



Master in Data Science

D5: NN-based DDI

Mining Unstructured Data

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Team members

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1 Introduction

This task revolves around **relation extraction**, aiming to extract relations between entities expressed in the text. Specifically, the objective is to extract relationships between drugs from biomedical texts, known as **drug.interaction(drug,drug)**.

This task also pursues a classification task of each drug-drug interaction according to one of the four following types: **advise**, **effect**, **mechanism**, **int**. Accordingly, the challenge called for a five-way classification of sentences for each drug-pair:

- **Advise**: the sentence notes a recommendation or advice related to the concomitant use of the two drugs. Ex: UROXATRAL should NOT be used in combination with other alpha-blockers.
- **Effect**: the sentence states the effect of the drug interaction, including pharmacodynamic effect or mechanism of interaction. Ex: Quinolones may enhance the effects of the oral anticoagulant, warfarin.
- **Mechanism**: the sentence describes a pharmacokinetic mechanism. Ex: Grepafloxacin is a competitive inhibitor of the metabolism of theophylline.
- **Int**: the sentence mentions a drug interaction but doesn't provide any additional information. Ex: "The interaction of omeprazole and ketoconazole has been established.")
- **None**: the sentence does not show an interaction between the two drugs.

To achieve accurate relation extraction and classification, we employ neural networks, exploring various architectures and configurations. By experimenting with different models and hyperparameters, we aim to determine the optimal setup that maximizes the performance of relation extraction from biomedical texts.

2 Experiments description

2.1 Experimented Architectures and Hyperparameters

2.1.1 Embedding Dimension

We experimented with different embedding dimensions to evaluate their impact on the model's performance.

2.1.2 Max Length and Suffix Length Values

Different maximum length and suffix length values were experimented with to determine the optimal configuration for input sequences.

2.2 Experimented Input Information

2.2.1 Number of LSTM Units

We experimented with different numbers of LSTM units (e.g., 30, 64, 128) to identify the best configuration for capturing sequential dependencies.

2.2.2 Used Optimizer

Various optimizers such as Adam, RMSprop, and SGD were tested to find the most effective optimization strategy for training the model.

2.2.3 Number and Kind of Layers or Activation Functions

The number and types of layers (e.g., LSTM, Conv1D) and activation functions were varied to explore different architectural configurations.

2.3 Combining LSTM and CNN Layers

We experimented with combinations of LSTM and Conv1D layers, adjusting parameters like the number of filters and kernel size to potentially capture more complex patterns.

2.4 Adding Dropout

Dropout layers with different rates were added to prevent overfitting and improve the generalization capability of the model.

2.5 Evaluation Metrics

The performance of different configurations was evaluated using precision, recall, and F1-score to ensure a comprehensive assessment of the models.

3 Code Description

3.1 Best Network Model

```
1 from tensorflow.keras.layers import Input, Embedding, Conv1D, GlobalMaxPooling1D,
   Bidirectional, LSTM, concatenate, Dropout, Dense
2 from tensorflow.keras.models import Model
3
4 def build_network(codes):
5     # sizes
6     n_words = codes.get_n_words()
7     max_len = codes.maxlen
8     n_labels = codes.get_n_labels()
9
10    # Input Layer
11    inpt = Input(shape=(max_len,))
12    emb = Embedding(input_dim=n_words, output_dim=300, input_length=max_len)(inpt)
13
14    # Convolutional Layers
15    conv1 = Conv1D(filters=128, kernel_size=5, activation='relu')(emb)
16    conv2 = Conv1D(filters=128, kernel_size=5, activation='relu')(conv1)
17    pool = GlobalMaxPooling1D()(conv2)
18
19    # Bidirectional LSTM Layer
20    lstm = Bidirectional(LSTM(units=128, return_sequences=True))(emb)
21    lstm = Bidirectional(LSTM(units=128, return_sequences=False))(lstm)
22
23    # Feature Combination
24    combined = concatenate([pool, lstm])
25    dropout = Dropout(0.5)(combined)
26
27    # Additional Dense Layer
28    dense = Dense(256, activation='relu')(dropout)
29
30    # Output Layer
31    out = Dense(n_labels, activation='softmax')(dense)
32
33    model = Model(inputs=inpt, outputs=out)
34    model.compile(loss='categorical_crossentropy', optimizer='adam', metrics=['
    accuracy'])
35
36    return model
```

Listing 1: Best Network Model Code

3.1.1 Explanation

The final model architecture consists of the following components:

- **Input Layer:** The input layer expects sequences of a maximum length (`max_len`).
- **Embedding Layer:** Converts input tokens into dense vectors of fixed size (300).
- **Convolutional Layers:** Two Conv1D layers with 128 filters and a kernel size of 5, both using the ReLU activation function, followed by a GlobalMaxPooling1D layer to reduce the dimensionality of the output.
- **Bidirectional LSTM Layers:** Two Bidirectional LSTM layers with 128 units each. The first LSTM layer returns sequences, while the second does not.
- **Feature Combination:** The outputs from the convolutional and LSTM layers are concatenated.
- **Dropout Layer:** A dropout layer with a dropout rate of 0.5 to prevent overfitting.

- **Dense Layer:** A dense layer with 256 units and ReLU activation.
- **Output Layer:** A dense layer with a number of units equal to the number of labels (`n_labels`) using the softmax activation function to output probability distributions over the classes.

The model is compiled using categorical cross-entropy loss and the Adam optimizer, with accuracy as the evaluation metric.

4 Experiments and results

To determine the optimal model, it's essential to assess both the machine learning algorithm and the capabilities of the feature extractor. Our evaluation of experiments will focus on key metrics such as **precision**, **recall**, and **F-1 score**.

4.1 Initial state

	tp	fp	fn	#pred	#exp	P	R	F1
brand	47	2	327	49	374	95.9%	12.6%	22.2%
drug	1561	123	345	1684	1906	92.7%	81.9%	87.0%
drug_n	7	43	38	50	45	14.0%	15.6%	14.7%
group	530	98	157	628	687	84.4%	77.1%	80.6%
M.avg	-----					71.8%	46.8%	51.1%
m.avg	2145	266	867	2411	3012	89.0%	71.2%	79.1%
m.avg(no class)	2220	191	792	2411	3012	92.1%	73.7%	81.9%

Figure 1: Initial state

4.2 Embedding dimension

4.2.1 50

	tp	fp	fn	#pred	#exp	P	R	F1
advise	72	34	69	106	141	67.9%	51.1%	58.3%
effect	134	69	178	203	312	66.0%	42.9%	52.0%
int	14	3	14	17	28	82.4%	50.0%	62.2%
mechanism	82	77	179	159	261	51.6%	31.4%	39.0%
M.avg	-----	67.0%	43.9%	52.9%				
m.avg	302	183	440	485	742	62.3%	40.7%	49.2%
m.avg(no class)	329	156	413	485	742	67.8%	44.3%	53.6%

4.2.2 300

	tp	fp	fn	#pred	#exp	P	R	F1
--	----	----	----	-------	------	---	---	----

advise	84	56	57	140	141	60.0%	59.6%	59.8%
effect	155	130	157	285	312	54.4%	49.7%	51.9%
int	15	2	13	17	28	88.2%	53.6%	66.7%
mechanism	82	71	179	153	261	53.6%	31.4%	39.6%
M.avg	-----	64.1%	48.6%	54.5%				
m.avg	336	259	406	595	742	56.5%	45.3%	50.3%
m.avg(no class)	387	208	355	595	742	65.0%	52.2%	57.9%

Embedding Dimension	Precision	Recall	F1 Score
150	71.8%	46.8%	51.1%
50	67.0%	43.9%	52.9%
300	64.1%	48.6%	54.5%

Table 1: Embedding Dimension

4.3 Max length and suffix length values

4.3.1 50

	tp	fp	fn	#pred	#exp	P	R	F1
advise			72	39	69	111	141	64.9% 51.1% 57.1%
effect			139	66	173	205	312	67.8% 44.6% 53.8%
int			14	4	14	18	28	77.8% 50.0% 60.9%
mechanism			82	109	179	191	261	42.9% 31.4% 36.3%
M.avg			-----	63.3%	44.3%	52.0%		
m.avg			307	218	435	525	742	58.5% 41.4% 48.5%
m.avg(no class)			328	197	414	525	742	62.5% 44.2% 51.8%

4.3.2 300

	tp	fp	fn	#pred	#exp	P	R	F1
advise			79	43	62	122	141	64.8% 56.0% 60.1%
effect			162	105	150	267	312	60.7% 51.9% 56.0%
int			14	2	14	16	28	87.5% 50.0% 63.6%
mechanism			83	68	178	151	261	55.0% 31.8% 40.3%
M.avg			-----	67.0%	47.4%	55.0%		
m.avg			338	218	404	556	742	60.8% 45.6% 52.1%
m.avg(no class)			372	184	370	556	742	66.9% 50.1% 57.3%

Max Length	Precision	Recall	F1 Score
150	71.8%	46.8%	51.1%
50	63.3%	44.3%	52.0%
300	67.0%	47.4%	55.0%

Table 2: Max Length

4.4 Conv1D Layer

Increased the **number of filters** and **kernel size** to potentially capture more complex patterns.

4.5 Number of LSTM units

We experimented with different numbers of LSTM units (30, 64, 128).

LSTM layer w 128 units

	tp	fp	fn	#pred	#exp	P	R	F1
advise			71	52	70	123	141	57.7% 50.4% 53.8%
effect			177	109	135	286	312	61.9% 56.7% 59.2%
int			17	7	11	24	28	70.8% 60.7% 65.4%
mechanism			118	66	143	184	261	64.1% 45.2% 53.0%
M.avg			----	63.6%	53.3%	57.9%		
m.avg			383	234	359	617	742	62.1% 51.6% 56.4%
m.avg(no class)			462	155	280	617	742	74.9% 62.3% 68.0%

Add a LSTM layer w 64 units

	tp	fp	fn	#pred	#exp	P	R	F1
advise			100	93	41	193	141	51.8% 70.9% 59.9%
effect			207	202	105	409	312	50.6% 66.3% 57.4%
int			18	2	10	20	28	90.0% 64.3% 75.0%
mechanism			166	153	95	319	261	52.0% 63.6% 57.2%
M.avg			----	61.1%	66.3%	62.4%		
m.avg			491	450	251	941	742	52.2% 66.2% 58.3%
m.avg(no class)			583	358	159	941	742	62.0% 78.6% 69.3%

Add a LSTM layer w 30 units

	tp	fp	fn	#pred	#exp	P	R	F1
advise			88	75	53	163	141	54.0% 62.4% 57.9%
effect			205	155	107	360	312	56.9% 65.7% 61.0%
int			17	7	11	24	28	70.8% 60.7% 65.4%
mechanism			114	47	147	161	261	70.8% 43.7% 54.0%
M.avg			----	63.1%	58.1%	59.6%		
m.avg			424	284	318	708	742	59.9% 57.1% 58.5%
m.avg(no class)			489	219	253	708	742	69.1% 65.9% 67.4%

LSTM Units	Precision	Recall	F1 Score
128	63.6%	53.3%	57.9%
64	61.1%	66.3%	62.4%
30	63.1%	58.1%	59.6%

Table 3: Number of LSTM Units

4.6 Combinations of LSTM and CNN layers

30 ,30

	tp	fp	fn	#pred	#exp	P	R	F1
advise			93	63	48	156	141	59.6% 66.0% 62.6%
effect			199	129	113	328	312	60.7% 63.8% 62.2%
int			18	1	10	19	28	94.7% 64.3% 76.6%
mechanism			128	90	133	218	261	58.7% 49.0% 53.4%
M.avg			----	68.4%	60.8%	62.7%		
m.avg			438	283	304	721	742	60.7% 59.0% 59.9%
m.avg(no class)			510	211	232	721	742	70.7% 68.7% 69.7%

60 - 60

	tp	fp	fn	#pred	#exp	P	R	F1
advise			83	53	58	136	141	61.0% 58.9% 59.9%
effect			171	69	141	240	312	71.2% 54.8% 62.0%
int			16	3	12	19	28	84.2% 57.1% 68.1%
mechanism			99	48	162	147	261	67.3% 37.9% 48.5%
M.avg			-----	71.0%	52.2%	59.6%		
m.avg			369	173	373	542	742	68.1% 49.7% 57.5%
m.avg(no class)			423	119	319	542	742	78.0% 57.0% 65.9%

16-16

	tp	fp	fn	#pred	#exp	P	R	F1
advise			95	80	46	175	141	54.3% 67.4% 60.1%
effect			169	109	143	278	312	60.8% 54.2% 57.3%
int			17	2	11	19	28	89.5% 60.7% 72.3%
mechanism			108	61	153	169	261	63.9% 41.4% 50.2%
M.avg			-----	67.1%	55.9%	60.0%		
m.avg			389	252	353	641	742	60.7% 52.4% 56.3%
m.avg(no class)			450	191	292	641	742	70.2% 60.6% 65.1%

Adding dropout of 0.1

	tp	fp	fn	#pred	#exp	P	R	F1
advise			69	53	72	122	141	56.6% 48.9% 52.5%
effect			197	144	115	341	312	57.8% 63.1% 60.3%
int			16	9	12	25	28	64.0% 57.1% 60.4%

mechanism	92	85	169	177	261	52.0%	35.2%	42.0%
-----------	----	----	-----	-----	-----	-------	-------	-------

M.avg	-----	57.6%	51.1%	53.8%
-------	-------	-------	-------	-------

m.avg	374	291	368	665	742	56.2%	50.4%	53.2%
m.avg(no class)	448	217	294	665	742	67.4%	60.4%	63.7%

kernel=5

Combination	Precision	Recall	F1 Score
30, 30	68.2%	60.8%	62.7%
64, 64	71.0%	52.2%	59.6%
16, 16	67.1%	55.9%	60.0%
30, 30 + Dropout 0.1	57.6%	51.1%	53.8%

Table 4: Combining LSTM and CNN Layers

4.7 Final model

The final model insights are described in the section 3.1.1. The network starts with an input layer for DDI sentences, followed by embedding and convolutional layers extracting features. Bidirectional LSTM layers capture context, and a dropout layer prevents overfitting. Concatenation and dense layers process features, with softmax output providing interaction category probabilities. This architecture effectively combines convolutional and recurrent layers for accurate drug-drug interaction classification.

	tp	fp	fn	#pred	#exp	P	R	F1
advise			96	81	45	177	141	54.2% 68.1% 60.4%
effect			178	76	134	254	312	70.1% 57.1% 62.9%
int			21	9	7	30	28	70.0% 75.0% 72.4%
mechanism			105	64	156	169	261	62.1% 40.2% 48.8%
M.avg	-----		64.1%	60.1%	63.1%			
m.avg	400	230	342	630	742	63.5%	53.9%	58.3%
m.avg(no class)	467	163	275	630	742	74.1%	62.9%	68.1%

4.8 Test

After training our final model, we evaluated its performance on the test dataset. The table below summarizes the results:

	tp	fp	fn	#pred	#exp	P	R	F1
advise	116	59	93	175	209	66.3%	55.5%	60.4%
effect	168	104	118	272	286	61.8%	58.7%	60.2%
int	6	8	19	14	25	42.9%	24.0%	30.8%
mechanism	171	114	169	285	340	60.0%	50.3%	54.7%
M.avg	-----		57.7%	47.1%	51.5%			
m.avg	461	285	399	746	860	61.8%	53.6%	57.4%
m.avg(no class)	531	215	329	746	860	71.2%	61.7%	66.1%

4.9 Conclusions

In summary, our project centered on developing a neural network-based approach for classifying drug-drug interactions (DDIs) from biomedical texts. After conducting a series of experiments and optimizations, we designed an advanced model that combines convolutional and recurrent layers. This model effectively captures both local and contextual information, yielding promising results across precision, recall, and F1-score metrics for various interaction categories. By leveraging deep learning techniques, our approach demonstrates the potential of neural networks in accurately extracting and classifying DDIs from unstructured biomedical data, contributing significantly to pharmacovigilance and drug safety research.