Benchmarking BioRelEx for Entity Tagging and Relation Extraction

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Abstract

Extracting relationships and interactions between different biological entities is still an extremely challenging problem but has not received much attention as much as extraction in other generic domains. In addition to the lack of annotated data, low benchmarking is still a major reason for slow progress. In order to fill this gap, we compare multiple existing entity and relation extraction models over a recently introduced public dataset, BioRelEx of sentences annotated with biological entities and relations. Our straightforward benchmarking shows that span-based multi-task architectures like DYGIE show 4.9% and 6% absolute improvements in entity tagging and relation extraction respectively over the previous state-of-art and that incorporating domain-specific information like embeddings pre-trained over related domains boosts performance.

1 Introduction

Extracting biological entities and determining relationships between them is particularly challenging due to the heterogeneous nomenclature of such entities. Besides, along with the rapid changes in molecular biology, there is a lack of consensus over a standardized dataset. While Khachatrian et al. (2019) attempt to address the issue of standardization by introducing BioRelEx, there is still plenty of room for improving the tagging and relation extraction of these entities.

Especially when there has been tremendous progress achieved by multi-task span-based architectures to extract entities and relations in various datasets within domains like news and scientific articles (Luan et al., 2019; Wadden et al., 2019), we attempt to seek if this success can be emulated to recent standardized biological literature, like BioRelEx.

We compare a range of classifiers; previously common generic ones like CRF and BiLSTM as well as recent state-of-the-art (SOA) multi-task span based architectures like Dynamic Graph IE (DYGIE) (Luan et al., 2018, 2019) in order to provide a stronger benchmark over BioRelEx (Khachatrian et al., 2019), a recently published dataset of 2010 sentences consisting annotations of biological entities and binding interactions between those entities. We also check the impacts of using DYGIE’s updated span representations obtained from relation and coreference graph propagation. Given the domain specificity of BioRelEx, we assess the impact of utilizing embeddings pre-trained on related domains.

2 Related Work

Most information extraction systems have looked at entity tagging as a flat sequence labeling problem and have employed feature-based CRFs and later neural architectures (Ma and Hovy, 2016; Peters et al., 2018). Lample et al. (2016) take inspiration from shift-reduce parsers to employ a transition based approach. Yu and Lam (2010); Miwa and Sasaki (2014); Li and Ji (2014); Zheng et al. (2017)
have jointly modelled entity tagging and relation extraction. Fu et al. (2019) use relation-weighted graph convolution networks for considering the interaction between named entities and relations. To incorporate the ability to tag overlapping spans, Katiyar and Cardie (2018); Wang and Lu (2018, 2019) devised neural methods applying hyper graph based representations on top of sequence labelling.

Fei et al. (2019); Dai et al. (2020) tag nested and discontinuous mentions in biomedical text. Lee et al. (2017, 2018) enumerate over all possible spans and apply bean pruning to reduce the number of candidate spans used for coreference resolution. Luan et al. (2018, 2019) further apply a multi-task graph based architecture incorporating relation, coreference and event based propagation to enhance span representations.

Lin et al. (2020) test how well do current NER models generalize in the absence of strong name regularity, high mention coverage and sufficient context diversity.

Khachatrian et al. (2019) introduce BioRelEx by annotating bio-medical texts with entities grounded with other databases, focusing on delineating biological and experimental entities and distinguishing between direct regulatory and indirect physical interactions.

3 Dataset & Evaluation

Khachatrian et al. (2019) have made publicly available 2010 annotated sentences (1405 for training and 201 for validation) consisting of annotations for 33 types of entities and relation annotations for binding interactions. We gauge the performance of all architectures over the validation dataset using the evaluation script of Khachatrian et al. (2019) namely measuring the micro-averaged precision, recall and F-score.

4 Entity Tagging

Entity Tagging (Figure 1) is the task of predicting the best entity type label for every span of words in a given piece of text. And Relation Extraction (Figure 2) involves predicting the best relation type for such entity spans.

4.1 Traditional Architectures

We evaluate various architectures traditionally common for the task of entity tagging which have displayed strong performances on other entity tagging datasets. As a baseline, we train a BiLSTM-CRF (Huang et al., 2015), a BiGRU-CRF and a CNN-CRF (Collobert et al., 2011) with 300-d Glove embeddings (Pennington et al., 2014) as input.

BioRelEx, like other bio-medical texts, belong to a knowledge intensive domain and hence we expect a considerable amount of domain-specific terms to appear. In accordance with that, we incorporate sub-word embeddings by taking advantage of

- Flair’s (Akbik et al., 2019) implementation of Contextual String Embeddings (Akbik et al., 2018) which use a character-language model
- Byte Pair Embeddings (Heinzerling and Strube, 2018)
- FastText Embeddings (Bojanowski et al., 2017)

as inputs to a BiLSTM. Table 1 compares the performance of these traditional architectures along with the various embeddings on BioRelEx’s validation dataset. Our experiments show that Flair embeddings provide a clear gain of 14% over other embeddings. However, flat architectures like BiLSTM unarguably lack the ability to model overlapping spans and hence in the next section, we attempt to use recently successful architectures like DYIE to check for performance gains.

4.2 Multi-Task Architectures

We choose to evaluate DYIEPP (Wadden et al., 2019) which has shown strong results on many entity tagging datasets and emphasized the importance of pre-training with text from similar domains like SciBERT (Beltagy et al., 2019).

In Table 2, we present different configurations of DYIEPP along with their results. Surprisingly, concatenation of ELMo Embeddings (Peters et al., 2018), Glove and Character Embeddings performs better than SciBERT for the BioRelEx dataset. Although, relation propagation do not seem to help much, coreference propagation shows an increase in the scores. Moreover, we observe that increasing the number of hidden units and layers boosts the scores. ¹

DYIEPP’s best configuration performs 3.2% better than the current SOA, SciERC (Beltagy et al., 2019; Khachatrian et al., 2019).

¹We find that keeping 400 hidden units and 2 layers in the BiLSTM works best for our case. So, we use this configuration in all our future experiments.
Table 1: Performance of Flat Architectures on Entity Tagging. News-* and Pubmed-* are character level embeddings (Akbik et al., 2018, 2019) used as inputs to a BiLSTM-CRF.

| System                                      | Precision | Recall | F-score |
|----------------------------------------------|-----------|--------|---------|
| BiLSTM-CRF (Glove)                          | 0.316     | 0.523  | 0.320   |
| BiLSTM-CRF (Glove)                          | 0.508     | 0.483  | 0.495   |
| CNN-CRF (Glove)                             | 0.541     | 0.500  | 0.520   |
| News-forward + News-backward + Glove        | 0.723     | 0.604  | 0.658   |
| Pubmed-forward + Pubmed-backward + BytePairEmbeddings | 0.743     | 0.596  | 0.662   |
| Pubmed-forward + Pubmed-backward + BytePairEmbeddings + FastText | 0.748     | 0.591  | **0.660** |

Table 2: Performance of Multi-Task Architectures on Entity Tagging. DYGIIEPP mentioned in the third row uses ELMo embeddings but without graph propagation. Also it has 400 BiLSTM units and 3 BiLSTM layers.

| System                                      | Precision | Recall | F-score |
|----------------------------------------------|-----------|--------|---------|
| DYGIIEPP (SciBERT)                         | 0.587     | 0.630  | 0.600 (-0.208) |
| DYGIIEPP (BERT-base)                        | 0.567     | 0.660  | 0.610 (-0.198) |
| DYGIIEPP                                    | 0.832     | 0.786  | 0.808   |
| +Relation Propagation (RP)                  | 0.845     | 0.766  | 0.803 (-0.005) |
| +Coreference Propagation (CP)               | 0.837     | 0.787  | **0.811 (+0.003)** |
| +RP, CP                                     | 0.832     | 0.767  | 0.798 (-0.010) |
| DYGIIEPP (200 BiLSTM units 1 layer)         | 0.836     | 0.769  | 0.801 (-0.007) |
| DYGIIEPP (400 BiLSTM units 2 layers)        | 0.826     | 0.773  | 0.800 (-0.008) |
| DYGIIEPP (512 BiLSTM units 3 layers)        | 0.852     | 0.771  | 0.810 (+0.002) |
| SciERC                                      | 0.864     | 0.710  | 0.779   |

Table 3: Impact of using Domain Specific Embeddings on Entity Tagging. We perform the experiments on DYGIIEPP with the same base configuration as that of the Section 4.2 (Table 2).

| System                                      | Precision | Recall | F-score |
|----------------------------------------------|-----------|--------|---------|
| +BioELMo                                    | 0.858     | 0.790  | 0.823 (+0.015) |
| +BioELMo, Relation Propagation (RP)          | 0.862     | 0.794  | 0.827 (+0.019) |
| +BioELMo, Coreference Propagation (CP)       | 0.858     | 0.792  | 0.824 (+0.016) |
| +BioELMo, RP, CP                            | 0.851     | 0.805  | **0.828 (+0.020)** |
| +BioELMo, 200 BiLSTM units 1 layer           | 0.836     | 0.807  | 0.821 (+0.013) |
| +BioELMo, 400 BiLSTM units 2 layers          | 0.859     | 0.790  | 0.822 (+0.014) |
| +BioELMo, BioWord2Vec                       | 0.844     | 0.793  | 0.818 (+0.010) |

Table 4: Relation Extraction Performance of Multi-Task Architectures. We use the same base configuration of DYGIIEPP as the one in Section 4.2 (Table 2).

| System                                      | Precision | Recall | F-score |
|----------------------------------------------|-----------|--------|---------|
| DYGIIEPP (SciBERT)                         | 0.241     | 0.139  | 0.176 (-0.379) |
| DYGIIEPP (BERT-base)                        | 0.239     | 0.109  | 0.150 (-0.405) |
| DYGIIEPP                                    | 0.592     | 0.523  | 0.555   |
| +Relation Propagation (RP)                  | 0.628     | 0.500  | **0.556 (+0.001)** |
| +Coreference Propagation (CP)               | 0.450     | 0.520  | 0.482 (-0.073) |
| +RP, CP                                     | 0.479     | 0.527  | 0.502 (-0.053) |
| DYGIIEPP (200 BiLSTM units 1 layer)         | 0.569     | 0.459  | 0.508 (-0.047) |
| DYGIIEPP (400 BiLSTM units 2 layers)        | 0.570     | 0.452  | 0.504 (-0.051) |
| DYGIIEPP (512 BiLSTM units 3 layers)        | 0.594     | 0.503  | 0.545 (-0.010) |
| SciERC                                      | 0.490     | 0.503  | 0.496   |

Table 5: Relation Extraction Performance of Domain Specific Embeddings over DYGIIEPP.
4.3 Domain-Specific Embeddings

Domain-specific embeddings have been essential to achieve high performances for entity tagging tasks especially in knowledge intensive domains. (Romanov and Shivade, 2018; Zhu et al., 2018). Since BioRelEx is a domain specific dataset, we experimented with embeddings trained on related domains as well as with embeddings pre-trained on BioRelEx.

We replaced the original ELMo embeddings in Wadden et al. (2019) with BioELMo (Jin et al., 2019) which have been pre-trained on 10M PubMed abstracts. We use Word2Vec embeddings trained on PubMed data (Pyysalo et al., 2013) too, which we will refer to as BioWord2Vec and also train Glove embeddings on the BioRelEx dataset. We present the results in Table 3. We observe that incorporating BioELMo boosts performance of DYGIEPP by an absolute 1.7% over ELMo embeddings. Using coreference propagation and relation propagation reveal slight improvement as well.

5 Relation Extraction

5.1 Multi-Task Architectures

Since the multi-task architecture proposed by Luan et al. (2018); Wadden et al. (2019) have attempted to leverage context across multiple sentences as well as incorporate coreference, relation and event information to enhance span representations, we verify if this success would easily apply to BioRelEx since this dataset contains a notable amount of coreferences and biologically nested entities like shown in Figure 1.

We summarise the results for relation extraction in Table 4. Here, the combination of ELMo, Glove and Character Embeddings performs remarkably better than SciBERT. Contrary to entity tagging, for relation extraction, enabling relation propagation gives us the best scores. Further increasing the layers and the number of units in the BiLSTM also helps a lot in this case.

5.2 Domain-Specific Embeddings

We follow the same steps as followed for entity tagging. We present the results for relation extraction in Table 5. We observe that whereas in case of entity tagging, using domain specific embeddings, specifically BioELMo shows a good improvement, for relation extraction, they show a slight decrease in the F-score. Comparing Table 5 to Table 4, we see a small reduction when using domain specific embeddings. Similar to entity tagging, here too, BioWord2Vec reduces the F-score.

6 Conclusion

We evaluate a number of architectures for entity tagging and relation extraction and perform extensive hyperparameter tuning over the BioRelEx dataset. Our experiments improve BioRelEx’s SOA for entity tagging and relation extraction by 4.9% and 6% F-score respectively. Our evaluations show that using ELMo, Glove and character embeddings improves the performance compared to BERT and SciBERT on multi-task architectures. Likewise, utilizing domain specific information in the form of pre-trained embeddings also leads to an improvement in performance for entity tagging.

7 Discussion

Multi-task architectures like DYGIE, by and large with domain-specific embeddings improve the predictions of BioRelEx. Interestingly, we find that contextual embeddings like ELMo and BioELMo exceed the performance of BERT (Devlin et al., 2018) and SciBERT by a large margin which is tangential to findings on other benchmarks like GLUE (Wang et al., 2018).

Besides, we observe that in a few cases, certain span annotations of entities are not being taken into account while converting to SciERC’s input format by the provided conversion script, but were being expected to be predicted during the evaluation process making it impossible for any model to go beyond a training set F-score of 91.2%. While this minor incorporation in BioRelEx might drastically improve F-scores for all of the architectures, relative differences of performances between the architectures might hardly change. We would still expect multi-task architectures to predict BioRelEx entities and relations better vis--vis traditional architectures as the F-scores display an appreciable leap of 15% to 30% already (Table 1 vs Table 2).

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