism, then it is fed to a clause-level sequence tagger to tag discourse labels.

$$D_{summ}[i,:) = A[i,:) \cdot D[i,:,\cdot] \in \mathbb{R}^d$$
A.3 Labels in BIO Schema

We convert the labels into BIO schema where none label represents $O$ and all other labels are converted into $B_{label}$ when the previous label type is different from the current label and $I_{label}$ when the previous label is the same as the current label. We use the labels in BIO schema to train all of our models (Baseline models do not use BIO schema).

A.4 Implementation and Training Details

The model is implemented using Keras (Chollet et al., 2015) with Tensorflow (Abadi et al., 2015) backend. We use early stopping mechanism with toleration of 5 epochs. We schedule the training by training the model with a learning rate of $lr$ for 100 epochs, and then the learning rate is decreased to 1/10 and fine-tuned with another 100 epochs. We use Adam (Kingma and Ba, 2014) for the optimizer. We use 5-fold cross validation F1 measure as our main performance measure and we report both F1 scores under BIO schema and the one removed BIO schema.

The optimal hyper-parameters and the attempted range if applicable are listed in Table 4.

| Hyper-Parameter | Used | Range             |
|-----------------|------|-------------------|
| $d_{BERT}$      | 768  | N/A               |
| $c$             | 30   | N/A               |
| $w$             | 55   | N/A               |
| $d$             | 300  | 200, 300, 768     |
| $d_2$           | 225  | 50 ~ 300          |
| $p$             | 110  | 25 ~ 150          |
| $h$             | 60   | 12 ~ 150          |
| $H$             | 200  | 50 ~ 350          |
| $lr$            | $10^{-3}$ | $10^{-4}$ ~ $10^{-2}$ |
| Validation Set Ratio | 0.1 | N/A               |
| Embedding dropout | 0.4 | 0 ~ 0.6          |
| Dense dropout   | 0.4  | 0 ~ 0.6          |
| Attention dropout | 0.6 | 0 ~ 0.6          |
| LSTM dropout    | 0.5  | 0 ~ 0.6          |
| Batch size      | 10   | 5, 10             |

Table 4: Optimal hyper-parameters and the range among which the hyper-parameter is tuned (some are not applicable)
| Embedding     | Attention Context | Sequence Tagger | BIO CV F1 | CV F1 | Test F1 | Note          |
|--------------|------------------|----------------|----------|-------|--------|---------------|
| BioBERT      | LSTM             | biLSTM+CRF     | 0.716    | 0.784 | 0.808  | Best Model    |
| BioBERT      | LSTM             | biLSTM         | 0.712    | 0.780 | 0.796  |               |
| BioBERT      | RNN              | biLSTM         | 0.707    | 0.778 | 0.808  |               |
| BioBERT      | No Context       | biLSTM+CRF     | 0.711    | 0.777 | 0.808  |               |
| BioBERT      | No Context       | biLSTM         | 0.706    | 0.777 | 0.802  |               |
| BioBERT      | RNN              | biLSTM+CRF     | 0.711    | 0.776 | 0.820  |               |
| BioGloVe     | LSTM             | biLSTM         | 0.698    | 0.772 | 0.805  |               |
| BioBERT      | LSTM             | LSTM           | 0.702    | 0.771 | 0.796  |               |
| BioBERT      | No Context       | LSTM           | 0.697    | 0.770 | 0.782  |               |
| BioBERT      | RNN              | LSTM           | 0.701    | 0.770 | 0.782  |               |
| BioGloVe     | LSTM             | CRF            | 0.694    | 0.768 | 0.808  |               |
| BioBERT      | No Context       | CRF            | 0.691    | 0.766 | 0.797  |               |
| BioBERT      | RNN              | CRF            | 0.688    | 0.765 | 0.785  |               |
| BioGloVe     | LSTM             | biLSTM+CRF     | 0.692    | 0.765 | 0.793  |               |
| BioGloVe     | RNN              | biLSTM+CRF     | 0.691    | 0.764 | 0.788  |               |
| BioGloVe     | RNN              | LSTM           | 0.688    | 0.763 | 0.800  |               |
| BioGloVe     | LSTM             | LSTM           | 0.686    | 0.760 | 0.802  |               |
| BioGloVe     | No Context       | biLSTM         | 0.678    | 0.759 | 0.808  |               |
| BioGloVe     | RNN              | CRF            | 0.685    | 0.759 | 0.761  |               |
| BioBERT      | LSTM             | CRF            | 0.679    | 0.759 | 0.794  |               |
| BioGloVe     | No Context       | CRF            | 0.680    | 0.758 | 0.765  |               |
| BioGloVe     | No Context       | biLSTM+CRF     | 0.682    | 0.757 | 0.769  |               |
| BioWord2Vec  | RNN              | LSTM           | N/A      | 0.746 | 0.774  | Dasigi et al. (2017) |
| N/A          | N/A              | CRF            | N/A      | 0.713 | 0.707  | Baseline      |
| N/A          | N/A              | SVM            | N/A      | 0.697 | 0.734  | Baseline      |
| BioBERT      | N/A              | biLSTM+CRF     | 0.581    | 0.666 | 0.691  |               |
| BioBERT      | N/A              | biLSTM         | 0.578    | 0.666 | 0.688  |               |
| BioGloVe     | N/A              | biLSTM+CRF     | 0.565    | 0.649 | 0.674  |               |
| BioGloVe     | N/A              | biLSTM         | 0.559    | 0.643 | 0.686  |               |
| BioBERT      | N/A              | LSTM           | 0.553    | 0.639 | 0.651  |               |
| BioGloVe     | N/A              | LSTM           | 0.548    | 0.633 | 0.653  |               |
| BioGloVe     | N/A              | CRF            | 0.513    | 0.611 | 0.632  |               |
| BioBERT      | N/A              | CRF            | 0.501    | 0.599 | 0.646  |               |

Table 5: Performance of models with different configurations sorted by original cross-validation F1 score