

Linguistically Informed Relation Extraction and Neural Architectures for Nested Named Entity Recognition in BioNLP-OST 2019

*Usama Yaseen^{1,2}, *Pankaj Gupta^{1,2}, Hinrich Schütze²

¹Corporate Technology, Machine-Intelligence (MIC-DE), Siemens AG Munich, Germany

²CIS, University of Munich (LMU) Munich, Germany

{usama.yaseen, pankaj.gupta}@siemens.com

Abstract

Named Entity Recognition (NER) and Relation Extraction (RE) are essential tools in distilling knowledge from biomedical literature. This paper presents our findings from participating in BioNLP Shared Tasks 2019. We addressed Named Entity Recognition including nested entities extraction, Entity Normalization and Relation Extraction. Our proposed approach of Named Entities can be generalized to different languages and we have shown it's effectiveness for English and Spanish text. We investigated linguistic features, hybrid loss including ranking and Conditional Random Fields (CRF), multi-task objective and token-level ensembling strategy to improve NER. We employed dictionary based fuzzy and semantic search to perform Entity Normalization. Finally, our RE system employed Support Vector Machine (SVM) with linguistic features.

Our NER submission (team:MIC-CIS) ranked first in *BB-2019 norm+NER task* with standard error rate (SER) of **0.7159** and showed competitive performance on *PharmaCo NER task* with F1-score of **0.8662**. Our RE system ranked first in the *SeeDev-binary Relation Extraction Task* with F1-score of **0.3738**.

1 Introduction

Extracting knowledge from scientific articles is a challenging but very important problem. This becomes especially critical for biomedical literature which is growing at an increasing rate of at least 4% per year, as of June 2019 there are 30 Million documents in PubMed (Lu, 2011). Named Entity Recognition (NER) (Settles, 2004; Gupta et al., 2016; Lample et al., 2016) in the context of biomedical domain refers to the task of identifying the name of the biological entities e.g. name of a bacteria. Relation extraction¹ (RE) (Kambhatla,

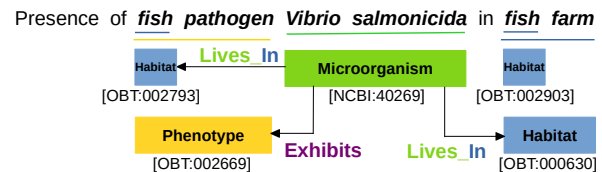


Figure 1: An illustration of (nested) NER + Normalization and Relation Extraction in Biomedical entities. Each rectangular box spans an entity, where the overlapping spans indicate nested entities. E.g., *fish* is a nested entity (a sub-concept) of type *Habitat* within the parent entity *fish pathogen* of type *Phenotype*. The identifiers (e.g. OBT:002669, NCBI:40269, etc.) refer to unique IDs in Biomedical databases (i.e., OBT → OntoBiotope Ontology and NCBI → NCBI Taxonomy), used to perform entity normalization (i.e., entity linking). The arrows indicate binary relationships.

2004; McDonald et al., 2005; Lever and Jones, 2016; Gupta et al., 2018) refers to identifying relations among biological entities (binary or n-ary).

Figure 1 illustrates an example of (nested) NER and RE consisting of five entities, where three entities participate in two distinct relationships. It is often required to link named entity(s) to a unique reference in database(s). For instance, one of the two occurrences of *fish* refers to *marine fish* while the second refers to a *farm fish*, where the two entities are linked (or normalized) to different identifiers (e.g., OBT:002793 and OBT:002903) in the biomedical database (e.g., OntoBiotope Ontology). The act of linking entities to standard entities with a unique identifier is known as entity normalization and is challenging as several entity mentions can correspond to the same standard entity (or unique identifier), e.g. *E. coli*, *Bacillus coli* and *Bacteriumcoli* refer to the standard entity *Escherichia coli* in the database. The linking process relies on knowledge base (KB) search (heuristic OR semantic) in order to resolve entities.

NER is a critical primitive step in the NLP

* Equal Contribution

¹Event extraction is treated as RE in this work

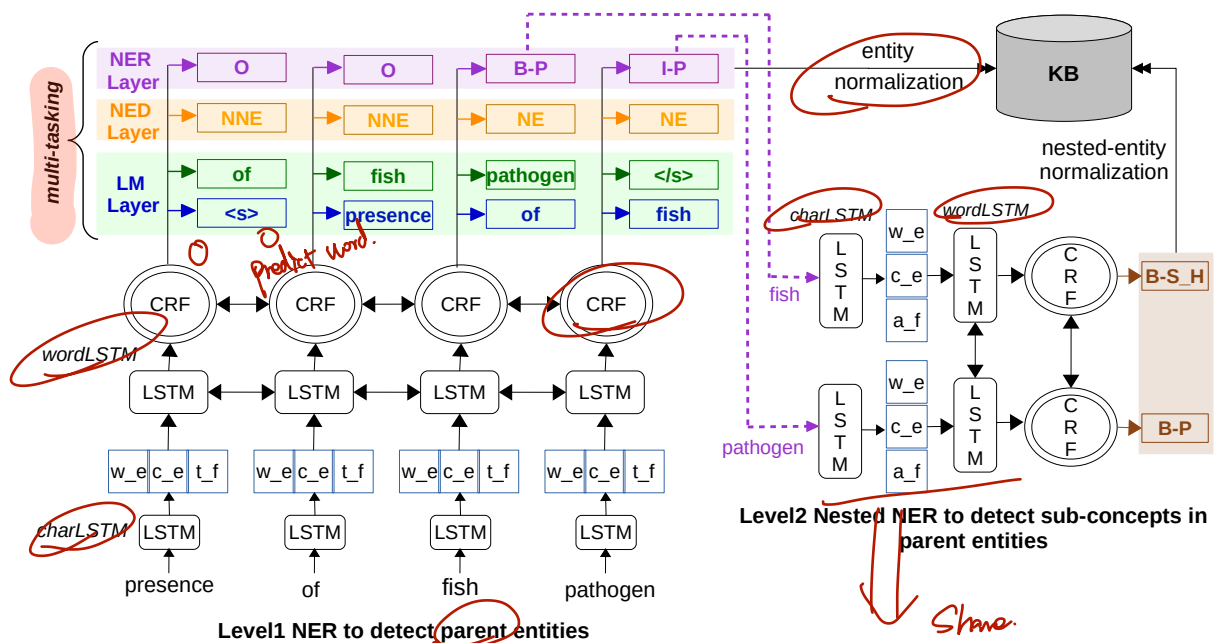


Figure 2: System Architecture for NER task, consisting of two bi-LSTM-CRF architectures: Level1 NER to detect parent entities and Level2 Nested NER to detect sub-concepts within the parent entities (output of Level1 NER). Here, w_e : a word embedding vector; c_e : an embedding vector for a word computed using character-level bi-directional LSTM; t_f : a vector of additional linguistic features; B_P: B_Pathogen; B-S_H: a sub-concept of type *Habitat* detected by the Level2 Nested NER run over the the parent entity.

pipeline as downstream tasks such as RE, text classification, Question Answering (QA) etc., depend on it. Even though several methods have been devised to engineer reliable NER systems; however, most of them don't explicitly address the extraction (or recognition) of nested entities, especially required in the biomedical domain. *Nested entity* is defined as an entity or sub-concept which is part of a longer entity (i.e., a parent). For instance in the Figure 1, *fish* is a nested entity as it is part of a parent entity *fish pathogen*. In this work, we have also investigated extracting nested entities via two bi-LSTM-CRF (Lample et al., 2016) networks: one for parent detection and another for nested entities with the parent entity.

2 Task Description and Contribution

We participate in the following three tasks organized by BioNLP workshop 2019: (1) **PharmaCoNER**: Recognition of pharmaceutical drugs and chemical entities in Spanish text. (2) **BB-norm+NER**: Recognition of *Microorganism*, *Habitat* and *Phenotype* entities and normalization with NCBI Taxonomy and OntoBiotope habitat concepts. (3) **SeeDev Binary RE**: Binary Relation extraction of genetic and molecular mechanisms involved in plant seed development.

Following are our multi-fold *contributions*:

1. To address NER tasks, we have employed neural network based sequence classifier, i.e., bi-LSTM-CRF and investigated multi-tasking of named entity detection (NED) and language modeling (LM). We further introduced hybrid loss including CRF and ranking. We also incorporated linguistic features such as POS, orthographic features, etc. We apply the proposed modeling approaches to both English and Spanish texts. Comparing with other systems, our submission (Team: MIC-CIS) is ranked 1st in *BB-norm+NER* task (Bossy et al., 2019) with standard error rate of 0.7159. In *PharmaCoNER* task (Gonzalez-Agirre et al., 2019), our submission scored F1-score of 0.8662.
2. To address RE task, we employed linguistic and entity features in SVM. Our submission (Team: MIC-CIS) is ranked 1st in SeeDev binary RE task (Chaix et al., 2016) with F1-score of 0.3738.

The code to reproduce our results is available at: <https://github.com/uyaseen/bionlp-ost-2019>.

multi-language

Many feature work

Features	Description
word-cap	capitalization features
POS	parts-of-speech tags
ortho	orthographic features e.g. <i>Egg Pulp</i> , 97 encoded as <i>Ccc Ccccp nn</i>
tri-gram	tri-gram as features
five-gram	five-gram as features
length	length of the word
sdp-rel	dependency relation tag
alpha-features	detect if certain linguistic pattern occurred in the current word or the next word

Table 1: Word-level features for NER. The features are encoded as embeddings, except the *alpha* features that are represented as one-hot vector.

3 Methodology

In the following sections we discuss our proposed model for NER and RE.

3.1 Neural Architectures for NER

Figure 2 describes the architecture of our model, where we design two sequence taggers *Level1 NER* and *Level2 Nested NER* to extract parent and nested entities respectively. Furthermore, Level1 NER can be configured in two modes: (1) LSTM-CRF (Lample et al., 2016) with word embeddings (w_e), character embeddings (c_e) and token-level features (t_f) such as POS, capitalization features, word shape, etc. (refer to table 1 for the complete list of word level features) (2) LSTM-CRF+Multi-task that performs entity detection and language modelling as auxiliary tasks. Note that Level2Nested NER only operates on the parent entities detected by Level1 NER. The parent and nested entities are then normalized to unique identifiers in KB by our entity normalization algorithm.

3.1.1 BiLSTM-CRF

The input to LSTM is a sequence of word features ($\mathbf{w}_1, \mathbf{w}_2, \dots, \mathbf{w}_n$) and they compute a hidden state for each element in the sequence ($\mathbf{h}_1, \mathbf{h}_2, \dots, \mathbf{h}_n$). This hidden state can be used to jointly model tagging decisions using CRF (Lafferty et al., 2001). CRF imposes ordering constraints on the tagging decisions e.g. I_Habitat should always be preceded by B_Habitat. For an input sentence,

$$\mathbf{W} = (\mathbf{w}_1, \mathbf{w}_2, \dots, \mathbf{w}_n),$$

we consider a matrix \mathbf{P} of scores output by the bidirectional LSTM. The size of \mathbf{P} is $n \times k$,

where k is the number of distinct tags, and $P_{i,j}$ corresponds to the score of the j^{th} tag of the i^{th} word in a sentence. For a sequence of predictions

$$\mathbf{y} = (y_1, y_2, \dots, y_n),$$

we define its score to be

$$s(\mathbf{X}, \mathbf{y}) = \sum_{i=0}^n A_{y_i, y_{i+1}} + \sum_{i=1}^n P_{i, y_i}$$

where the matrix \mathbf{A} express transition scores such that $A_{i,j}$ represents the score of a transition from the tag i to tag j . We add start and end tag to the set of possible tags, therefore, the size of \mathbf{A} is $k + 2$. During training, we minimize the negative log-probability of the correct tag sequence:

$$\begin{aligned} \log(p(\mathbf{y}|\mathbf{X})) &= s(\mathbf{X}, \mathbf{y}) - \log \left(\sum_{\tilde{\mathbf{y}} \in \mathbf{Y}_{\mathbf{X}}} e^{s(\mathbf{X}, \tilde{\mathbf{y}})} \right) \\ &= s(\mathbf{X}, \mathbf{y}) - \log \text{add}_{\tilde{\mathbf{y}} \in \mathbf{Y}_{\mathbf{X}}} s(\mathbf{X}, \tilde{\mathbf{y}}), \quad (1) \end{aligned}$$

$$loss_{CRF} = -\log(p(\mathbf{y}|\mathbf{X})) \quad (2)$$

3.1.2 Hybrid Loss: CRF + Ranking

We use a variant of ranking loss function proposed by dos Santos et al. (2015). Ranking maximizes the distance between the true label y^+ and the most competitive label c^- :

$$loss_{ranking} = \max(0, 1 + (\gamma * (m^+ - y^+)) + (\gamma * (m^- + c^-)))$$

where γ is the scaling factor that penalizes the predictions, m^+ and m^- are margins for correct and incorrect labels respectively. We follow Vu et al. (2016) to set the values of margins.

The hybrid loss function hence is the sum of CRF tagging loss and ranking loss:

$$loss_{hybrid} = loss_{CRF} + \alpha \cdot loss_{ranking}$$

where $\alpha \in [0, 1]$, weighs the contribution of ranking loss in the overall loss value. During training we minimize the hybrid loss and found it to improve the F1 score for both *BB-norm+NER* and *PharmaCoNER* tasks.

3.1.3 Multi-Tasking of Named Entity Recognition, Detection and Language Modelling

We employed auxiliary objectives of named-entity detection (NED) (Aguilar et al., 2017) and bidirectional language modelling (LM) (Rei, 2017) in our

Algorithm 1 Entity Normalization

Input: NE, NE_Type
Output: RF_ID
Output: NE_PRED (Optional)

```
1: RF_ID = None
2: IF NE_Type == 'Microorganism':
3:   found, RF_ID = exact_match(NE, NCBI)
4:   if not found:
5:     found, RF_ID = fuzzy_match(NE, NCBI)
6:   return RF_ID
7: ELSE
8:   found, RF_ID = exact_match(NE, NCBI)
9:   if not found:
10:    found, RF_ID = fuzzy_match(NE, NCBI)
11:   if found:
12:     # LABEL UPDATE !
13:     NE_PRED = 'Microorganism'
14:     return RF_ID, NE_PRED
15:   found, RF_ID = exact_match(NE, OBT)
16:   if not found:
17:     found, RF_ID = semantic_search(NE, OBT)
18: return RF_ID
```

model. Usually these auxiliary objectives acts as regularizes (Collobert and Weston, 2008) and improves the overall performance. With these multi-tasking objectives, for each word token our model predicts the NED tag, next word, previous word and the NER tag². LM and NED layers in figure 2 realizes NED and LM objectives respectively. Note that Multi-tasking is only enabled at train time and requires no additional labelling.

3.1.4 Nested Entities

The dataset of *BB-norm+NER* task contains 17.4% nested entities³ which cannot be extracted by standard Bi-LSTM CRF model. We employed two Bi-LSTM-CRF models: *Level1* NER model to detect parent entities and *Level2* Nested NER model to detect nested entities. Figure 2 (right) shows the architecture of Level2 Nested NER. The parent entities detected by Level1 NER are fed to Level2 Nested NER to detect nested entities in the parent entities. Level2 Nested NER has the same architecture as Level1 NER but without the multi-tasking objectives. It is easy to see that current architecture can only detect nested entities at level 2. The final output of model is the aggregation of parent entities and nested entities.

3.1.5 Entity Normalization

The goal of entity normalization (entity linking) is to map noisy predicted entities in text to canonical

entities in knowledge base (KB). This is challenging because: (1) not all variations of textual forms for a canonical entity exists in the KB, (2) syntactic variations in the predicted entity mentions due to misspellings, abbreviations, acronyms and boundary errors.

For *BB-norm+NER* task, we used two Biomedical databases *OntoBiotope Ontology* and *NCBI Taxonomy*. *OntoBiotope Ontology* contains 3,602 canonical forms of type *Habitat* and *Phenotype*. *NCBI Taxonomy* contains 1,082,401 records for type *Microorganism*. We employed exact, fuzzy and semantic (embedding) search to perform entity normalization. Algorithm 1 illustrates the detailed steps of our algorithm, note that type and order of search depends on the predicted named entity type. We also employed *caching* to minimize pairwise comparisons and improve the overall run-time efficiency.

3.1.6 Post-processing for NER+norm

Our model (see Figure 2) employs CRF at decoding step to impose boundary ordering constraints on the predicted named entity types e.g. *I* should always be preceded by a *B* token. But our model does not always respect such ordering constraints and therefore, we resolve boundary inconsistencies at inference time to make the NER labels consistent. *Post-processing* column in the Table 3 illustrates the post-processing resolving inconsistent labels after the voting on majority labels, consider row *r3* where post-processing correctly imposes the semantics of boundary ordering by changing *I-Habitat* to *B-Habitat*.

3.2 Relation Extraction

Deep Learning based methods are state of the art in relation extraction (Wu and He, 2019; Wang et al., 2016) but they require large amount of labelled training data. In cases when enormous training data is not available than Kernel methods like Support Vector Machines (SVM) are an optimal choice. We employed SVM for performing relation extraction. One of the downsides of SVM is that they usually require lots of hand-crafted features to train properly. Table 2 lists computed general and entity features.

Our best model was trained with Radial Basis Function (RBF) Kernel with value of penalty parameter *C* determined by grid search for each dataset. We employed oversampling and class-weight penalization to handle imbalanced data.

²we used IOBES tagging scheme

³<https://groups.google.com/d/msg/bb-2019/A2MuFYiPQIY/9YtMmakeBQAJ>

General Features	Description	Entity Features	Description
bow	bag-of-words (bow) representation of the complete sentence	entity-pos	position of entity in the bow representation
bow-partial	bow representation of the between context (i.e. word tokens between target entities) including three words to the target entities	entity-type	type of the entity mentions
bow-lemma	bow representation of the lemmatized tokens in the between context	dist-entities-cat	distance between target entities as categorical
pos-tags	part-of-speech tags	dist-entities	distance between target entities
sdp	shortest dependency path as bow	entity-count	count of entities in between context
sdp-len	length of shortest dependency path as scalar	entity-count-cat	count of entities in between context as categorical
sdp-rel	dependency relation tag	e1 type = e2 type	if type of e1 and e2 is same
emb-sdp	average embeddings of sdp	sdp-entity	sdp with entity as bow
keyword-vec	if current word is part of feature list of relations	entity-patterns	check if certain linguistic patterns occur in the vicinity of target entities

Table 2: General and Entity features used in Relation Extraction

	Tokens	Models			Voting	Post-processing
		M1	M2	M3		
r1	Presence	O	O	O	O	O
r2	of	O	O	B-H	O	O
r3	fish	I-H	B-H	I-H	I-H	B-H
r4	pathogen	I-H	I-P	I-P	I-P	B-P
r5	Vibrio	B-M	B-M	B-M	B-M	B-M
r6	salmonicida	I-M	O	I-M	I-M	I-M
r7	in	B-H	O	O	O	O
r8	fish	B-H	O	B-H	B-H	B-H
r9	farm	I-H	O	I-M	I-H	I-H
r10	.	O	O	O	O	O

Table 3: NER: Ensembling and Post-processing correcting individual models mistakes. Here, B, P and M refer to Habitat, Phenotype and Microorganism, respectively.

Surprisingly oversampling did not provide any performance improvement therefore, final models were trained only with higher class weights for minority classes. We did not normalize any input feature as it resulted in reduced performance.

In relation extraction participating entities are not known in advance, the usual practise is to test every valid pair of entities for a relation. We employed heuristic of *token counts* between entities to filter the probable invalid relations. The value of token counts was determined using cross-validation.

3.3 Ensemble Strategy

Bagging is a helpful technique to reduce variance without impacting bias of the learning algorithm. We employed a variant of *Bagging* (Breiman, 1996) which makes sure that every sample in the training set is part of the development set at least

once and vice versa. We created three data folds and trained the model using optimal configuration on each fold, prediction on test involves majority voting among the *three* trained models.

The commonly used tagging schemes (BIO, BIOES etc..) for NER contains information about the boundary of an entity along with the class of an entity, which is spitted by the model at each time-step. Due to this dual information in a single output, maximum voting is not trivial as models can not only disagree on the class but also on the boundary of an entity. Empirically we found that our model is better at predicting the class of an entity rather than the boundary of an entity, therefore, we followed the strategy *class determines the boundary*. In cases when voting results in a tie, we take the prediction of the *confident* model, we treat the model trained on original train/dev split as the confident model. We also experimented with an extreme version of ensembling where we aggregate the output of every model with distinct spans, as expected this improves the recall but with the cost of reduced precision. One possible optimization to this ensemble strategy is to only aggregate the non-overlapping spans to control reduction in precision without much decrease in recall, we will explore this as a future work. Table 3 shows the ensemble correcting individual model’s erroneous predictions.

In case of ensemble for RE, we followed the straight forward approach of majority voting at sentence level for each test sample.

Task	Train	Dev	Test
Sentence Counts			
PharmaCo	8068	3748	3930
SeeDev	644	308	466
BB-norm+ner	822	413	735
PharmaCoNER Entities			
NORMALIZABLES	2304	1121	859
PROTEINAS	1405	745	973
UNCLEAR	89	44	34
NO-NORMALIZABLES	24	16	10
BB-norm+NER Entities			
Habitat	1118	610	-
Microorganism	739	402	-
Phenotype	369	161	-

Table 4: Dataset statistics for NER

4 Experiments and Results

4.1 Dataset and Experimental Setup

Data: We employed bagging (discussed in section 3.3) to split the annotated corpus into 3-folds. We used pre-processed versions of datasets for BB-norm+NER⁴ and SeeDev⁵ provided by the organizers. This pre-processed version comes with sentence splitting, word tokenization and POS tagging.

PharmaCoNER: The dataset consists of four entity types with very few mentions of type *UNCLEAR* and *NO-NORMALIZABLES* as shown in table 4. Entities of type *UNCLEAR* are ignored in the evaluation of this shared task but we still treat them as regular entities.

BB-norm+NER: The dataset consists of three entity types with few mentions of type *Phenotype* (see table 4). The dataset also contains 3.6% *disconnected entities*⁶, we did not employ any strategy to handle disconnected entities and instead treat them as separate (regular) entities.

SeeDev: The dataset consists of 22 binary relations among 16 entity types. The dataset is highly imbalanced with zero instances of type *Regulates_Molecule_Activity* and *Composes_Protein_Complex* in the default development set.

⁴<https://sites.google.com/view/seedev2019/supporting-resources>

⁵<https://sites.google.com/view/bb-2019/supporting-resources>

⁶<https://groups.google.com/d/msg/bb-2019/A2MuFYiPQIY/9YtMmakeBQAJ>

Hyper-parameter	Value
NER	
learning rate	0.005
character (char) dimension	25
hidden unit::char LSTM	25
POS dimensions	25*, 50 ⁺
Ortho dimension	25*, 50 ⁺
hidden unit::word LSTM	200*, 100 ⁺
word embeddings dimension	200*, 100 ⁺
length dimension	10
sdp_rel	10
alpha_features	2
ranking loss:: α	1.0
ranking loss:: γ	1.0
RE	
kernel	RBF
class-weights	10.0

Table 5: Hyper parameter settings for NER and RE. * and + denote the optimal parameters for BB-norm+ner and PharmaCoNER respectively.

Experimental Setup: We found sub-word information to be very helpful in identifying entities and relations in biomedical domain and all our experiments used word embeddings trained using FastText (Bojanowski et al., 2017). For tasks in English language we used FastText embeddings trained on PubMed (Zhang et al., 2019). We don’t employ any strategy for handling imbalanced classes for NER but have used class weighting by a factor of 10 for all positive classes for RE. Table 5 lists the best configuration of hyper-parameters for all the tasks.

PharmaCoNER: We used *SPACCC-POSTAGGER* (Soares and gonzalez agirre, 2019) for sentence splitting, word tokenization and POS tagging. We trained FastText embeddings on the following corpora: IBECS (Rodríguez, 2002), IULA-Spanish-English-Corpus (Marimon et al., 2017), MedlinePlus (Miller et al., 2000), PubMed (Lu, 2011), ScIELO (Goldenberg et al., 2007) and PharmaCoNer (Gonzalez-Agirre et al., 2019). We trained embeddings on two variants of corpora: (1) Include train and development set of PharmaCoNER (2) Include complete dataset of PharmaCoNER. We concatenated these two embeddings to provide complementary information and found them to empirically work better than the embeddings trained on individual corpora variant. We compute micro-F1 using the script

	Configuration	PharmaCoNER			BB-norm+NER			
		P	R	F1	P	R	F1	SER
		Fold=1			Fold=1			
r1	<i>BiLSTM-CRF</i>	.884	.773	.824	.809	.474	.598	.576
r2	+ <i>word-emb</i>	.892	.857	.874	.831	.526	.644	.524
r3	+ <i>ortho</i>	.909	.846	.877	.823	.515	.633	.533
r4	+ <i>POS</i>	.906	.851	.877	.827	.523	.641	.526
r5	+ <i>multi-task</i>	.907	.851	.878	.806	.528	.638	.531
r6	+ <i>length</i>	-	-	-	.842	.487	.617	.545
r7	+ <i>ranking</i>	.912	.860	.885	.827	.535	.650	.520
r8	+ <i>search</i>	-	-	-	.810	.600	.690	.489
		Fold=2			Fold=2			
r9	<i>BiLSTM-CRF</i>	.915	.890	.902	.630	.400	.489	-
r10	<i>all features</i>	.934	.889	.911	.719	.513	.599	-
		Fold=3			Fold=3			
r11	<i>BiLSTM-CRF</i>	.899	.873	.886	.784	.699	.739	-
r12	<i>all features</i>	.917	.877	.896	.813	.764	.788	-

Table 6: Scores on dev set using different features on *PharmaCoNER* and *BB-norm+NER* tasks. Here, + signifies feature accumulation to the last row.

provided by the organizers on the dev set⁷.

BB-norm+NER: For training NER model we compute macro-F1⁸ (Tsai et al., 2006) on the dev set. NER and Entity normalization together are evaluated using *Standard Error Rate (SER)* (Bossy et al., 2015). During the entity normalization step, the fuzzy and semantic search can resolve an entity mention to multiple normalization identifiers. Our algorithm returns top 5 matched identifiers, however, we empirically found selecting the top most identifier gives superior performance.

SeeDev: We adopted two strategies to create negative relation instances for train and dev+test set: (1) *Train*: only consider sentences not participating in any positive relation (2) *Dev+Test*: consider all the sentences. Negative relation instances are always created only among the valid combination of entity types. We also employed an extended version of keywords match of Li et al. (2016) as a feature (referred as keyword vectors in table 2).

4.2 Results on Development Set

To investigate the impact of features we incrementally enabled them and observe the affect on performance on dev set.

NER: Table 6 shows the score on dev set for *PharmaCoNER* and *BB-norm+NER*. Observe that *FastText* embeddings (row r2) outperform randomly initialized embeddings (row r1) and con-

⁷<https://github.com/PlanTL-SANIDAD/PharmaCoNER-CODALAB-Evaluation-Script>

⁸evaluation measure with strict boundary detection

	Features	P	R	F1
r1	<i>bow-between</i>	.0	.0	.0
r2	+ <i>class-weights</i>	.214	.196	.205
r3	+ <i>entity-type</i>	.157	.589	.248
r4	+ <i>sdp-entity</i>	.204	.540	.296
r5	+ <i>emb-sdp</i>	.212	.479	.294
r6	+ <i>lemma</i>	.220	.478	.301

Table 7: Scores on dev set using different features on *SeeDev* task. Here, + signifies feature accumulation to the last row.

tribute to biggest performance boost for both datasets. Subsequently, *Orthographic* (row r3) and *POS* (row r4) features⁹ improve the scores for *PharmaCoNER* but surprisingly lower the score for *BB-norm+NER*. In row r5, we perform multi-tasking with auxiliary task of NED leading to improvement only for *PharmaCoNER*. Next, we incorporate hybrid loss including ranking (row r7) which consistently improves the score on both datasets. In row r8, we employed Brute Force Search (discussed in section 4.3) that significantly reduce SER for *BB-norm+NER*. Finally, we create an ensemble of (r7, r10, r12) and (r8, r10, r12) on test set for *PharmaCoNER* and *BB-norm+NER* respectively.

RE: Table 7 shows the score on dev set for *SeeDev*¹⁰. In row r1, negative instances dominate the training set resulting in no learning. Observe that introduction of class weights (row r2) compensate the dominance of negative instances leading to F1 score of 0.205. Next, we added *entity-type* (row r3) and *sdp-entity* (row 4) features, both of these features significantly improves F1 score i.e. by an absolute value of more than 4.0. Subsequently, *emb-sdp* (row r5) and *lemma* (row r6) contribute to incremental improvements. Finally, we create an ensemble of row r6 on all three data folds.

4.3 Analysis on Development Set

BB-norm+NER: We also explored approaching the problem of NER and entity normalization in a reverse manner by matching every entity mention from the biomedical databases (i.e. *NCBI Taxonomy* and *Ontobiotope*) in every sentence. This

⁹Additionally, we have employed document-topic proportion from neural topic models (Gupta et al., 2019a), however, no significant gains were observed.

¹⁰Results are only reported for standard data fold as it was not trivial to change evaluation script for non-standard folds.

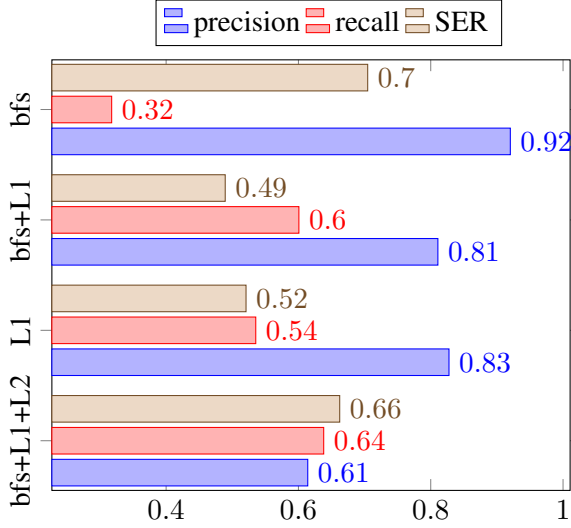


Figure 3: *BB-norm+NER*: Impact of brute-force search, Level1 NER and their aggregation on SER. Here bfs, L1 and L2 refer to *brute-force search*, *Level1 NER* and *Level2 Nested NER* respectively.

matching is indeed exhaustive search, we refer to it as *Brute-force search*. Figure 3 shows the comparison of: (1) *brute-force search* (2) *Level1 NER* (3) aggregation of *brute-force search* and *Level1 NER* (4) aggregation of *brute-force search*, *Level1 NER* and *Level2 NER*. Brute-force search yields high precision but a moderately low recall with SER value of 0.7. In comparison, Level1 NER has significantly higher recall with a little reduction in precision yielding SER value of 0.52. The aggregation of brute-force search and Level1 NER improves recall and lowers SER value to 0.49. Finally, aggregation of brute-force search, Level1 NER and Level2 NER results in a balanced precision and recall values but an overall higher value of SER. Our submission on test set employed aggregation of *brute-force search* and *Level1 NER*.

SeeDev: We employed the heuristic of token counts between target entities to filter potential negative relation instances. With this heuristic in place, we only consider sentences with entity distance less than or equal to threshold parameter τ . Figure 4 shows the impact of different values of τ on system performance. The value of $\tau \leq 20$ gives significant boost in precision with minor decrease in recall. Our submission employed the threshold value of $\tau \leq 20$ between entity tokens.

4.4 Comparison with Participating Systems

SeeDev: Table 8 (left) is the official result of SeeDev Shared Task. Our submission *MIC-CIS*

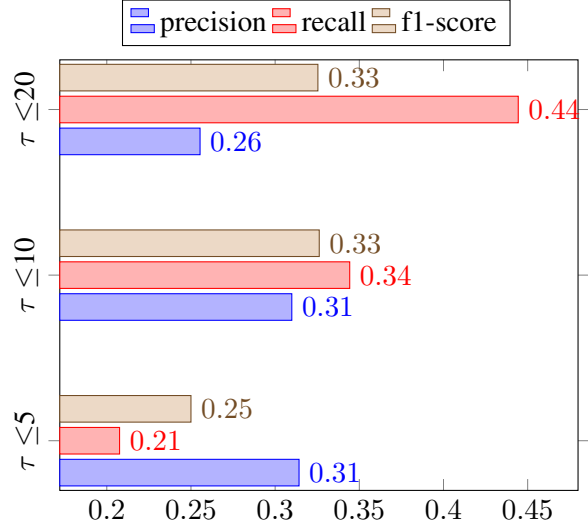


Figure 4: *SeeDev*: Impact of 'token counts between target entities' heuristic on system performance.

Task: SeeDev				Task: BB-norm+NER			
Team	P	R	F1	Team	P	R	SER
MIC-CIS	.294	.511	.373	MIC-CIS-1	.624	.433	.715
YNU-junyi-1	.272	.458	.341	MIC-CIS-2	.560	.449	.786
Yunnan_University-1	.045	.132	.067	BLAIR_GMU-1	.496	.467	.793
Yunnan_University-2	.020	.132	.035	BLAIR_GMU-2	.499	.466	.805
YNBY-1	.011	.070	.019	baseline-1	.572	.327	.823

Table 8: Comparison of our system (MIC-CIS) with top-5 participants: Scores on Test set for SeeDev and BB-norm+NER

achieves the best score among all participating systems with F1 score of **0.373** showing compelling advantage. The system attains the highest precision (0.294) and recall (0.511). Precision and recall are not balanced however, and our system need an improvement to bring down false positives.

BB-norm+NER: Table 8 (right) shows the comparison of performance among participating teams on BB-norm+NER test set. Our two submissions (MIC-CIS-1, MIC-CIS-2) ranked first and second with standard error rate (SER) of **0.7159** and 0.7867 respectively. The second submission employed Level2 NER to extract nested entities and hence has higher recall but with reduced precision. *MIC-CIS-1* has the highest precision 0.6242 and *MIC-CIS-2* has the recall close to the best recall of *BLAIR_GMU-1* with score 0.4676. Precision and recall are not balanced, we hypothesize improvement in nested entities extraction and modelling discontinuous entities will improve the system recall.

5 Conclusion and Future Work

In this paper, we described our system with which we participate in *PharmaCoNER*, *BB-norm+NER* and *SeeDev* shared tasks. Our NER system employed linguistic features, multi-tasking via auxiliary objectives and hybrid loss including ranking loss to extract flat and nested entities in English and Spanish text. Our RE system employed SVM with linguistic features. Compared to other participating systems, our submissions are ranked 1st in BB-norm+NER and SeeDev task. Our system demonstrates competitive performance on PharmaCoNER with F1-score of 0.8662.

In future, we would like to explore improved modelling strategies for nested NER and discontinuous entities extraction. Further, in this work we only addressed intra-sentence RE, we would be interested to explore approaches for inter-sentence RE (Peng et al., 2017; Gupta et al., 2019b). Moreover, we would like to investigate interpretability of LSTMs for NER and RE (Gupta and Schütze, 2018).

Acknowledgment

This research was supported by Bundeswirtschaftsministerium (bmwi.de), grant 01MD19003E (PLASS, plass.io) at Siemens AG - CT Machine Intelligence, Munich Germany.

References

- Gustavo Aguilar, Suraj Maharjan, Adrián Pastor López-Monroy, and Tamar Solorio. 2017. A multi-task approach for named entity recognition in social media data. In *Proceedings of the 3rd Workshop on Noisy User-generated Text, NUT@EMNLP 2017, Copenhagen, Denmark, September 7, 2017*, pages 148–153.
- Piotr Bojanowski, Edouard Grave, Armand Joulin, and Tomas Mikolov. 2017. Enriching word vectors with subword information. *TACL*, 5:135–146.
- Robert Bossy, Louise Deléger, Estelle Chaix, Mouhamadou Ba, and Claire Nedellec. 2019. Bacteria Biotope at BioNLP Open Shared Tasks 2019. In *Proceedings of the BioNLP Open Shared Tasks 2019 Workshop*.
- Robert Bossy, Wiktor Golik, Zorana Ratkovic, Dialekti Valsamou, Philippe Bessièrès, and Claire Nedellec. 2015. Overview of the gene regulation network and the bacteria biotope tasks in bionlp’13 shared task. In *BMC Bioinformatics*.
- Leo Breiman. 1996. Bagging predictors. *Machine Learning*, 24(2):123–140.
- Estelle Chaix, Bertrand Dubreucq, Abdelhak Fatihi, Dialekti Valsamou, Robert Bossy, Mouhamadou Ba, Louise Deléger, Pierre Zweigenbaum, Philippe Bessièrès, Loïc Lepiniec, and Claire Nedellec. 2016. Overview of the regulatory network of plant seed development (seedev) task at the bionlp shared task 2016. In *Proceedings of the 4th BioNLP Shared Task Workshop, BioNLP 2016, Berlin, Germany, August 13, 2016*, pages 1–11.
- Ronan Collobert and Jason Weston. 2008. A unified architecture for natural language processing: deep neural networks with multitask learning. In *Machine Learning, Proceedings of the Twenty-Fifth International Conference (ICML 2008), Helsinki, Finland, June 5-9, 2008*, pages 160–167.
- Saul Goldenberg, Regina Célia Figueiredo Castro, and Fernando Redondo Moreira Azevedo. 2007. [scielo (scientific electronic library online) statistical data interpretation]. *Acta cirurgica brasileira*, 22 1:1–7.
- Aitor Gonzalez-Agirre, Montserrat Marimon, Ander Intxaurre, Obdulia Rabal, Marta Villegas, and Martin Krallinger. 2019. Pharmaconer: Pharmacological substances, compounds and proteins named entity recognition track. In *Proceedings of the BioNLP Open Shared Tasks (BioNLP-OST)*, Hong Kong, China. Association for Computational Linguistics.
- Pankaj Gupta, Yatin Chaudhary, Florian Buettner, and Hinrich Schütze. 2019a. Document informed neural autoregressive topic models with distributional prior. In *The Thirty-Third AAAI Conference on Artificial Intelligence, AAAI 2019, The Thirty-First Innovative Applications of Artificial Intelligence Conference, IAAI 2019, The Ninth AAAI Symposium on Educational Advances in Artificial Intelligence, EAAI 2019, Honolulu, Hawaii, USA, January 27 - February 1, 2019*, pages 6505–6512.
- Pankaj Gupta, Subburam Rajaram, Hinrich Schütze, and Thomas A. Runkler. 2019b. Neural relation extraction within and across sentence boundaries. In *The Thirty-Third AAAI Conference on Artificial Intelligence, AAAI 2019, The Thirty-First Innovative Applications of Artificial Intelligence Conference, IAAI 2019, The Ninth AAAI Symposium on Educational Advances in Artificial Intelligence, EAAI 2019, Honolulu, Hawaii, USA, January 27 - February 1, 2019*, pages 6513–6520.
- Pankaj Gupta, Benjamin Roth, and Hinrich Schütze. 2018. Joint bootstrapping machines for high confidence relation extraction. In *Proceedings of the 2018 Conference of the North American Chapter of the Association for Computational Linguistics: Human Language Technologies, NAACL-HLT 2018, New Orleans, Louisiana, USA, June 1-6, 2018, Volume 1 (Long Papers)*, pages 26–36.
- Pankaj Gupta and Hinrich Schütze. 2018. LISA: explaining recurrent neural network judgments via layer-wise semantic accumulation and example to

- pattern transformation. In *Proceedings of the Workshop: Analyzing and Interpreting Neural Networks for NLP, BlackboxNLP@EMNLP 2018, Brussels, Belgium, November 1, 2018*, pages 154–164.
- Pankaj Gupta, Hinrich Schütze, and Bernt Andrassy. 2016. Table filling multi-task recurrent neural network for joint entity and relation extraction. In *COLING 2016, 26th International Conference on Computational Linguistics, Proceedings of the Conference: Technical Papers, December 11-16, 2016, Osaka, Japan*, pages 2537–2547.
- Nanda Kambhatla. 2004. Combining lexical, syntactic, and semantic features with maximum entropy models for extracting relations. In *Proceedings of the ACL 2004 on Interactive Poster and Demonstration Sessions, ACLdemo '04*, Stroudsburg, PA, USA. Association for Computational Linguistics.
- John D. Lafferty, Andrew McCallum, and Fernando C. N. Pereira. 2001. Conditional random fields: Probabilistic models for segmenting and labeling sequence data. In *Proceedings of the Eighteenth International Conference on Machine Learning (ICML 2001)*, Williams College, Williamstown, MA, USA, June 28 - July 1, 2001, pages 282–289.
- Guillaume Lample, Miguel Ballesteros, Sandeep Subramanian, Kazuya Kawakami, and Chris Dyer. 2016. Neural architectures for named entity recognition. In *NAACL HLT 2016, The 2016 Conference of the North American Chapter of the Association for Computational Linguistics: Human Language Technologies, San Diego California, USA, June 12-17, 2016*, pages 260–270.
- Jake Lever and Steven J. Jones. 2016. VERSE: event and relation extraction in the bionlp 2016 shared task. In *Proceedings of the 4th BioNLP Shared Task Workshop, BioNLP 2016, Berlin, Germany, August 13, 2016*, pages 42–49.
- Chen Li, Zhiqiang Rao, and Xiangrong Zhang. 2016. Litway, discriminative extraction for different bio-events. In *Proceedings of the 4th BioNLP Shared Task Workshop, BioNLP 2016, Berlin, Germany, August 13, 2016*, pages 32–41.
- Zhiyong Lu. 2011. Pubmed and beyond: a survey of web tools for searching biomedical literature. *Database*, 2011.
- Montserrat Marimon, Jorge Vivaldi, and Núria Bel. 2017. Annotation of negation in the IULA Spanish clinical record corpus. In *Proceedings of the Workshop Computational Semantics Beyond Events and Roles*, pages 43–52, Valencia, Spain. Association for Computational Linguistics.
- Ryan T. McDonald, Fernando C. N. Pereira, Seth Kulick, R. Scott Winters, Yang Jin, and Peter S. White. 2005. Simple algorithms for complex relation extraction with applications to biomedical IE. In *ACL 2005, 43rd Annual Meeting of the Association for Computational Linguistics, Proceedings of the Conference, 25-30 June 2005, University of Michigan, USA*, pages 491–498.
- Naomi Miller, Eve-Marie Lacroix, and Joyce E. B. Backus. 2000. Medlineplus: building and maintaining the national library of medicine’s consumer health web service. *Bulletin of the Medical Library Association*, 88 1:11–7.
- Nanyun Peng, Hoifung Poon, Chris Quirk, Kristina Toutanova, and Wen-tau Yih. 2017. Cross-sentence n-ary relation extraction with graph lstms. *TACL*, 5:101–115.
- Marek Rei. 2017. Semi-supervised multitask learning for sequence labeling. In *Proceedings of the 55th Annual Meeting of the Association for Computational Linguistics, ACL 2017, Vancouver, Canada, July 30 - August 4, Volume 1: Long Papers*, pages 2121–2130.
- Joaquín Alberto Carballido Rodríguez. 2002. [the spanish bibliographic index of the health sciences (ibecs) and actas urológicas españolas]. *Actas urológicas españolas*, 26 6:381–3.
- Cícero Nogueira dos Santos, Bing Xiang, and Bowen Zhou. 2015. Classifying relations by ranking with convolutional neural networks. In *Proceedings of the 53rd Annual Meeting of the Association for Computational Linguistics and the 7th International Joint Conference on Natural Language Processing of the Asian Federation of Natural Language Processing, ACL 2015, July 26-31, 2015, Beijing, China, Volume 1: Long Papers*, pages 626–634.
- Burr Settles. 2004. Biomedical named entity recognition using conditional random fields and rich feature sets. In *Proceedings of the International Joint Workshop on Natural Language Processing in Biomedicine and its Applications, NLPBA/BioNLP 2004, Geneva, Switzerland, August 28-29, 2004*.
- Felipe Soares and Aitor gonzalez agirre. 2019. Spaccpos-tagger. Funded by the Plan de Impulso de las Tecnologías del Lenguaje (Plan TL).
- Richard Tzong-Han Tsai, Shih-Hung Wu, Wen-Chi Chou, Yu-Chun Lin, Ding He, Jieh Hsiang, Ting-Yi Sung, and Wen-Lian Hsu. 2006. Various criteria in the evaluation of biomedical named entity recognition. *BMC Bioinformatics*, 7:92.
- Ngoc Thang Vu, Pankaj Gupta, Heike Adel, and Hinrich Schütze. 2016. Bi-directional recurrent neural network with ranking loss for spoken language understanding. In *2016 IEEE International Conference on Acoustics, Speech and Signal Processing, ICASSP 2016, Shanghai, China, March 20-25, 2016*, pages 6060–6064.
- Linlin Wang, Zhu Cao, Gerard de Melo, and Zhiyuan Liu. 2016. Relation classification via multi-level attention cnns. In *Proceedings of the 54th Annual Meeting of the Association for Computational Linguistics, ACL 2016, August 7-12, 2016, Berlin, Germany, Volume 1: Long Papers*.

Shanchan Wu and Yifan He. 2019. Enriching pre-trained language model with entity information for relation classification. *CoRR*, abs/1905.08284.

Yijia Zhang, Qingyu Chen, Zhihao Yang, Hongfei Lin, and Zhiyong Lu. 2019. Biowordvec, improving biomedical word embeddings with subword information and mesh. In *Scientific Data*.