Supplementary Material

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Architecture of i-biRNN

Figure 1 illustrates the architecture of inter-sentential Connectionist Bi-directional Recurrent Neural Network (ibiRNN). Consider two sentences S1 and S2, where S1 consists of words $[v_1^1, [v_2^1]_{e1}, v_3^1, v_4^1]$ and S2 consists of words $[w_1^2, w_2^2, [w_3^2]_{e2}, w_4^2]$. v_2^1 and w_3^2 are *entity1* and *entity2* respectively spanning sentence boundary.

The input to the i-biRNN is the concatenation of S1 and S2 where;

- ullet V: the weights matrix between hidden units and input in forward and backward network used to condition the input word vector, $\mathbf{x_t}$
- ullet W_f : the weights matrix connecting hidden units in forward network
- ullet W_b : the weights matrix connecting hidden units in backward network
- $\mathbf{h_f}$: the forward hidden unit computed at time step, t, accumulating the semantic meaning given the input word $\mathbf{x_t}$ and history
- h_b : the backward hidden unit computed at time step, t, accumulating the semantic meaning given the input word $\mathbf{x_t}$ and the future context, $\mathbf{h_{b_{t+1}}}$, that is accumulated and conditioned on the future words.
- W: the recurrent weight matrix connecting combined hidden units, \mathbf{h}_t through time;
- **h**_t: the hidden vector that accumulates the semantics obtained from the combination or sum of forward and backward units at time step, t
- N: total number of words in S1 and S2
- U: the output weight matrix, connecting to the softmax layer

Data Description

The BioNLP shared task (2011 and 2013) consists of extracting bacteria localization events of given species i.e., *Localization* or *PartOf* relations. For *Location*, the participating entity types are Bacterium and type Localization (Host

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Parameter	Value(s)			
Training epoch	500			
Hidden size	100, 200			
initial learning rate	0.001, 0.005, 0.010			
activation	tanh, cappedrelu			
context window size	1, 3			
L2 weight	0.0001			
mini batch size	1			
optimizer	gradient descent			
gradient norm clipstyle	rescale			
gradient norm cutoff	5.0, 10.0, 20.0			
word embedding dimension	200			
PI/POS embedding dimension	5			
sentence range, k	$=0, \leqslant 1, \leqslant 2, \leqslant 3$			
weight initialization	identity			
bias initialization	zero			
W sharing in bi-RNN	True			
W sharing in ADP and SDP	True, False			

Table 1: Hyperparameters for BRNN and iDepNN

| HostPart | Geographic | Environment | Food | Soil | Water), while *PartOf* has *HostPart* and *Host* entity types. The BioNLP ST 2016 focuses on extraction of *Lives_in* events among *Bacteria*, *Habitat* and *Geographical* entities.

Hyperparameters

See Table 1. We run graphLSTM for 100 iterations with learning rate of 0.02, batch size 10 and 150 hidden dimension.

Feature Analysis on BioNLP ST 2011 and 2013 datasets

See Table 2.

Development Scores (official) on BioNLP ST 2016 data set to determine the value of training parameter, k

See Table 3.

Dataset: BioNLP ST 2013							
Features		SVM		iDepNN			
reatures	P	R	F1	P	R	F1	
iSDP	.848	.740	.769	.911	.875	.889	
+ PI + ET	.853	.786	.808	.915	.921	.918	
+ POS	.934	.904	.917	.938	.945	.942	
+ Dependency	.937	.926	.931	.970	.938	.951	

Dataset: BioNLP ST 2011

Features		SVM		iDepNN			
reatures	P	R	F1	P	R	F1	
iSDP	.830	.777	.794	.919	.933	.926	
+ PI + ET	.831	.790	.803	.931	.916	.923	
+ POS	.915	.918	.915	.955	.922	.938	
+ Dependency	.930	.931	.930	.928	.957	.942	

Table 2: SVM Vs iDepNN: Performance of different features used in inter-sentential ($k \le 1$) training and inter-sentential ($k \le 1$) evaluation. iSDP + dependency refers to iDepNN-ADP.

train	Model	Development scores at different values of \boldsymbol{k}							
param	Model	k = 0			$k \leqslant 1$				
		pr	$\mathbf{F1}$	\mathbf{R}	P	pr	$\mathbf{F1}$	\mathbf{R}	P
	i-biRNN	113	.497	.378	.726	132	.591	.475	.781
$k \leqslant 1$	iDepNN-SDP	139	.524	.431	.669	167	.641	.568	.737
	iDepNN-ADP	138	.536	.438	.688	161	.630	.549	.740
	i-biRNN	129	.493	.393	.659	145	.613	.511	.764
$k \leqslant 2$	iDepNN-SDP	149	.531	.449	.651	180	.598	.545	.661
	iDepNN-ADP	142	.534	.443	.675	161	.619	.539	.726
	i-biRNN	112	.514	.388	.759	129	.603	.482	.806
$k \leqslant 3$	iDepNN-SDP	142	.506	.417	.641	173	.610	.548	.688
	iDepNN-ADP	139	.530	.435	.676	158	.626	.539	.747

Table 3: BioNLP ST 2016 development set: Performance comparison to determine the value of training parameter k. Observe that the parameter $k \le 1$ is optimal during training and evaluation (on development set) for relationships within and across sentence boundaries. P, R and F1 are official scores.

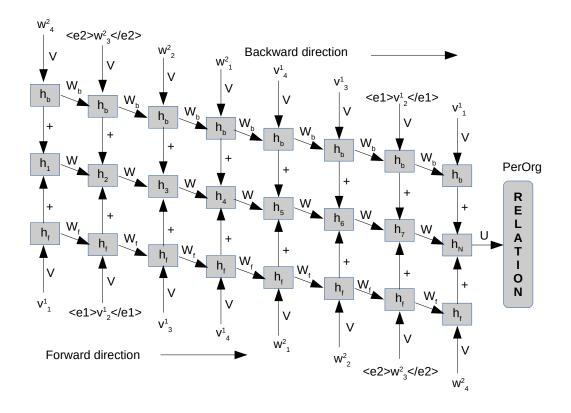


Figure 1: Architecture of i-biRNN. In our structures, we share the weights in forward, backward and combined networks, in order to reduce parameters, i.e., \mathbf{W} is being shared in the three networks.