Drug Reaction Discriminator within Encoder-Decoder Neural Network Model: COVID-19 Pandemic Case Study

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***Abstract*—Social networks become widely used for understanding patients shared experiences, and reaching a vast audience in a matter of seconds. In particular, many health-related organizations used sentiment analysis to automatically reporting treatment issues, drug misuse, new infectious disease symptoms. Few approaches have proposed in this matter, especially for detecting different drug reaction descriptions from patients generated narratives on social networks. Most of them consisted of only detecting adverse drug reaction(ADR), but may fail to retrieve other aspect, e.g, the beneficial drug reaction or drug retroviral effects such as "relieve intraocular pressure associated with glaucoma". In this study, we propose to develop an encoder-decoder for drug reaction discrimination that involves an enhanced distributed biomedical representation from controlled medical vocabulary such as PubMed and Clinical note MIMIC III. The embedding mechanism primarily leverages contextual information and learn from predefined clinical relationships in term of medical conditions in order to define possible drug reaction of individual meaning and multi-word expressions in the field of distributional semantics configuration that clarifies sentence's similarity in the same contextual target space, which are further share semantically common drug description meanings. Furthermore, the bidirectional sentiment inductive model are created to enhance drug reactions vectorization from real-world patients description whereby achieved higher performance in terms of disambiguating false positive and/or negative assessments. As a result, we achieved an 85.2% accuracy performance and the architecture shows a well-encoding of real-world drug entities descriptions.**

***Index Terms*—Biomedical distributed representation, Drug reaction, Encoder-Decoder, medical concepts, Sentiment information.**

I. Introduction

Information on social networks can have an immediate influence on patients' decisions to seek a second opinion or choose a specific provider, particularly for people who are coping with a chronic condition or managing their medication-related adverse drug events and reactions. Nowadays, patients widely seek out second opinions, searching the interconnection that helps them to discover possible alternatives to diagnoses and treatments[1]. An estimated of 27% of patients comment or post status updates based on health-related experiences. Patients care about other patients and want to provide as much information as possible, or collect as much information as possible, to make the most trustworthy determinations and decisions. In particular, online platforms play a large role in global pandemic combat. Massive online everyday discussions are sharing and disseminating information, misinformation, and harmful experiencesan estimated[2] 23 per cent of social network users, especially, those are living with a chronic health condition, have gone online to find others with similar health conditions and frequently capture varied elements ranging from medication issues, new COVID-19 symptoms to various drug reactions. Many Healthcare and research communities aim at defining a powerful online solution and use social networking to discover and share safety information. Since enormous numbers of contaminated persons are buying themselves candidate medications to treat or ovoid COVID-19 symptoms just by consulting people online conversations, they are also cheap, already available local drug stores, and relatively free of side effects.

Tremendous patients' narratives widely know this pandemic period on social networks, characterized by vigorous activity, fresh dynamism into global pandemic combat. Such a huge amount of biological concepts, citations and related-medication terms, as depicted in Fig.I, are affectively and semantically associated in different contexts. Neural Networks addresses such issues in the context of natural language processing (NLP) through a multi-disciplinary approach that aims to bridge the gap between statistical NLP and many other disciplines that are necessary for understanding human language. In this study, we propose to design a based neural network method to mine related-drug events from online patient narratives. Indeed, this method consists of defining a medical configuration policy to effectively mimic corresponding nontechnical and descriptive real-world expressions to formal medical candidate formats in the controlled medical vocabularies such as PubMed.

[1]https://www.pwc.com/us/en/industries/health-industries/library/health-care-social-media.html

[2]http://www.cdc.gov/chronicdisease/resources/ publications/index.htm

> Laura Ingraham CONTINUES to pimp out #hydroxychloroquine as a magic bullet for #COVID19 FDA cautioned AGAINST the use of it as a treatment. Doctors IRRESPONSIBLY went on FOX & said there were NO side-effects. That's a LIE.

Fig. 1. Twitter post on COVID-19

A wide variety of techniques have been proposed in this context range from dictionary-based methods based on encoded knowledge as lexical resources, supervised methods to completely unsupervised methods. Deep Learning approaches provide many advantages: rich embedding representation, dimensionality reduction, and long-term dependencies over large datasets. But, lowmedical natural concepts observations from shared experiences would lead to inferior method accuracy. This study uses the process to model the underlying drug reaction detection and considers another aspect of related-drug events like beneficial drug reactions or retroviral effects such as stimulate appetite for people with AIDS wasting syndrome. Many existing methods fail to define positive responses that deal with considerable errors in other related computation steps such as extracting the speaker's subjectivity of given drug reaction; it results in false positives and negatives. The failure of defining drug reactions from patients' narratives on social networks factors is studied, and an optimal level of drug reaction abstraction is proposed. Thus, A discussion is opened to define the relation between the two models is discussed, leading to a new cost model. After that, the results raised the need to coordinate efforts to include the collection of information on adverse incidences related to a particular target (drug, disease.etc.) and seek related-medication indicators which enable defining unsuspected drug events. It considered the most crucial task which has been involved a degree of medication errors comprehension and preventability of adverse drug reactions (ADRs) through comprehending multiple related medical concepts in the overwhelming self-reported experiences.

The remainder of this paper is structured as follows. Section(2) provides a summary of the literature review of various related-medical approaches. Section(3) presents the proposed Encoder-Decoder methods. Section(4) offers large social network experimentation outputs convolving large biomedical embeddings. Section 5 concludes this paper and provides some perspectives.

II. Literature Background

In this section, we present an overview of recent studies performed in the context of online related-drug knowledge detection. We seek to demonstrate its role to enhance the performance of related sentiment analysis tasks and the applicability of SA in the context of drug reaction extraction.

A. Medical concepts normalization

The fresh dynamism into global pandemic combat conduct to huge related-medication information spreading in many formats: commonly drugs used and their minute reactions. In this section, we present some contributions that provide the distributed representation of many medical knowledge and vocabularies. Thus, we resume related studies that deal, especially, with Drug reaction detection and normalization.

1) Drug reaction detection: As discussed in Section.I, these platforms are becoming an increasingly preferable place for sharing personal health-related narratives, and discussing various drug problems, e.g. adverse drug reactions, which is considered among the top causes of morbidity and mortality. Adverse Drug reaction becomes a significant public health concern by various communities and researchers, especially, pharmacovigilance groups. However, its value for pharmacovigilance has been scantly studied - with health-related forums and community support groups preferred for the task [1]. Such an example of massive studies that presented an annotated corpus from social networks, it is a corpus of 10,822 tweets. It consists of annotating the presence or absence of ADR mentions, with a mutation to formal ADR description in the Unified Medical Language System (UMLS). Likewise, it is widely used conditional random fields (CRFs) to extract mentions that known deterministic features and many problems, other researchers solved that [2] by involving machine learning-based approach to achieve a variety of features, including a novel feature for modeling words' semantic similarities from a highly informal text in social media. But, it slowly converges for detecting unformal drugs and predicting the possible ADRs of a new medicine or/and new disease/virus. Profound learning potential advantages of leveraging contextual and semantic information into unique dense representation, deducing possible relationships in terms of similarities, reasoning correlate concepts, and multi-word expressions in long-term dependencies, it helped to cover many limitations. Several baselines in this context, [3] developed a recurrent neural network (RNN) model that labels words in an input sequence with ADR membership tags. Still, they reached optimal performance with fewer training examples than the other baselines.

Recently, many researchers combined many Deep learning algorithms and techniques to enhance model capabilities, for example, [4] used embeddings to represent the chemical, biological, and biomedical information to automatically detect potential ADRs of drugs and also predicting the possible ADRs of a new drug. But, data have been gathered in local windows in terms of drugs or diseases, and it time-depend, which were only recorded in 2012 with 1325 ADRs.

Because of the sensitivity of detecting adverse drug reactions to public health effects, it mainly required more credible models and personalizable parameters. In this sense, many competitions have been involved; one of them is the Social Media Mining for Health (SMM4H)-2017 shared task [5]. They launched many tasks to improve model quality in terms of mining related-drugs information such as automatic classification of self-reports of 1) adverse drug reactions (ADRs) and 2) medication consumption, from medication-mentioning tweets, and 3) normalization of ADR expressions. It characterized by massive training data consisted of 15 717 annotated tweets for (1), 10 260 for (2), and 6650 ADR phrases and identifiers for (3); and exhibited typical properties of social-media-based health-related texts. Systems were evaluated using 9961, 7513, and 2500 instances for the three subtasks, respectively.

2) Biomedical embedding: Medical concepts have known huge diversity sources of varied concepts, definitions and structures. Biomedical concepts (biomedical named entities and their related concept) can then be annotated to automatically tagged text such as many pre-trained taggers and models in the state-of-the-art: ezTag[3], TaggerOne[4], GNormPlus[5], and tmVar [6]...etc. But, tagging medical entities' performance dramatically drops when applied on online narratives and results in the very weak recall due to disambiguate nontechnical and descriptive format. Since neural networks approaches got huge success in resolving many text representation challenges. Many distributions took the alternatives and successfully performed several improved biomedical word embedding of formal vocabularies and ontologies such as widely-used biomedical controlled vocabulary Medical Subject Headings (MeSH) [6] and PubMed. MeSH is for indexing and searching multiple biomedical works of literature and to help better PubMed searching by utilizing MeSH and MeSH-derived topical terms, called Meshable, together, these literature databases expertly cover the entire available biomedical domain scientific literature, including PubMed abstracts, PubMed Central full-text articles, and other medical ontologies with subword information and MeSH [7]. Thus, MeSH terms and subheadings are organized in a hierarchical structure and used to indicate the topics of an article. Biologists can use either MeSH terms as queries or the MeSH interface provided in PubMed for searching PubMed abstracts. Thus, distributed word representation at sentence-level showed optimal representation that contributes to many related applications' success. [8] 700-dimensional sentence embeddings trained with over 30 million documents from both scholarly articles in PubMed and clinical notes in the MIMIC-III Clinical Database.

III. Encoder-decoder Model

Millions of related COVID-19 posts pour into varied platforms. Patients and health consumers are storming intentionally their medications experiences and their related-treatment opinions on Social media that describe all the incredible complex processes happening in real-time treatment. For people living with chronic health conditions (one that is persistent and long-lasting, such as arthritis, asthma, high blood pressure, cancer, or HIV/AIDS). An assessed Social network tool developed mainly to extract COVID-19 related-medication insights through Sentiment Analysis.

Before digging into architecture details, we choose to highlight the originality of the study in response to the COVID-19 crisis. A survey conveyed by Oxford concerning COVID-19 disease and conditions and treatments[7], assumes the inexistence of drugs for COVID-19. Thus, it reports possible outcomes and effects of drugs bought by many people as pre-medication to avoid or treat this pandemic. The goal is to standardize common terminology through individual processes developed for raising awareness of Health Care Professionals about preventable ADRs. In the future, we aim to design a dynamic system for reporting and Medication Errors learning.

The exploitation of such overwhelming unstructured data on social media is of critical importance. They frequently need analysis at the features extraction level which can be difficult without sufficient background knowledge of the formal medical contexts. In this work, we propose an Encoder-Decoder Model based on Biomedical distributed representation From Controlled Medical vocabulary. It consists of an extended transition-based Medical concept recognition. Furthermore, we validate the effectiveness of distracting drug reaction components on retrieving the relevant positiveness and negativeness. An additional Neural Network layers based-sentiment computation process is shared between Medical-NER and Sentiment discrimination. Indeed, Medical-Named Entity Recognition incorporates the MEDLINE database of references and abstracts on life sciences and biomedical topics and Pubmed primarily. As depicted in Fig.2, the approach is summarized as follow:

- Based-keywords crawling system is created, raw tweets are collected through Twitter APIs. For the collection of focused Twitter data, we use a list of related-COVID-19 Keywords $Corona$, and $Chloroquine$. Indeed, we are interested in getting information attributed by : ['id','created_at', 'source', 'original_text', 'retweet_count', 'ADR', 'original_author', 'hashtags', 'user_mentions', 'place', 'place_coord_boundaries']. The Table V summarizes statistics of raw data grouped in terms of some related-drugs keywords in differents slice of time.
- N-grams biomedical embedding Matrix construction by involving distributed biomedical at sentence-level generation [8]. A distributed representation of 700 dimensions that are trained on PubMed and Clinical notes MIMIC-III whereby achieved an 0.848 of accuracy. Indeed, it has been evaluated BioSentVec for clinical sentence pair similarity tasks. they used the BIOSSES [8] and the MedSTS[9] benchmarking datasets.The statistics of the two corpora PubMed and the clinical notes from MIMIC-III Clinical Database have described in Table VI.
- Additional Salient Twitter features are convolved to summarize varied online criteria.
- Bidirectional, Sentiment inductive model, is created to validate drug reactions discrimination from real-world patients' descriptions.

[3] https://eztag.bioqrator.org/
[4] https://www.ncbi.nlm.nih.gov/research/bionlp/Tools/taggerone/
[5] https://www.ncbi.nlm.nih.gov/research/bionlp/Tools/gnormplus/
[6] https://www.ncbi.nlm.nih.gov/research/bionlp/Tools/tmvar/
[7] https://www.health.harvard.edu/diseases-and-conditions/treatments-for-COVID-19
[8] https://tabilab.cmpe.boun.edu.tr/BIOSSES/DataSet.html
[9] https://arxiv.org/ftp/arxiv/papers/1808/1808.09397.pdf

TABLE I
RELATED-COVID19 TWEET AND THEIR DRUG REACTION SPANS FROM REAL-WORLD DESCRIPTIVE ENTITIES.

Tweet	Medical concepts	drug reaction span
@covid19crusher poor clinical outcome morocco lead switch hydroxychloroquine march twentythree average time covid19a remdesivir people died	covid19 hydroxychloroquine remdesivir	died
laura ingraham continues pimp hydroxychroloquine magic bullet covid19 fda cautioned use treatment doctors irresponsibly went fox said sideeffects lie fog	hydroxychroloquine bullet	fog
make tik tok video misguide people spit food item deliver hide information affect people bea patient lupus rationing rx severe patient gt50 improve amp discharge hospital	gt50 lupus	spit food amp rx gt50
fda approves widespread use drug covid19 limit effectiveness grave side effect base stu tired tolerant	base stu	tired tolerant
addict take #hydroxychroloquine follow 500ml glass dettol per presidential instruction lie comfortable position cover clean white sheetcall undertaker	hydroxychroloquine dettol	addict

TABLE II
EVALUATION RESULTS WITH TWO BENCHMARKS DATASETS BIOSSES AND MEDSTS.

	BIOSSES	MedSTS
Our embeddings	**0.85**	**0.83**
BioSentVec (PubMed)	0.817	0.750
BioSentVec (MIMIC-III)	0.350	0.759
BioSentVec (PubMed + MIMIC-III)	0.795	0.767

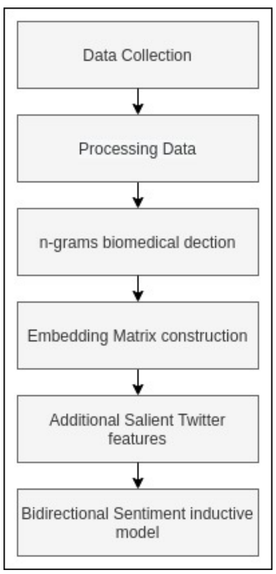

Fig. 2. The whole model description.

IV. IMPLEMENTATION AND EXPERIMENTS

One of the most potent ideas in deep learning is that sometimes you can take knowledge the neural network has learned from one task and apply that knowledge to a separate study. It called transfer learning. Transfer learning makes sense when you have a lot of data for the problem you are transferring from and usually relatively less data for the issue you are transferring to. In this study, we aim at imitating and retrieve the corresponding of real-word related drug entities in the formal medical ontologies by adopting a distributed representation of two databases PubMed and MIMIC III Clinical notes as described in Table VI. To summarize, we aim at developing an approach that takes unstructured data as input, constructing the embedding matrix by incorporating biomedical vocabulary, and discriminating possible drug reaction multi-word expressions. Finally, these representations are exploited for inferring positives and negative reports through operating sentiment scale we proposed.

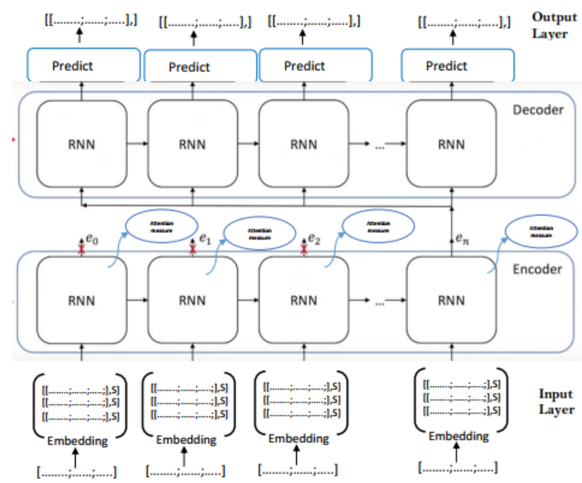

Fig. 3. Architecture of proposed approach.

The overall framework of this study is exhibited in Fig.3, as shown in this figure. This framework involves three stages: (1) build an enhanced sentence-level distributed biomedical representation, (2) Construct Encoder-Decoder model to discriminate and infer Drug reactions from texts, Which is a n-grams based embedding-trained model, and (3) Sentiment Induction based on Bidirectional LSTM. This model maps any body of text into 700-dimensional embeddings. The embedding matrix leverages contextual and information meaning from the sentence context to define the multi-word expression of drug reaction individual meaning in the field of distributional semantics configuration, which clarifies sentence's similarity in the same contextual target space, which are further share

TABLE III
THE EFFICIENCY COMPARISON BETWEEN THREE ALGORITHMS

Dataset	Corpora	Accuracy %
LSTM	Our Embeddings	0.73
SVM	Our Embeddings	0.61
BILSTM	Our Embeddings	**0.85**
	Biomedical Embeded sentence(PubMed)	0.81
	Clinical notes MIMIC III	0.79

TABLE IV
EXPERIMMENTS RESULTS OVERVIEW ON TWITTER DATA USING THREE SENTIMENT LEXICONS.)

SA lexicon	neural network algorithm	Accuracy (%)
SenticNet	LSTM	77 %
	BiLSTM	**85.3 %**
	stacked-LSTM	79%
SentiWordNet	LSTM	79.5 %
	BiLSTM	**86%**
	Stacked LSTM	74 %
AFINN	LSTM	79.5 %
	BiLSTM	**87%**
	Stacked LSTM	78 %

TABLE V
STATISTICS OF RAW DATA GROUPED IN TERMS OF SOME RELATED-DRUGS KEYWORDS IN DIFFERENTS SLICE OF TIME

related-drugs keywords	Number of tweets	Including drug reactions
COVID-19	20938	209
chloroquine	3299	107
remdesivir	2918	76

semantically common drug description meanings.
In addition, distributed representation of medical multi-words expression relies on automatic semantic identification of medical n-grams from patients narratives regarding definitions-related policy by investigating patterns and relationships from various embeddings of highly pre-defined medical controlled vocabulary and exploiting feature dynamism setting. It consists of both comprehending related-medication words, phrases and their semantics, which they are employed to fit conceptual and affective associations in high generalization performance. In the experiments, we examined four cases for deriving the embedding based vectors effectiveness. The first involved training on a pretrained vectors of the two corpora PubMed and the clinical notes from MIMIC-III Clinical Database have described in Table VI on the given training data. As the second use word2vec model on biomedical text corpus [10] that

[10]http://bio.nlplab.org.

Sources	Documents	Sentences	Tokens
PubMed	28,714,373	181,634,210	4,354,171,148
MIMIC III Clinical notes	2,083,180	41,674,775	539,006,967

TABLE VI
BIOMEDICAL CORPORA AND MEDICAL ONTOLOGIES STATISTICS USED FOR BIOMEDICAL DISTRIBUTED REPRESENTATION.

consists of over five billion words, which is further provided in the word2vec binary format. Moreover, this process was developed from PubMed, the PubMed Central texts, and their combination using the word2vec tool as follow: methods include training the embeddings based on (1) the average surrounding context words, such as the continuous bag-of-words (cbow) model in word2vec [9], (2) weighted context words, such as the skip-gram model in word2vec, (3) global cooccurrence statistics, such as GloVe [10], and (4) word n-grams, such as fastText [11]. The first mechanism got in consistence recall in term of defining meaning of medical multi-word expressions.
Since the related-drug reaction should extract from the whole context of the sentence, we propose a model for generating sentences from keywords using multiple RNN components with self-attention as a discriminator among these artificial neural networks. Specifically, the RNNs Encoder-Decoder structure uses an encoder to hold the biomedical embeddings information that represents drug reaction as the span of text in tweets reporting ADRs, and it is annotated corpora from Social Media Mining for Health (SMM4H) 2017 shared tasks [5]. It is benchmark training data that consists of 15 717 annotated tweets for adverse drug reactions (ADRs), 10 260 for medication consumption, from medication-mentioning tweets, and 6650 ADR phrases and identifiers for normalization of ADR expressions. It achieved an accuracy of 88.7%, outperforming individual systems. The decoder is the second network that convolves the output of the encoder and gives the best match to the actual input or intended drug reactions. The encoders are trained with the decoders. There are no labels (hence unsupervised). The loss function is based on computing the delta between the actual and reconstructed input. The optimizer will try to train both encoder and decoder to lower this reconstruction loss. Also, the keyword for input to the encoder of the generator is input together with words similar to oneself. This method contributes to the creation of sentences containing words that have similar meanings to the multi-word expressions.
We conduct many training developments to achieve good recognition accuracy, we used large patient narratives datasets from Twitter, as described in Table V. Table III present an overview of related-COVID19 tweets and their drug reaction spans from real-world descriptive entities. Likewise, we evaluated the biomedical distributed configuration space for clinical sentence pair similarity tasks. We used two benchmarks datasets dedicated for biomedical evaluation, the 100 sentence pairs from BIOSSES, and the 1068 sentence pairs

from MedSTS, as illustrated in Table II.

V. Evaluation: Sentiment Analysis Fine-tuning Task

Sentiment Analysis (SA) has got massive attention from healthcare organizations, using SA approaches to automatically detect medication issues, drug misuse, new infectious diseases symptoms, understanding patients shared experiences and reaching a vast audience in a matter of seconds is of critical importance. Since [12] cited many related-drug extraction challenges, [13] propose an optimal solution to get reliable and credible insights from those related-drug narratives. Moreover, [14] provide a novel mechanism to create medical distributed N-grams by enhancing convolutional representation, which is dedicated mainly to featuring text under medical setting and clarifying related sentiment at the same level. Indeed, [15] proved how drug reaction presence in text fails to retrieve the relevant sentimental status. They frequently need analysis at the features extraction level, which can be difficult without sufficient background knowledge of the formal medical contexts. Many experiments have been done in previous studies [13], [14] explain why sentiment analysis systems are able to perform sentiment analysis towards a given entity and services reasonably well but fare poorly on clarifying sentiment towards a medical concepts or multi-words expressions that may refer to an adverse drug reaction. The paper investigates the challenges of considering biomedical aspects through sentiment tagging task. An automatic approach to generate sentimental based-aspect with regard to drug reaction multi-word expressions towards varied related medication contexts, it considered as domain-specific sentiment lexicon by considering the relationship between the sentiment of both words features and medical concepts features. From our evaluation on large Twitter data set, we proved the efficiently of our encoder-decoder biomedical representation of drug reaction, which is dedicated to matching expressions from everyday patient self-reports. At this end, we chose to validate and enhance representations by learning real-world natural concepts and validating on additional task such as sentiment classification. We developed a based BiLSTM classifier that took the output of encoder-decoder representations to induce sentiment value from large patient self-reports about the COVID-19 pandemic. It is designed mainly to deploy the dynamic embeddings of medical concepts dependencies on huge shared data.

Since polarity is strongly connected to attitudes and feelings, we chose to use the popular sentimental lexicons to synthesize the full range of emotional medication experiences in terms of positivity and negativity, and we used three sentiment lexicons as follow:

- **SenticNet** [16]: knowledge base based on the sentic computing that provides semantic information, sentics and polarity associated with more than 50,000 natural language concepts. To bridge the conceptual and affective gap between word-level natural language data and the concept-level opinions and sentiments conveyed by them.
- **SentiWordNet** [17]: SentiWordNet is a public lexical resource, containing opinion information on terms extracted from the WordNet database. It is widely used in a variety of applications, such as emotional (or sentiment) analysis, and opinion mining. It also provides sentiment scores of positive, negative scores for each word, by using semi-supervised learning, automatic annotation of WordNet, and a random-walk approach.
- **AFINN** [18]: the AFINN lexicon measures sentiment with a numeric score between -5 and 5, while the other two lexicons categorize words in a binary fashion, either positive or negative. To find a sentiment score in chunks of text throughout the novel, we will need to use a different pattern for the AFINN lexicon than for the other two.

The evaluation models have slightly different results on Twitter data, where LSTM does well in this case. The based stacked-LSTM and BiLSTM model consistently improved the sentiment classification performance but is efficient when we exploit proposed configuration on a big online dataset. We proposed to exploit two-grams or three-grams using BiLSTM network to trickle the emotion aspects for new multi-word expressions that are inserted into the vocabulary, which are all fast operations. Therefore, it works even faster than classical sentiment lexicon approaches. Even drug reactions that are not in the vocabulary are selected as possible drug reactions. However, it deserves to be noted that if we replace tokens with n-grams and train on small datasets, which is encoder-decoder architecture with the obtained biomedical distributed representations on top of those features, then we may get whopping 5.3 bumps in the accuracy. It succeeds our accuracy to 87 per cent. We end up by learning some more in-depth representations. Table IV provides an overview of obtained results and classical models on large training set then it makes sense to use classical approaches.

VI. Conclusion

In this research, we developed an Encoder-decoder drug reaction Discriminator by involving an enhanced distributed biomedical n-grams representation from Controlled medical vocabulary (PubMed and Clinical note MIMIC III). Thus, we investigated the Bi-LSTM based neural network approach are used to generate sentiment scale powered by additional statistical salient for medical concept-aspects sentiment Inference.

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