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Learning sentiment and affects from large scale patients' narratives and biomedical documents using Neural Networks and Sentic computing: COVID-19 Case Study

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I would like to dedicate this thesis to my loving parents

To my husband

To my family

Declaration

I hereby declare that except where specific reference is made to the work of others, the contents of this dissertation are original and have not been submitted in whole or in part for consideration for any other degree or qualification in this, or any other university. This dissertation is my own work and contains nothing which is the outcome of work done in collaboration with others, except as specified in the text and Acknowledgements. This dissertation contains fewer than 65,000 words including appendices, bibliography, footnotes, tables and equations.

Hanane GRISSETTE
December 2021

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Abstract

Sentiment analysis is the computational study of people's opinions, sentiments, affects, evaluations, attitudes, moods, and emotions. The notion of sentiment in the context of medicine concerns a patient's health status, critical events, unexpected situations or specific medical conditions, the outcome or effectiveness of a treatment or judgment of medical conditions, experiences or opinions of treatments or a sort of drug, the certainty of a diagnosis. To evaluate this information properly, assessing positive or negative clinical outcomes or judging the impact of a medical condition on patients, several algorithms have been developed, each sermonizing a different research analysis or question. However, sentiment analysis for medical information requires a domain-specific sentiment source and complementary context-dependent features to be able to correctly emphasize on the explicit and implicit sentiment conveyed towards bio-medical data objects and their attributes. This thesis posits a case for constructing depend-domain comprehension of different bio-medical components within the text, as a means to better understand the natural language of generated patient narratives on social networks.

The automatic generation of features without human intervention is the most critical task for biomedical sentiment analysis. Regarding the high dynamicity of shared patient narrative data on social networks, the lack of formal medical language sentiment dictionaries prevents retrieval of the appropriate sentiment, which is unapproachable and can be prone to annotator bias. By designing affective approaches to model both unstructured texts and structured bio-medical knowledge, we can incorporate additional evidence from drug-related patterns structures beyond texts and allow sentiments to flow from concept to concept based on the dependency relation of the input sentence, in particular, a better understanding of the contextual role of each concept within the sentence is achieved.

This thesis thoroughly explains the definitions and theoretical preliminaries of representation learning methods, sentic computing theory, transfer learning, and associative learning and describes a list of the bio-medical concepts knowledge and their parameters, which contribute to the generation of semantics and contexts of medical information. Next, by examining the importance of biomedical knowledge in constructing category information and context information and developing the idea of incorporating depend-domain knowledge, a brief

review of the general area of sentiment analysis and an examination of the work undertaken so far in the bio-medical domain is presented. In particular, this thesis proposes insights on the evolution of sentiment analysis research from heuristics to discourse structure, from coarse-to fine-grained analysis, and from keyword to concept-level polarity detection.
To achieve our goals, we present different approaches to construct medication-related information by incorporating the existing concept-based bio-medical relations, as well as performing deep content analysis with some of the well-developed neural networks methods. As this detailed analysis will demonstrate, while some problems in performance remain despite the development and implementation of the different neural networks methods, sentiment analysis of patient-generated narratives is indeed viable and achieves a classification accuracy of 91.4% on the gathered data from varied social networks platforms such as Twitter. Furthermore, the models and data can serve as a great tool to automatically report treatment issues, drug misuse, new infectious disease symptoms, especially for detecting different drug reaction descriptions from patients generated narratives on social networks. This requires a suitably annotated patient-generated texts dataset for drug-related data objects, for both analysis and experimentation. Following the construction and detailed analysis of such a resource, a series of deep learning experiments study the impact of different models, features, and health-related texts types to the problem. These experiments examine the transferability and applicability of the selected methods and demonstrate that model and feature choice may not be a significant issue in sentiment generation, whereas bio-medical entities related to the extraction of different data-object properties, and contextual-semantics dependencies that the models train and test across does affect the outcome of sentiment analysis models in the context of medicine.

Keywords: *Sentiment Analysis, Affective Analysis, Sentic Computing, Neural networks, Patients' Narratives, Social Networks*

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Nomenclature

Roman Symbols

$Affinity(P)$	Affinity function
C	Compound Matrix
D	Patients narratives corpus
W	Weights Matrix

Greek Symbols

λ	The regularization parameter

Superscripts

j, i, k	superscript indexes

Subscripts

T	subscript index

Other Symbols

$e(i)$	Embedding vector for target sentence i
$g_{PL}, g_{AT}, g_{SE}, g_{AP}$	g_X is the level of activation predicted by the ELM where l_X is the corresponding sentic level
$l_{PL}, l_{AT}, l_{SE}, l_{AP}$	Sentic level (affective dimensions for Pleasantness, Attention, Sensitivity, and Aptitude respectively).

Acronyms / Abbreviations

ABSA	Aspect-Based Sentiment Analysis

ADR	Adverse Drug Reaction
BiLSTM	Bidirectional Long Short-term Memory
CHV	Consumer health vocabulary
CNN	Convolutional neural network
ELM	Extreme Learning Machine
LMs	Language Models
LSTM	Long Short-term Memory
MeSH	Medical Subject Headings
NLP	Natural Language Processing
PD	Parkinson's Disease
PROMs	Patient-Reported Outcome Measures
RNN	Recurrent neural network
SA	Sentiment Analysis
SIDER	Side Effect Resource
SUDEP	The Sudden, Unexpected Death of someone with Epilepsy
SVM	Support vector machine

Chapter 1

INTRODUCTION

> *"The secret of getting ahead is getting started."*
>
> — Mark Twain

1.1 Context

1.1.1 Motivations of Research in Sentiment Analysis and Patient Narratives

Out of 7.82 billion is the world's total population, 50.64% are interconnected via social networking sites[1]. Particularly, more than 40% of users say that information found via social networks platforms affects the way they deal with their health, where 90% of respondents from 18 to 24 years of age said they would trust medical information shared by others [2]. Information on social networks can have an immediate influence on patients' decisions to seek a second opinion, searching the interconnection that helps them to discover possible alternatives to diagnoses and treatments[3]. An estimated 27% of patients comment or post status updates based on health-related experiences and want to provide as much information as possible, or collect as much information as possible, to make the most trustworthy determinations and decisions[4].

Within the coronavirus outbreak period, social networks platforms play a large and crucial

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[1] 2021's statistics in :https://backlinko.com/social-media-users

[2] 24 Outstanding statistics and figures on how social media has impacted health care industry. Referral MD; 2017. https://getreferralmd.com/2013/09/healthcare-social-media-statistics/. Accessed 26 Sep 2017.

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

[4] https://getreferralmd.com/2017/01/30-facts-statistics-on-social-media-and-healthcare/

Table 1.1 Some related-concepts have cited in many stated natural remedies used for some ailments

Concept	Description
CBD Oil	CBD is one of over 100 chemical compounds known as cannabinoids found in the cannabis or marijuana plant, Cannabis sativa .
Cannabidiol	Cannabidiol is a popular natural remedy used for many common ailments.
THC	tetrahydrocannabinol (THC) is the main psychoactive compound in marijuana that gives the high sensation.

role in global living combats through information generation, dissemination, and consumption. It has vital importance in surveying public attitudes, identifying infodemics, assessing mental health, and detecting or predicting COVID-19 cases, etc. An estimated 1,342,1037 original discussions opened with 465,721 comments from 3,734,815 different users have been reported in one month by authors in (Cinelli et al., 2020). Indeed, a 57% of respondents are concerned about the amount of misinformation about COVID-19 others may be getting and 81% of users said that they were seeing banners, pop-ups, and upfront notices about the coronavirus[5]. Refers to authors in (González-Padilla and Tortolero-Blanco, 2020), a good example can be seen with the peak of searches for information on the Internet and social media platforms in China preceding the peak of incidence in COVID-19 cases by 10-14 days, with which Internet and social media networks searches have demonstrated correlation with the incidence of disease.

Multiple examples of unsafe and incorrect treatment recommendations are shared everyday, misinformation, and harmful experiences across the world. Sentiment Analysis (SA) has fared extremely well in identifying breakpoints in health-related public opinion. By considering different data objects attributes, it is highly used to discriminate and identify salient information that contains medical information. In particular, the notion of sentiment in the context of medicine concerns a patient's health (a change or reflection of the health status), a medical condition (critical events, unexpected situations or specific medical conditions, the outcome or effectiveness of a treatment or judgment of medical conditions, etc.), or treatment and experience regarding a sort of drug or the certainty of a diagnosis (more details can be seen in Section 2.2.2 and Fig 2.1). That is explicitly valuable in emerging situations, for example, (1) alleviating the symptoms that can help to discover the risk of a disease at an early stage, (2) detecting misunderstanding of drug related-information or side effects, (3) and ensuring a competitive edge to better understanding patients' experiences in a given condition, etc.

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[5] https://www.ofcom.org.uk/research-and-data/tv-radio-and-on-demand/news-media/coronavirus-news-consumption-attitudes-behaviour/interactive-data

- ambiguate incidence and high case **fatality** rate of \#**COVID19** in patients with active \#**epilepsy** & **epilepsy**, **COVID-19**
- **amepilepsysoc** terrific leadership team great paners advancing **epilepsy awareness** treatment thank sharing chi **amp**
- **aeds antiepileptic drugs** besides \#epilepsy also treat **mood disorders #chronicpain**
- @adrienneolivier @tiaank89 year ago today able add **vagus nerve** implant peters **treatment condition** been…
- @**aspiringheadr** frequency **takotsubo cardiomyopathy** \#epilepsy-related **hospitalizations** among adults impact in-hospit…

Fig. 1.1 A sample of tweets medication-related COVID-19

1.1.2 Bio-medical Sentiment Analysis

Sentiment analysis models are mostly used to evaluate affects and sentiments conveyed by patient narratives gathered from multiple information sources, determine positive or negative clinical outcomes and judge the impact of drugs and medical conditions. Indeed, sentiment can be conveyed through diseases, treatments, medical conditions and they impact a patient's life quality and health status. The models' effectiveness depends mainly on how well they recognize entities, concepts, events, and their aspects regarding varied medical targets such as treatments, conditions, symptoms, and drug events.

Sentiment analysis approaches have been broadly categorized into knowledge-based approaches, machine learning-based approaches, and hybrid approaches that rely on ensemble methods. Knowledge-based approaches, including corpus-based methods and lexicon-based methods, mainly rely on an already developed knowledge base such as SentiWordNet (Baccianella et al., 2010) by which the polarity value is computed based on the co-occurrences of the term with other positive or negative seed words in the knowledge base. The problem is that the coverage of knowledge bases as most of the available knowledge bases contain general knowledge (not affective knowledge) which is insufficient to determine the polarity of shared patient narratives. Machine learning-based approaches are more popular for the identification of emotions and polarity from unstructured raw text, where it is possible for the methods to not only learn the sentimental valence of affect input but can also take into account the valence of other unseen input.

In training a classification algorithm, we need to discover what features give the statement a positive or negative sentiment. Advanced machine learning algorithms are designed to discover patterns and associations in historical training data, which aim at defining relevant features that construct the semantics and contexts. The main challenge is the identification and learning of the principal and relevant features for the sentiment analysis algorithms.

Feature selection and feature extraction techniques are used to mine the prominent features

Table 1.2 Frequent medical concept used for epilepsy treatment

Concept	Description
SUDEP	SUDEP sudden unexpected death in epilepsy
AEDS	anti-epileptic drugs (aeds), and therapeutic drug monitoring for phenytoin, carbamazepine, phenobarbital ..etc
SCN2A	Movement disorders seem to be common in patients with epileptic encephalopathy. SCN2A encodes an alpha subunit in a voltage-gated sodium channel.

and are preferred when only discrimination is required but may not be a good choice for bio-medical data objects when interpretation is required. Since is been widely used for hand-crafted features to identify bio-medical entities such as diseases, drugs, symptoms, and also relations types such as cures, causes, etc, feature selection is preferably used for drug-related algorithms as does not alter the data and hence offers better interpretability. Most of the existing feature selection techniques, used for sentiment analysis, may not consider the redundancy among features where feature extraction methods result in irrelevant and redundant features. Extraction techniques based on medical concepts should be involved so as to collectively detect different concepts of related drugs regarding the dynamism of various medical situations. An intuitive solution is to take into account the properties and attributes of medical data objects, domain-dependent semantics and relationships among entities, and additional online attributes such as natural language concepts.

Different from the traditional use of machine learning algorithms, deep neural networks allow an extensive coverage of the raw data. Among the most successful SA models are those based on deep learning techniques, which rely commonly on two main functionalities that are feature learning algorithm and classification neural network-based algorithm.

Attempts to understand components of medical information and affects and its generation are complicated by many factors, one of which concerns the problem of bio-medical entities identification, leading to inefficient feature learning precision. In particular, feature learning requires careful engineering and considerable domain expertise to shape and recognize entities that the learning subsystem used for training. Existing SA services might fit good at understanding the whole sentiment assessment but fairly poor at shaping bio-medical concepts structures and tracking sentiment conveyed towards the bio-medical set of components as input target. This failure can be strongly associated with many problems, in particular the lack of formal medical language sentiment dictionaries, which is unapproachable and can be prone to annotator bias. However, neural networks-based methods become a more suitable solutions for patient narratives feature learning tasks, which offer a rich representation and allow identifying the relations among words, offering interesting qualitative, historically, semantically, and contextually information. Indeed, they have been widely used in learning efficient pattern and linguistics structures in the context of medicine through exploiting richer features in both semantic and context directions because of their ability to learn deep patterns and relationships through distributed representations and are further used for medical concept normalization and recognition, sentiment tagging, and adverse drug reaction detection. etc. Embedding is a popular neural network-based method that provides informative, rich, and semantic representations. Existing embeddings focus on the word structure and spatial characteristics to encode words meanings and semantics (Yang et al., 2021). Many alternatives have been done, Word2Vec (Mikolov et al., 2013a) and Global vector (GLOVE) (Pennington et al., 2014a) are the first generations of semantic space models and are successfully capturing important characteristics in a word-level distribution. Word2Vec algorithm is widely used as an unsupervised method that seeks to place words with similar context close together in the embedding space. Despite their performance in many SA fine-tuning tasks, these methods have certain limits and are being underemployed for medical use cases such as detecting multiple sentiment polarities regarding different contexts and identifying complex bio-medical components, e.g, drug reactions. They merely take into account word distributions free-context and do not emphasize properties from depend-domain context (Li et al., 2017). Thus, pretrained vectors mostly ignore the relationships between terms that have never occurred in the vocabulary, especially bio-medical dependencies (Shuang et al., 2018). Importantly, a good embedding can capture and summarize data-objects attributes, properties, semantics, and fine-grained relationships. The best accuracy is achieved by exploring bidirectional contextual information from a large knowledge-based dataset since the accuracy of sentiment classification mainly relies on the quality of the annotation, word score, and entity tagging techniques (Zuo et al., 2020; Ke et al., 2021).

One of the major obstacles that have to be faced when applying automatic emotion recognition to realistic patients notes and drug-related interactions is the sparsity and ambiguity of unlabeled data that may seriously affect learning relevant features. Given the limitation of manually labeled data, supervised approaches on small datasets are obtained to be more suitable (Pesaranghader et al., 2019), yet they do not allow handling different concept nuances and their ambiguities types from social networks. Unsupervised approaches hardly involve a degree of medical language comprehension to build medical concept vs. senses meaning, which is mostly used to clarify contextual senses generated by inferring such a sense of the distributed representation of a sentence. A wide range of sense disambiguation approaches has been applied to the question of discriminating various ambiguities in bio-medical and clinical documents (McInnes and Stevenson, 2014). The current systems implement mostly different complicated graphical tasks based on advanced distributed solutions or the classic Natural Language Processing (NLP) techniques to extract and disambiguate complex entities and relations in texts (Halioui et al., 2018). They have progressed steadily to the point where

Table 1.3 Examples of related-concepts senses.

Concept	Possible meanings	Statistics (freq)
aed	Anti-epileptic drugs (AEDs) are the main type of treatment for most people with epilepsy.	298
	Automated external defibrillator, is used to help those experiencing sudden cardiac arrest.	22
	The AED (United Arab Emirates Dirham) is the currency abbreviation.	5
SUDEP	SUDEP as : Epilepsy Fondation	493
	SUDEP : Sudden Unexpected death	1007
	SUDEP action labeled as Making every epilepsy death count	284
	SUDEP institute	190
	SUDEP purpleday: Sudep Event	480
	Epilepsy Sudep awarness	383
	sudden infant death syndrome (SIDS).	290
seizure	epileptic seizure (a sudden attack of illness)	137
	Jacksonian seizures symptomb	121
	seizure of power by the military	2

sense disambiguation methods achieved consistent levels of succeeding accuracy on a variety of ambiguities[6]. Recent studies improve the accuracy of recognition of medical entities by linking social media data to their correspondence from the health-related databases and pharmaceutical clusters. Where it is computational and software costly to centralize all these knowledge from resources around the world.

Embedding techniques can make complete use of the information represented in generated narratives to extract and disambiguate contextual senses (Li et al., 2019). However, they made limited progress in addressing contextual concept polarity detection from medication-related short text, and thus far, advanced machine learning-based NLP techniques have been underutilized (Nikfarjam et al., 2015b). Indeed, they mostly do not offer lexical depend-domain distinction, especially medical multi-word expressions that are undisambiguated regarding concept aspect-based senses. Bio-medical data loss increases rapidly and holds highly biased medical concepts towards a given aspect and undistinguishable senses and therefore their accuracies drop. Advanced embeddings are more general and flexible in nominating similar context-based meanings. In particular, concept embedding offered an improved knowledge reward over the state-of-the-art bio-medical WSD methods using medical ontologies such as the MSH WSD dataset (Sabbir et al., 2017; Antunes and Matos, 2017; Li et al., 2019b), being responsible for assigning the proper concept to an ambiguous term. But, according to authors in (Calvo et al., 2019), the problem of these meaning disambiguation methods of concepts results in a specialization in a single set of words, which has been underutilized

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[6] doi:10.4249/scholarpedia.4358

regarding medication-related text challenges. Then again, medical aspect-based relations have been lacking.

1.1.3 Problem Context and Research Questions

The automatic analysis of patient shared narratives require primarily skilled natural concept recognition capabilities and huge labeled medical data, which are unaffordable. The problem is that the existing methods fail because they do not properly focus on the medical components related to extracting different properties, concepts, medical events, and people from data objects, which should be used to formulate interactions, semantics, dependencies, and inter-relations. Text accumulation errors and linguistic sub-problems such as noisy (insignificant) and informal texts often occur due to the inability to resolve the ambiguity of these medical elements and define drug-related entities, resulting in a lower recall than desired. This motivates the overall problem of this thesis: *Learning sentiment and affects from large scale patients' narratives and biomedical documents*. The main research question discussed through this thesis can be presented on five important sub-problems corresponding to most of the unique characteristics of patient shared narratives to achieve this goal.

Sub-problem 1 : *Bio-medical data Structure particularities on social networks and informality:* Different from raw data mostly used for classification or regression, patients self-reports on social networks frequently capture varied elements ranging from medical issues, product accessibility issues to potential side effects or adverse drug reactions. Patient narratives can represent a combination of meaning, structure, and events. As shown in Fig. 1.1, patient narratives highly cite various concepts and entities that may be ambiguated. Indeed, high-level features such as concepts can not be detected due to noisity and informality.

The major issue is the inability of existing SA methods to accurately detect their attached medication-related sentiments regarding varied aspects such as treatment, medication or condition. they are becoming less efficient due to data sparseness, informal medical language, structural ambiguities, and got in low accuracy due to non-consideration of medical entities and contexts. Because they learn from general-scope data and are not adapted or incorporated the specific lexicon used in the formal medical contexts.

The informality of varied medical entities in the text leads to ignoring such components and prevents detection of the real target and meanings. Referring to previous qualitative analysis in this sense provided in our earlier experiments (Grissette and Nfaoui, 2020b), most SA approaches generally classify subjective medical events or sensitive medical entities as a negative sign of every polar story, which can seriously fail to recover the corresponding feeling. Thus, no study considers these entities as an analysis target, which aims to detect the relevant sentiment towards these entities for a given aspect. As an example in (Grissette and Nfaoui, 2019), the sentiments conveyed towards the concept of "$Epilepsy$"[7] are all considered negative where this disease can also appear in positive stories and quotes. As shown in Fig. 1.1, it has appeared in both several positive patient reports, as well as negative patient reports, due to the frequent associations with SUDEP concepts as a life-threatening complication that generally seemed to arise when a person with epilepsy dies so unexpected and was previously in its usual state[8] of health. An estimated study reported that SUDEP takes more lives each year in the United States than other epilepsy-related deaths such as Sudden Infant Death Syndrome (SIDS), and their concepts have appeared frequently in accounts of epilepsy in different ways, Table 1.2 highlighted these related concepts and their specific meaning in the context of epilepsy.

Additionally, many related natural remedies are flagged up in online conversations as treatment issues or usage descriptions, as shown in the Table. 1.1, unfortunately, related concepts have been ignored by controlled bio-medical vocabularies such as manganese, taurine, seizure reduction, and CBD oil, which is variously cited in terms of side effects and problems treatment without formal reports by medical experts. In this work, a lexicon's expansion is proposed based on a neural network that aims at extracting, aggregating, and computing relevant features for each new term, which are further used as sentimental former vectors to average emotions' overall dimensions and tokens of vocabulary.

Twitter case study: The subject of the research is comprehensively studied as an example of a phenomenon of concretization, within the context of a living case study. Twitter Sentiment Analysis (TSA) also has great success in analyzing real-world cases, especially in the COVID-19 pandemic period, many studies have done (Lu and Zheng, 2020; Peng et al., 2020). Twitter data involve additional linguistics properties: language diversity, brevity, short and limited expressions, acronyms, named entities, hashtags, informal medical language, emoticons, etc. They might exhibit additional natural language challenges, such as excessive use of abbreviations, acronyms, alternatives, and misspellings of medical entity citations. For example, in the dataset used in this study, we have found 1489 COVID-19-related spellings, e.g., 'postcovid', 'covidiots', 'noncovid', and 'covidale'. In addition, the annotated corpora proposed in this area are very few. Moreover, current annotation systems primarily focus only on common concept types such as genes and diseases (Chen et al., 2020). Consequently, the limited amount of training data available increases bio-medical data loss. To overcome

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[7] https://www.mayoclinic.org/diseases-conditions/ epilepsy/symptoms-causes

[8] https://www.epilepsy.com/learn/early-death-and-sudep/sudep/

this limit, controlled medical languages and their data object components, which contain rich semantic information, are incorporated to build and learn medical word embeddings (Chen et al., 2020; Zhang et al., 2019a; Chen et al., 2019) from generated narratives.
To show the importance of considering bio-medical terms, authors in (Denecke and Deng, 2015) perform an intrinsic and extrinsic evaluation using various datasets from patients' clinical records and generated narratives on social media platforms with respect to word usage and changeable sentiment in a given situation. m

Sub-problem 2 : *Affect bio-medical concept-level encoding.* Existing neural networks-based solutions offer rich embedding and long-term dependencies over large datasets. But, low medical natural concepts observations from shared experiences would lead to inferior method accuracy. One of the primary challenges is associated with the capability of extracting sentiment conveyed towards bio-medical entities within the text. The major research questions discussed in this stage are listed below:

(1) How can the exactness of medical fact assessments be enhanced by studying varied medical concepts from many self-reported experiences?

(2) What embedding strategy should be considered for deploying entity interactions, dependencies, contextual semantics, and their sentics for improved biomedical sentiment analysis by considering the aspects in which they are extracted?

(3) How can salient online information be identified to focus on a given person, target or entity?

(4) What does demonstrate that integrating a prior sentiment knowledge in the embedding process participate in enhancing model reliability, and help to investigate sentiment value for unseen items.

However, we discuss which the best knowledge, parameters, layers are efficient to boost the model's ability to learn medication-related affective associations. The proposed strategies were on two main alternatives as follows:

Alternative 1: *A based sentic computing and neural network approach.* We propose a novel method that defines and normalizes bio-medical concepts and events and synthesizes contextual semantics and their assembled sentics.
Contextualized embedding is a critical step in bio-medical sentiment analysis. To support the credibility and correctness of our bio-medical representations, we use label propagation at the first model layer by integrating a large number of well-coordinated samples of highly controlled vocabulary from PubMed. Additionally, we enhance our connotation by integrating extreme learning machine cognitive capabilities into our neural network model. The obtained

embeddings are then used to build and recognize affective semantics and sentics based on extreme learning machines.

Alternative 2: *An associative learning-based approach.* This alternative mainly aim at defining capabilities for automatic sentiment decomposition of unsupervised representations from large-scale patients' narratives.
Considering the various medical components in the text, the proposed associative learning mechanism offers better results in terms of capacities of conceptualization, generalization, and recognition of medical familiarity and categorization based on aspects. The efficacy of this approach can be attributed to the ability to capture, quantify, and memorize a dependency measure considering online dynamicity by formulating bidirectional associative memory properties. Associative learning is mainly about expressing ideas and experiences reinforcing each other, which are furthermore interrelated, making it a powerful learning strategy (Enquist et al., 2016). It increases the levels of abstraction with communication between compound patterns, as well as patterns of learning feeling and inference. In particular, this alternative investigated an associative learning approach through multiple convolutions to build a dynamic configuration space from unsupervised medical concepts representations, which imitates such a learning process to learn the network parameters. Furthermore, the model promised to allow modeling medical patterns by identifying every time and inserting them into space with corresponding sentimental value with little support evidence.
Finally, The model also has the ability to calculate the completion of various medical patterns that have been missed or observed informally by convolving multiple convolutional neural network channels on the basis of old associative characteristics based on concepts. Those former patterns will be deployed later by our bio-medical sentiment decomposition aspect-based algorithm.

Sub-problem 3 : *Bio-medical concepts meaning ambiguity:* One of the most significant challenges in processing short text is the problem of ambiguity. This problem arises wherever addressing context and social knowledge where dictionary-based knowledge of the world is limited. Bio-medical meaning is only meaningful in reference to, and in distinction from, other meanings that need to be justified according to the sentential context in which the concepts occur, especially multiple sense modalities of an individual concept. As an example; Epilepsy disease has many key signs and symptoms and a spectrum of illnesses such as "Sudden Unexpected Death in Epilepsy (SUDEP)" that may have varied senses regarding multiple meanings in different contexts, where it is still subject to the aspect-specific extraction sub-issues. Table 1.3 illustrates some related multi-word expressions that may refer to "SUDEP".

"A few slices of raw ginger root in boiling water may help soothe a cough or sore

> *throat"* is one of many home remedies that widely have been shared on social networks. Home remedies and nontechnical traditional medicine entities identification is a fair challenge. More entities can be appeared on those remedies descriptions and might have serious side effects and be widely used for serious disease medications such as cancer. For case, Cannabidiol (publicly spelled as "CBD") is one of over 100 chemical compounds known as "cannabinoids" found in the cannabis or marijuana plant, Cannabis sativa, which is a popular natural remedy used for many common ailments. Cannabidiol is most commonly used for seizure disorder (epilepsy). It is also used for anxiety, pain, a muscle disorder called dystonia, Parkinson disease, Crohn disease, and many other conditions, but there is no good scientific evidence to support this uses[9].

The above problem prevents from defining sentimental information conveyed towards different data objects and their target meanings. Meanings are multiple, changing, and contextual. Since the meanings of words change, the sentimental attitudes that they conveyed also alter. Retrieving information about alternative meanings relies on the ability to deal with other ambiguities, type extraction, and relationships(semantics). Then the bio-medical entity recognition difficulties increase computational complexity which further increases the training difficulties of deep neural networks for online shared experiences.

For a given input sentence, most existing automated related-sense lexical databases and glosses, which offer sentiment value within a synset, rely only on computing related-sentiment or emotional valence by describing how the words and phrases of the text match vocabulary, e.g. WordNet lexical database that addresses the word ambiguity problem by providing various WordNet-based word sense disambiguation algorithms. They do not define sentimental relatedness of multiple meanings of given bio-medical aspect-based targets. To deal with those sub-issues, recent studies leverage deep learning ensemble methods to define related sentiment of varied senses by (i) exploring bidirectional contextual real-world definitions based on a core set of seed terms, (ii) logical reasoning or by (iii) evaluating similarities in document corpora. Whereas, those models cannot meet the requirements of large-scale complex medication-related narratives due to limited dictionaries of real-world knowledge and weak sentiment-sense associative capabilities that concern the dynamicity of sentiment towards aspects over a while, namely sentiment evolution. Besides, non-stable or absolute sense and sparsity present a fair challenge to clarify and distinct sentiment regarding appropriate senses and contextual definitions (Choi et al., 2017). Consequently, there are fewer studies that conquer these limitations.

Through this study, we aim to respond to the following research questions:

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[9] https://medlineplus.gov/druginfo/natural/1439.html

(1) With a massive influx of patients generated narratives on social networks, how controlled bio-medical vocabularies can help efficiently extract, define, and synthesize correct sense and what the best combination of these bio-medical resources is needed

(2) how do explore unsupervised learning to deal with the serious loss of bio-medical data of unstructured plain text

(3) what training parameters and enough data have to be involved to ensure models performance in term of dynamicity, sentiment evolution, and ambiguity varieties.

We produced three main contributions: First, we propose a sense disambiguation method training knowledge and learning mechanisms that serve to discover well-coordinated medication-related senses patterns and generate contextualized embeddings. Second, deploy a typical deep learning component to leverage concept-centric synsets and data-objects properties, whereby, attempt to understand the effect meaning of elementary sense vs context units that make up the whole meaning toward a given target in the text. Finally, we compute the conveyed aspect-based sentiments by leveraging the bag of affect former of each sense pattern constituent of the document. The intrinsic and extrinsic evaluations demonstrate that the model can leverage relevant senses features better than traditional WSD methods and baselines regarding bio-medical-data properties, ambiguity type, relational mapping between aspect and contextual dependencies.

Sub-problem 4: *Learning Approaches Adaptability and Transferability deficiency for biomedical data:* Massive examples of deep learning sentiment services have been provided which explore rich embedding benefits, dimensionality reduction, and long-term dependencies on large dataset conversion (training) examples. Each worked perfectly in the setting in which they were trained, but their performance decreased sharply when they became accustomed to analyzing patient stories online. They often lose ground in the face of more flexible knowledge-based challenges. Indeed, the language used by patients on social networks is highly informal. As Fig 1.1 Illustrates, it frequently involves various real-world natural concepts, descriptive entities, nontechnical medical citation, and pragmatic observations.

The problem is that, for a given aspect of analysis, it relies on appropriate material extracted to support intuitive knowledge, to verify expectations, pre-set explanations, and assumptions, to allow linguistic phenomena to be quantified, and to find proof for existing theories or to retrieve illustrative samples. Where the coverage of knowledge bases as most of the available knowledge bases contain general knowledge (not affective knowledge) which is insufficient to determine the polarity of unseen medical components. Generative Models for both Sentiment analysis (SA) and Natural Language Understanding (NLU), and Medical Named Entity (Medical-NER) learning tasks assuming the existence of medical human-labeled data or making use of resources for weak supervision that operates with the ignorance and the inability to define related-medication targets, and results in inaccurate sentiment prediction performance. To assist in these situations, we adopt a transfer learning configuration (see Chapter 2) with respect to the bio-medical entities varieties.

Sub-problem 5 : *Identification of adverse drug reactions.* Efficient bio-medical sentiment inference involves drug-related component distinction. In this regard, the proposed method has the advantage of considering drug reaction identification, which consists of natural bio-medical concept comprehension and drug reaction extraction. Most of them consisted of only detecting adverse drug reaction(ADR), but may fail to retrieve other aspects, e.g, the beneficial drug reaction or drug retroviral effects such as "relieve intraocular pressure associated with glaucoma".

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 stimulating 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 a 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 main finding of this thesis are as follows:

Feature learning representation

- Semantic relations among the words in the text have useful cues for sentiment analysis. Embedding algorithms conquer various text-linguistics limitations and annotated data deficiency, which provides a better understanding of the patient narrative text that improves the performance of the sentiment analysis. we demonstrate the effectiveness of integrating deep-learning-based cognitive capabilities for both enhancing distributed biomedical definitions and inferring sentiment compositions from many patient self-reports on social networks.

- The problem of data sparseness is alleviated by neural networks-based feature learning algorithms, which in turn improves the performance of the sentiment analysis. The deep architectures work significantly better than the classical approaches, especially when adding convolutions in the feature learning components, e.g, managing scarcity and reducing dimensionality through the downsampling step.
- Sentic Computing theory has great potential to define affect of complex components. By considering sentics vectors on top of the formed embeddings, a semisupervised LSTM-BiLSTM achieved an accuracy of 87.5%. The evaluations of unsupervised learning approximated the results of the previous model when dealing with a serious loss of biomedical data.
- Bidirectional associative memory algorithm has the ability to compute the completion of unseen bio-medical patterns, where comprehensive bio-medical distributed representations are used for representing the formal medical connections from PubMed databases. It achieved an average performance of 87% on varied large online datasets. It also outperforms baselines in discovering and identifying medical natural concepts.

Aspect-Target Class specification

- High sentiment analysis performances require more attention to the aspects and contexts regarding varied medical targets such as treatments, conditions, symptoms, and drug events. So too we argue that primary natural medical language understanding toward specific aspects has to be considered as intrinsic settings for medical vocabulary development. Indeed, natural medical concepts processing, from online generated narratives; has become a mandatory step to better match formal semantics from a widely used biomedical controlled vocabulary. This is specially provided in the context of semisupervised aspect-based learning for sentiment analysis.
- Semisupervised LSTM-BiLSTM model for biomedical sentiment classification algorithm with normalized features performs better than machine learning classi-

fiers for sentiment analysis such as support vector machines, especially for big online datasets.

- The model offers a significant rate of bio-medical natural concept discrimination by critically analyzing constraints from conjunctions of the positive or negative contextual semantics. Further, the experiments on multi-source data from Twitter and health-related forums have overshadowed sentiment assessment and achieved an accuracy of 91% regarding concepts-based medical aspects.

Domain Transferability

- By illustrating the importance of including bio-medical aspects in analyzing related medication text. we are conducting a comparative study between state-of-the-art deep learning algorithms utilizing bio-medical embeddings features for bio-medical sentiment analysis tasks. Indeed, we examined four cases of efficient vector derivation based on bio-medical embedding inclusion, whereby we discuss the quality of the study by performing an explanatory analysis using the positive and negative messages of the patients on Twitter.
- The experienced results provide fresh insights about how investigating medical knowledge,e.g Medical Subject Headings (MeSH) and PubMed, to clarify correspondence of various bio-medical descriptive entities, definitions, and data properties from shared medication-related content.
- Considering the importance of the feature with respect to the bio-medical domain improves the performance of the sentiment analysis. Both intrinsic and extrinsic evaluation proved how neural fusion-based mechanism succeeded to prune contextual senses-features generation and show strong agreement for bio-medical data properties parameterization and ambiguity type extraction.

To the community

- The relevant encoding of affective information conveyed regarding medication subjects clearly reveals defined roles and expectations that can have a positive impact on public health.
- The necessity of multi-properties analysis has been observed, it is been proceeded by an explanatory analysis. Those observations hold when controlling for age, income, education, ethnicity, and overall health status through all of which are also associated with doing health-related activities online.

- We provide meaningful support to bio-medical sentiment analysis applications on social networks. Indeed, the facets of this study might be used in many health concerns such as: analyzing changes in health status or unexpected situations.

1.2 Thesis Outline

This chapter has presented the motivation for this thesis and the methodology that has been used. The rest of this thesis is structured as follows:

- ***The second chapter*** provides a summary of the most important definitions and theoretical preliminaries for understanding the remainder of the thesis, including representation learning methods, aspect-based sentiment analysis in the field of medical information, sentic computing theory, and a list of the bio-medical concepts knowledge and their parameters, which are exploited to build the embeddings. Indeed, this chapter lays the groundwork for the thesis and the motivation for approaching a concept-level understanding of patients' self-reports and explores further what type of settings make the use of medical terminologies and ontologies from biomedical literature efficient to derive category information and context information. Finally, an introductory overview describing transfer learning theory adaptation for transferable characteristics of semantic models applied to biomedical sentiment annotation.

- ***The third chapter*** presents a summary of the literature review of sentiment analysis in the context of medicine and biomedical literature. This chapter describes and reviews previous research work done in the area of bio-medical sentiment analysis approaches, and how the development of the field has branched off to tackle the task of sentiment classification in the clinical domain. The chapter presents an introduction of biomedical distributed representation as an imperative step for concept-level sentiment analysis and the explanation of its key shifts, which highly differentiate it from standard embedding algorithms for unsupervised representations recognition.

- ***The fourth chapter*** presents the proposed architecture for *an affective concept-based encoding of patient narratives via sentic computing and neural networks* with more problem definition details. This chapter presents a large social network experimentation outputs and comparisons of state-of-the-art sentiment lexicons and sentence-level biomedical distributed systems. This chapter also discusses some linguistic gaps through analyzing huge patient narratives.

- ***The fifth chapter*** introduces *the bidirectional deep associative learning approach utilizing unsupervised representation from large scale patients' narratives* . This chapter formalizes a deep associative learning method to learn the properties of data objects from unstructured data, in conjunction with medical comprehensive medical vocabularies. An associative neural network computation in which future values mimic such a learning process from well-understood biomedical patterns, in which the former patterns have been deployed for sentiment decomposition regarding the aspects in which they are extracted. Indeed, this chapter examines four cases of efficient vector derivation based on biomedical inclusion, whereby we discuss the quality of the study by performing an explanatory analysis using the positive and negative messages of the patients on Twitter. The experiments have proven the effectiveness of the abstraction of medical concepts and demonstrated how good the proposed method is.
- With this in mind, ***The sixth chapter*** describes the development of drug reaction extraction method, details the identification of drug-related concept process, and finally, gives a corpus analysis of real-world COVID-19 discussions. This chapter aims to analyze word representation taxonomies in the context of medicine by analyzing word-level distributions. Following the construction and detailed analysis of such a resource, a series of machine learning experiments study the impact of different models, features, and review types on the problem. These experiments examine the applicability of the selected methods to improve model reliability and leverage the different conceptual and contextual distributed insights by incorporating unlabelled data into the training process from online examples. The analysis examines the suitability and of the concept-level representation learning for sentiment classification, and therefore proposing n-gram convolutions vocabulary scheme for drug-related data objects extraction. which produces medical concept normalization under distributed dependency.

1.3 List of Publications

Journal Papers:

- GRISSETTE HANANE; NFAOUI EL HABIB (2021). Affective Concept-Based Encoding of Patient Narratives via Sentic Computing and Neural Networks. Cognitive Computation. Springer. 2021; Available from: https://doi.org/10.1007/s12559-021-09903-z.(IF: 5.418,Q1)
- GRISSETTE HANANE; NFAOUI EL HABIB (2021). Deep associative learning approach for biomedical sentiment analysis utilizing unsupervised representation from large-scale patients' narra-

tives. Personal Ubiquitous Computing, Springer, 2021; Available from: https://doi.org/10.1007/s00779-021-01595-4.(IF: 3.006,Q2)

- GRISSETTE HANANE; NFAOUI EL HABIB (2020). Enhancing convolution based sentiment extractor via dubbed N-gram embedding-related drug vocabulary. Network Modeling Analysis in Health Informatics and Bioinformatics, Springer 9(1):42. (IF: 5.418,Q1)

Conferences:

- GRISSETTE HANANE; NFAOUI EL HABIB (2021). Adversarial LSTM-Based Sequence-to-Sequence Model for Drug-Related Reactions Understanding. In:Proceedings of Sixth International Congress on Information and Communication Technology. Lecture Notes in Networks and Systems, vol 216. Springer, Singapore. https://doi.org/10.1007/978-981-16-1781-2_6; p. 49–59, London, UNITED KINGDOM.
- GRISSETTE HANANE; NFAOUI EL HABIB (2021). Embedded Techniques Comparison for Bio-Medical Sentiment Analysis: A Corpus-Based Case Study of COVID19 Drug-related Reviews. The Second International Conference on Embedded Systems and Artificial Intelligence (ESAI). Fez, MOROCCO.
- GRISSETTE HANANE; NFAOUI EL HABIB (2021). The Impact of COVID-19 on Parkinson's Disease Patients from Social Networks. In:Networking, Intelligent Systems and Security. Smart Innovation, Systems and Technologies, vol 237. Springer, Singapore. https://doi.org/10.1007/978-981-16-3637-0_60, Kenitra, MOROCCO.
- GRISSETTE HANANE; NFAOUI EL HABIB (2020). Drug Reaction Discriminator within Encoder-Decoder Neural Network Model: COVID-19 Pandemic Case Study, 2020 Seventh International Conference on Social Networks Analysis, Management and Security (SNAMS), 2020, pp. 1-7, doi: 10.1109/SNAMS52053.2020.9336561, Paris, FRANCE.
- GRISSETTE HANANE; NFAOUI EL HABIB (2020). The Impact of Social Media Messages on Parkinson's Disease Treatment: Detecting Genuine Sentiment in Patient Notes, International Work Conference on Bioinspired Intelligence (IWOBI), COSTA RICA.
- GRISSETTE HANANE; NFAOUI EL HABIB (2019). Daily life patient's Sentiment Analysis model based on well-encoded embedding vocabulary for related-medication text, The 2019 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining, Vancouver, CANADA.
- GRISSETTE HANANE; NFAOUI EL HABIB (2018). A Conditional Sentiment Analysis Model for the Embedding Patient Self-report Experiences on Social Media. 10.1007/978-3-030-11884-6_6. Advanced Intelligent Systems for Sustainable Development, Springer. Tangier,Morocco.
- RISSETTE HANANE; NFAOUI EL HABIB; BAHIR ADIL (2017). Sentiment Analysis Tool for Pharmaceutical Industry; Healthcare, Transactions on Machine Learning and Artificial Intelligence, 5(4). https://doi.org/10.14738/tmlai.54.3339. Tetouan, MOROCCO.

Posters:

- GRISSETTE HANANE, NFAOUI EL HABIB(2020). Drug Reaction Detector through Multi-Folds Machine Translation mechanism. Deep Learning and Reinforcement Learning (DLRL) Summer School, Edmonton, CANADA.

- GRISSETTE HANANE, NFAOUI EL HABIB (2019). The impact of Social Media messages on Parkinson's disease treatment: Towards building Emotion Parkinson's Assisted Tool. Deep Learning and Reinforcement Learning (DLRL) Summer School, Edmonton, CANADA.
- GRISSETTE HANANE, NFAOUI EL HABIB(2019). Sentiment Analysis Model Based-CNN and extended transition-based Medical Concepts Recognition. Data Science Summer School (DS3), École Polytechnique Paris, France. Polythechnique Paris, FRANCE.
- GRISSETTE HANANE, NFAOUI EL HABIB(2018). A dynamic Sentiment Analysis Model based on associative learning for Defining the Minute Insights from passive and active Patients state self-reported on Social Media. Machine Learning Summer School (MLSS), Madrid, SPAIN.

Chapter 2

BACKGROUND

> *"There are only two ways to live your life.*
> *One is as though nothing is a miracle.*
> *The other is as though everything is a miracle. "*
> —Albert Einstein

2.1 Introduction

Sentiment Analysis concerns the study of capturing, quantifying, and measuring public sentiments through different methods, tools, and techniques. Quantifying sentiment in the context of medicine is difficult to capture in a few words, which may concern a patient's health, a medical condition, or treatment. The facets of sentiment in patient-related narratives (texts) may be manifested in (1) a change or reflection of the health status, (2) critical events, unexpected situations or specific medical conditions, (3) the outcome or effectiveness of a treatment or judgment of medical conditions, (4) experiences or opinions of treatments or a sort of drug, (5) the certainty of a diagnosis, etc (Denecke and Deng, 2015). However, sentiment analysis for medical information requires a domain-specific sentiment source and complementary context-dependent features to be able to correctly interpret the implicit sentiment. In this chapter, we describe the most important definitions and theoretical preliminaries for understanding the remainder of the thesis, including representation learning methods, sentic computing theory, transfer learning, and a list of the bio-medical concepts knowledge and their parameters. Indeed, this chapter lays the groundwork for the thesis and the motivation for approaching a concept-level understanding of patients' self-reports and explores further what type of settings make the use of medical terminologies and ontologies from biomedical literature efficient to derive category information and context information.

2.2 Sentiment Analysis

Sentiment analysis is the computational study of people's opinions, sentiments, affects, evaluations, attitudes, moods, and emotions. It aims mainly of capturing and extracting main interactions, relationships, contextual, and semantics of subjective information in given aspects, and therefore exploiting social contexts or common senses real-world knowledge.

2.2.1 Definition

In practice, sentiment is the underlying feeling, attitude, evaluation, or emotion associated with an opinion. Sentiment concerns four main cascaded constitutes: holder, target, aspect, entity, and polarity. Each component corresponds to specific tasks in a system.

Opinion : A view, attitude, or appraisal of an object, which can have a positive, negative or neutral orientation. An opinion can primarily considered as a quintuple (Kunić, 2019),

$$(e,a,s,h,t), \tag{2.1}$$

where e is the target entity, a is the target aspect of entity e on which the opinion has been expressed, s is the sentiment of the opinion on aspect a of entity e, h is the holder, and t is the time when the opinion is expressed.

Sentiment : positive or negative evaluation expressed through a language is called sentiment.

Aspect: denotes both feature and attribute.

Holder (entity) : denotes the entity that holds the sentiment.

Target : identifies the entity or a part or attribute of the entity selected as the aim of the sentiment.

Polarity or intensity: polarity is the property of sentiment. Polarity can be binary-folds (positive and negative), three-folds (positive, negative and neutral), or multi-labels (sad, happy, angry.etc.). Sentiment intensity might be seen as probability output showing the levels of strength or intensity, and each sub-interval from $[-1,1]$ assigned to a sentiment label.

2.2.2 Sentiment Analysis Levels

The corresponding growth of this field has resulted in the emergence of various subareas, each addressing a different level of analysis regarding various aspects and targets (entities, events, or persons) (Schouten and Frasincar, 2016). Sentiment Analysis can be performed at three main levels: at the document level, at the sentence level, and at aspect or entity level.

Sentiment at document level consists of measuring sentiment based on the whole content information. This level of analysis assumes that each document expresses opinions on a single entity.

Sentiment at sentence level, sometimes called topic-level, is one of the main direction in sentiment analysis area, which aim at recognizing the overall polarity of the sentence (e.g. positive, neutral, negative), according to semantic information learned from the textual content of the whole sentence.

Sentiment at aspect or entity level, also called feature-level, aspect-level is considered as a more finer-grained level of analysis. Instead of focusing on language items to extract expressed sentiment at documents, paragraphs, sentences, clauses or phrases, aspect level is mainly based on the idea that an opinion consists of a sentiment (a positive or a negative) and a target.

Target: identifies the entity selected as the aim of the sentiment.

Entity: can be a product, person, event, organization, or topic on which an opinion is expressed (opinion target). An entity can be considered as a taxonomy of components and sub-components where each component can have a set of attributes. In the biomedical domain, entities are assumed strictly to be defined by a set of components, for example, a disease has a set of symptoms, set of possible diagnoses, treatment, medication where the sub-components of medication may be case uses, side effects, drug interactions, etc., the attributes of which could be the state, quantity and the weight. Each component and attribute both constitute an aspect.

Aspect: defines the particular part or feature of the target that the sentiment is expressed towards. Extracting patient opinion towards various aspects of health services is closely related to aspect-based sentiment analysis. The sentimental aspect is a description of the expected overarching emotional response, this could be about the emotional effect of various components.

2.2.3 Aspect-Based Sentiment Analysis in the Field of Medical Information

Aspect-Based Sentiment Analysis (ABSA) is the practice of analyzing sentiments regarding a given aspect of a given entity, in which sentiments are analyzed, aggregated over time,

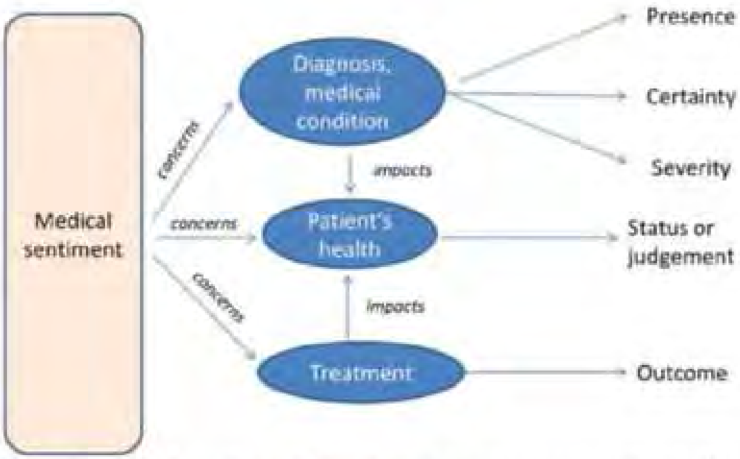

Fig. 2.1 The notion of medical sentiment. Sentiment can concern patient's health, a medical condition or treatment. For each aspect, sentiment can occur in different forms ((Denecke and Deng, 2015)).

and synthesized. The success of new SA approaches can be assessed by aspects potential in contributing to new theoretical approaches and in applications to real-world problems (Anand and Naorem, 2016; Sindhu et al., 2019; Sabeeh and Dewang, 2019).

Where medical sentiment concerns different diagnoses, medical conditions, treatments, medical events, drug interactions, and their side effects, many aspects are considered in the latest contributions. The supervised methods are more successful in getting accurate results for analyzing certain disease use cases and their aspects. Authors in (Salas-Zárate et al., 2017) present an aspect-level sentiment analysis method for diabetes based on ontologies in the diabetes domain. The semantic annotation was carried out through Stanford NLP with a domain ontology that describes **diabetic complications, drugs, laboratory physical examinations, diabetes**. The sentiment of the aspects is calculated by considering the words around the aspect which are obtained through N-gram methods. Among the main aspects included are **clinical presentation, physical manifestation, diagnosis, treatment, laboratory tests, and course of development**. The polarity of the closest words to the aspect identified is calculated by using SentiWordNet, after disambiguating the sense using Babelfy. Where Smith and Lee (2012) studied another aspect of sentiment in patient feedback from corpus from NHS Choices, namely **discourse functions such as expressive and persuasive**.

Recently, ABSA is getting much attention in infodemiology analysis such as COVID-19 use case. For instance, authors in (Jang et al., 2021)performed a local study on Twitter in North America. They particularly used ABSApp[1], a weakly supervised ABSA, to choose

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[1] https://arxiv.org/abs/1909.05608

and define aspects and they defined 545 aspect terms (eg, **"vaccines," "economy,"** and **"masks"**). The problem is that studies produced tools specifically for their research regarding specific diseases or medical conditions. A study was performed by (Jang et al., 2021) with the objective of understanding which tools would be available for sentiment analysis of Twitter health care research and determining which method would work best in the health care settings where they found none of the examined methods are extensively tested against a corpus of health care messages to check their accuracy. This study suggests that there is a need for an accurate and tested tool for sentiment analysis of tweets trained using a health care setting–specific corpus of manually annotated tweets first.

Issues and complex scenarios for AbSA have appeared regarding the very large number of medical concept citations within numerous medication-related reports that are affectively and semantically associated in different contexts. The conceptualization and development of multi-faceted sentiment analysis models to adequately capture observed opinion-sensitive information are imperative. The heart of the effective quantification of aspect-based sentiments relating to drugs, disease, and symptoms hardly involves a degree of medical concept comprehension. A **concept-level distillation** process for efficient sentiment analysis becomes apparent.

2.2.4 Main Properties of Concept-Level Sentiment Analysis in the Contexts of Medicine

A concept is a knowledge structure that offers sufficient and important cues about sentiments. For instance, the concept "grow movement" indicates anger and struggle (Shah et al., 2016). Feature learning approaches widely consider textual concepts (e.g., grow movement, grand mal) as textual metadata or a description of polar fact. We propose four properties of the feature learning approach specific to extracting concept-level sentiments conveyed towards bio-medical entities and aspects.

Property 1: ***Medical Concept is related to which aspects are extracted for automatically analyzing sentiment and its evolution.***

A concept is an abstract idea and may express specific semantics whereby conveys different affects. Extracting conceptual and affective information associated with natural language concepts is of critical importance. Due to the lack of resources that annotated the sentimental value conveyed towards medication-related concepts, few AbSA approaches consider medication-related concepts and their aspects such as disease or condition (Yu et al., 2020; Grissette and Nfaoui, 2019). Notably, they mostly neglect concepts and detect emotional valence only by scoring the text at the sentence level or word level by describing how words and phrases match the sentiment vocabulary.

Property 2: ***Concept affects is contextual.***

Each concept in the specified environment is given a score based on the way sentiment words relate to the concept and its associated score. Similar affects can be achieved through conceptually related meanings in a given context. Semantics are concepts that are most semantically related to the input concept, and affects are sentiment categorization values expressed by seeking constraints from conjunctions of the positive or negative semantics of aspects-based sentiment information.

Property 3: ***Natural language concepts distillation requires a specific setting to meet the massive requirement of online shared data.***

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 report treatment issues, drug misuse, new infectious disease symptoms. Few approaches have been proposed in this matter, namely multi-word medical concepts identification and drug-related descriptions that denoted vast connections for understanding patients' shared experiences. Therefore, this property assumes to explore the problem of mutual forms of drug interactions including beneficial drug effects. Most of them consisted of only detecting adverse drug reactions (ADR), but may fail to retrieve other aspects, e.g, the beneficial drug reaction or drug retroviral effects such as "relieve intraocular pressure associated with glaucoma". This mainly leverages and memorizes concepts' details and relationships to form a drug description that compactly with highly informed embeddings seeks multi-word related-drug descriptions from online generated narratives.

Property 4: ***The connectedness of concept types nuances are strongly emotionally correlated and must be determined for contributing to the sentiment decomposition approach***

Concept-based approaches, in fact, can analyze multi-word expressions that do not explicitly convey emotion but are related to concepts that do so. In the biomedical domain, concepts assume having a pervasive number of related concepts, components, relations, and subrelations. Concept Embedding is an ultimate solution to tackle important semantics and relationships defined in dependency space. Dependency vectors capture semantic and biomedical concept connections and then learn contexts properties and data object meta-data from large-scale biomedical semantic indexing maps and vocabularies such as PubMed. By considering the domain-depend relationship network, the embedding gain greatly improves the performance of the downstream computational prediction models and great ability to recognize the meaning of each concept,e.g, drug names, multi-word drug reaction expressions, disease symptoms, symptoms, and related-therapy terms.

2.3 Representation learning methods and bio-medical knowledge

2.3.1 Embedding Definition and Formulation

Word embedding approaches are traditionally used to map a discrete word to continuous vector representation, which tackles the semantic, linguistic relationships, and further encapsulate the contextual, ignoring the information present in the internal structure of words or any information available in domain-specific structured resources such as bio-medical ontologies. Although, such resources hold great potentials for enhancing the word representation relevancy and quality.

By considering a text corpus that is represented as a sequence S of words, $(w_1, w_2, ..., w_N)$. Distributed representations of words associate each word w_i with a dense feature vector h_{w_i}. Traditional word embedding techniques aim to learn a global word embedding matrix $E \in \Re^{V \times d}$, where V is the vocabulary size and d is the number of dimensions. Specifically, each row e_i of E corresponds to the global embedding of word type i in the vocabulary V. Given a window size t as the number of words on a single side, w_i is the target word and $(w_{(i-t)}, ..., w_{(i-1)}, w_{(i+1)}, ..., w_{(i+t)})$ is the context of word w_i. Contextual embeddings associate each word w_i with a representation that is a linear function of the entire input sequence S, i.e. $h_{w_i} = f(w_{(i-t)}, ..., w_{(i-1)}, w_{(i+1)}, ..., w_{(i+t)})$, where each input word w_j is usually mapped to its non-contextualized representation e_{w_j} first, before applying a linear function f. Several linear methods have been proposed :

Concatenation embeddings. With this method, context embedding involves concatenating the vector of the context words into a larger word vector:

$$h_{w_i} = (e(w_{(i-t)}), ..., e(w_{i-1}), e(w_{i-1}), ..., e(w_{i+t}) \tag{2.2}$$

Average embeddings. This method involves calculating the average of surrounding word embeddings. The sense of the contexts is expressed by averaging:

$$h_{w_i} = \sum_{\substack{j=i-t \\ j \neq i}}^{j=i+t} \frac{e(j)}{2t} \tag{2.3}$$

Weighted sum of embedding. This method sets a weight for each word, and the context embeddings are computed by weighted sum of the embeddings of the surrounding words. The common setting method is based on the distance from the target word:

$$h_{w_i} = \sum_{\substack{j=i-t \\ j \neq i}}^{j=i+t} e(j)\frac{t-|i-j|}{t} \tag{2.4}$$

These methods only have simple linear operations on neighbor words of the target word. In order to represent the entire sentential context as a whole.

Bio-medical Embedding. A different open set of biomedical word vectors/embeddings that combines subword information from unlabeled biomedical text such as abstracts with a widely-used biomedical controlled vocabulary, e.g, Medical Subject Headings (MeSH). Various biomedical sources and databases are used such as PubMed [2], the clinical notes from MIMIC-III Clinical Database, and unstructured electronic health record(EHR).etc. For example, BioWordVec Zhang et al. (2019a) and BioSentVec Chen et al. (2019) were trained to apply the word2vec method using text corpora from PubMed and the clinical notes from MIMIC-III Clinical Database (as summarized in Table 2.1). BioWordVec used a corpus of 10,876,004 English abstracts of biomedical articles from PubMed to estimate the relatedness of two words, and combine subword information from unlabeled biomedical text with a widely-used biomedical controlled vocabulary(the medical subject headings). The recent version of BioWordVec provides FastText word embeddings trained using PubMed and MeSH vocabulary. es in PubMed and clinical notes in the MIMIC III Clinical database to prove the effectiveness of

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[2] https://pubmed.ncbi.nlm.nih.gov/ is a free search engine that primarily accesses the MEDLINE[3] database of references and abstracts on life sciences and biomedical topics that comprises more than 29 million citations for biomedical literature, journal of life sciences and books online.

features of discriminating expressions by employing pair similarity tasks on different genres of biomedical texts. Table 4.2 presents statistics of biomedical embeddings, which have been thoroughly evaluated in a range of applications in this thesis.

Distributed representation has improved the learning recall of many related-pattern discovering tasks, which is capable to leverage data definitions in low-dimensional representative vectors (Weston et al., 2013; Khattak et al., 2019). But, they fail to deal with structural ambiguities and define unobserved related-medication concepts from tremendous unrelated patient experiences that need other predefined knowledge.

2.3.2 Embedding benchmarks

Publicly available pre-trained embeddings such as Glove are low dimensional, learned continuous vectors, visualize varied concept-relation associations. Most of them may not be the best fit to capture medical semantics of unsupervised feature-based approaches (Caliskan et al., 2017), where can not define word-vector for a word that does not occur in the training data. Such restrictions are because these embeddings were trained on general-scope data such as Wikipedia, google news.

Another critical challenge is the unidirectional training; transformers overcome some of these existing limitations of commons embedding methods, especially for representing categorical variables. Contextual embeddings, such as ELMo (Peters et al., 2018) and BERT (Devlin et al., 2019), move beyond global word representations like Word2Vec and have achieved impressive results.

Contextual embeddings assign each word a representation based on its context, thereby capturing uses of words across varied contexts and encoding knowledge that transfers across languages. BERT becomes the state-of-the-art of language representation model, which stands for Bidirectional Encoder Representations from Transformers. Unlike recent language representation models, BERT is designed to pre-train deep bidirectional representations from unlabeled text. Thus, the differences in pretraining model architecture, BERT is a profoundly bidirectional transformer.

Language models have many advantages over structured knowledge bases. Considering language models (LMs) as based knowledge bases, pre-trained LMs already capture commonsense knowledge such as BERT and ELMo, BERT contains relational knowledge competitive with traditional NLP methods that have access to oracle knowledge (Petroni et al., 2019). BERT as an unsupervised open-domain language model has a strong ability to learn and recall factual knowledge and prove itself in many fine-tuning tasks. It performs well, but all models perform poorly on many-to-many relations using varied knowledge bases such

Table 2.1 Statistics of biomedical corpora and Medical ontologies used for pre-trained biomedical embeddings training

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
PubMed Central	2,083,180	41,674,775	539,006,967

as ConceptNet [4] and Wikidata [5]. Others proved that BERT with ConceptNet knowledge base, data from Wikipedia, Performed worse than supervised methods on ConceptNet but is more likely to generalize to different domains. Supervised methods for commonsense knowledge under-perform when evaluated on novel data (Feldman et al., 2020). LMs mostly pick up lexical cues, where no model solves commonsense reasoning to date. In a recent study, we used BERT pretrained model, which becomes surprisingly good at representing natural concepts, facts and their attributes. Primarily, extended versions on social networks have known good ability to capture entities mentions (Poerner et al., 2019) and their related meanings.

Table 2.2 A summary of pre-trained embeddings for biomedical words and phrases using medical databases such as PubMed (abstracts,concepts...etc.) and MIMIC-III clinical notes

Biomedical Word Embedding	**Embedding**	**Parameter settings**	**Text Copora**
BioWordVec[6] Zhang et al. (2019a)	FastText	200-dimensional word embeddings, where BioWordVec vector 13GB in Word2Vec bin format and BioWordVec model 26GB.	PubMed and clinical note from MIMIC-III clinical Database
BioSentVec[7] Chen et al. (2019)	Sent2Vec	700-dimensional sentence embeddings. We used the bigram model and set window size to be 20 and negative examples 10.	PubMed
BioASQ3[8] Kosmopoulos et al. (2015)	Word2Vec	1,701,632 distinct word vectors and biomedical types	10,876,004 English abstracts of biomedical articles from PubMed.
BioConceptVec[9] Chen et al. (2020)	CBOW skip-gram glove fastText	It covers genes, mutations, chemicals, diseases and cellines. The trained embeddings contain over 400,000 concepts.	The entire PubMed biomedical concepts. PubTator to annotate biomedical concepts in the PubMed.

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[4] https://conceptnet.io/

[5] https://www.wikidata.org/wiki/Wikidata:Main_Page

2.4 Benchmarks for Drug-related Knowledge

According to (Denecke and Deng, 2015), sentiment analysis from medical documents requires a domain-specific sentiment source and complementary context-dependent features to be able to correctly interpret the implicit sentiment. Most of the state-of-the-art models rely on the use of medical terminologies and ontologies from biomedical literature to derive category information and context information. Here, we draw upon the most known benchmarking datasets used for both evaluation and training systems.

1. ***NCBI Disease Corpus :*** A resource for disease name recognition and concept normalization; a collection of 793 PubMed abstracts fully annotated at the mention and concept level. Each PubMed abstract was manually annotated by two annotators with disease mentions and their corresponding concepts in medical subject headings or Online Mendelian Inheritance in Man (OMIM). The public release of the NCBI disease corpus contains 6,892 disease mentions, which are mapped to 790 unique disease concepts. Of these, 88% link to a MeSH identifier, while the rest contain an OMIM identifier.

2. ***A corpus*** [10] ***for mining drug-related knowledge from Twitter chatter (Sarker and Gonzalez, 2017).*** The data set we are releasing consists of 267,215 Twitter posts made during the four months—November 2014 to February 2015. The posts mention over 250 drug-related keywords. The language models encapsulate the semantic and sequential properties of the texts.

3. ***PsyTAR (Zolnoori et al., 2019).*** This dataset contains 891 patients' drug-reviews. 4813 ADRs mentions were detected, 590 WDs mentions, 1219 SSIs mentions, and 755 DIs mentions. All identified entities mapped to his corresponding UMLS Metathesaurus concepts(916) and SNOMED CT concepts(755).

4. ***DrugBank database (Wishart et al., 2018).*** The DrugBank database is a comprehensive, freely accessible, online database containing information on drugs and drug targets. DrugBank contains 13,466 drug entries including 2,622 approved small molecule drugs, 1,351 approved biologic that combines detailed drug data with comprehensive drug target information. Because of its broad scope, comprehensive referencing and unusually detailed data descriptions, DrugBank is more akin to a drug encyclopedia than a drug database.

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[10] http://diego.asu.edu/Publications/Drugchatter.html

5. ***SMM4H corpus* *(Sarker et al., 2018b)*.** This dataset consists of 10 260 annotated tweets, and the normalization of ADR expressions consisted of 6650 ADR phrases and identifiers. Systems were evaluated using 9961, 7513, and 2500 instances for the 3 subtasks, respectively.

6. ***ADR Corpus (ADRMINE)* *(Nikfarjam et al., 2015b)*.** Drug-related corpus from social media, it is considered mainly for mining Adverse Drug Reaction Mentions using Sequence Labeling with CRF and word embedding Cluster features. it has known for extracting mentions of adverse drug reactions (ADRs) from a highly informal text in social media, and for modeling words' semantic similarities.

7. **MSH WSD Corpus**[11] **Jimeno-Yepes et al. (2011) :** The MSH WSD data set contains 203 ambiguous words. Each instance containing the ambiguous word has been assigned a UMLS Concept Unique Identifier (CUI) linked to the MeSH heading. The corpus consists of 203 ambiguous entities. Each ambiguous term/abbreviation contains a maximum of 100 instances per sense obtained from MEDLINE.

8. **ADAM**[12] **Zhou et al. (2006) :** Database of abbreviations in MEDLINE. This vocabulary covers frequently used abbreviations and their definitions (or long-forms), including both acronyms and non-acronym abbreviations. ADAM includes 59,405 distinct abbreviation/long-form pairs. Each record has a preferred abbreviation, variants of the abbreviation, long-form and variants, score, and frequency of instances.

9. **RxNorm**[13] **Nelson et al. (2011) :** RxNorm is an ensemble of UMLS Metathesaurus of source vocabularies. Many relationships (primarily synonymous), concept attributes, and some concept names are derived from the names provided by the source vocabularies. RxNorm provides the following attributes: concepts, concept names and their vocabulary sources, attributes, relationships, and other data about RxNorm. RxNorm is organized by concept or meaning, which are semantically associated and assigned at least one semantic type from the Semantic Network. Because of the huge source diversity of RxNorm, they provide an additional attribute as atom string for items that look similar but have different meanings in order to save the correct meaning for a given string from a particular source.

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[11] https://wsd.nlm.nih.gov/collaboration.shtml

[12] http://arrowsmith.psych.uic.edu/arrowsmith_uic/adam.html

[13] https://uts.nlm.nih.gov/license.html

2.5 Sentic Computing

2.5.1 Sentic Computing theory

Sentic computing is a pioneering multi-disciplinary approach to natural language understanding and processing at the crossroads between affective computing, information extraction, and common-sense reasoning, and exploits both computer and human sciences to better interpret and process social information on the Web Cambria and Hussain (2015). Cognitive and affective modeling, understanding social network dynamics and social influence mainly rely on identifying semantics enabled by the adoption of the bag-of-concepts model instead of simply counting word co-occurrence frequencies in text. Working at the concept level entails preserving the meaning carried by multi-word expressions.

Sentic computing is implemented via several feature-based sentiment analysis APIs and concept-level knowledge bases such as SenticNet, where the affective commonsense knowledge associated with natural language opinions has to be objectively assessed. Indeed, It implemented by allowing sentiments to flow from concept to concept based on the dependency relation between clauses. Recently, contextual polarity is assigned to concepts with regard to aspect information and emotions patterns via neural networks methods; sentic computing leverages sub-symbolic methods such as deep neural networks and multiple kernels learning to infer syntactic patterns from data and symbolic models such as semantic

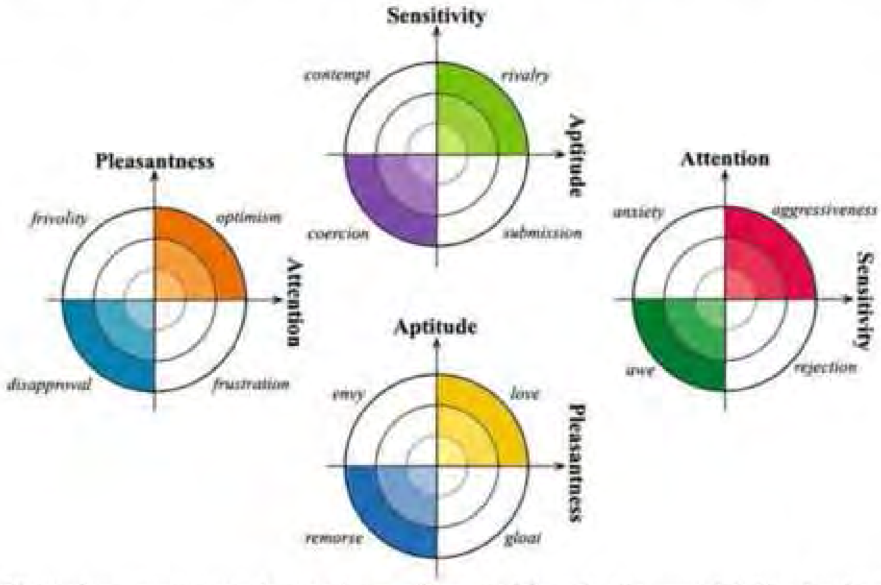

Fig. 2.2 Hourglass compound emotions of second level. By combining basic emotions pairwise, it is possible to obtain complex emotions resulting from the activation of two affective dimensions(Cambria and Hussain (2015))

networks and conceptual dependency representations to encode meaning, which is performed by means of sentic patterns and semantics.

Semantics are associated conceptual features, sentics are defined through sentic patterns or dimensions such as Pleasantness, Attention, sensitivity, aptitude, and the Polarity is float number between -1 and +1 (intensity), which is calculated in terms of the sentics and specifies the input concept positivity or negativity. Sentics can be converted to emotion labels, e.g., "joy", "eagerness" and are provided by the variable moodtags, by using the Hourglass model. Inferring sentic vector is mainly based on mining and exploiting the Hourglass model of emotions[14], in particular, to measure affective information regarding main affective components (dimensions) such as:

1. ***Pleasantness***: How much the user is amused by interaction modalities
2. ***Attention*** : How much the user is interested in interaction contents
3. ***Aptitude*** : How much the user is comfortable with interaction dynamics
4. ***Sensitivity***: How much the user is confident in interaction benefits

Each affective dimension is characterized by six levels of activation (measuring the strength of an emotion), termed *"sentic levels"*, which represent the intensity thresholds of the expressed or perceived emotion. For example, the Attention's levels are : *Vigilance*, *Anticipation*, *Interest*, *Distraction*, *Surprise*, *Amazement*. These twenty-four levels are correlated or characterized by a set of compounds, e.g., from the activation of two affective dimensions such as Attention and Sensitivity, we can obtain complex emotions or affects(As 2.2 described), and finally, sentic vector is float vector that can potentially synthesize the full range of emotional experiences in terms these dimensions and their levels and is computed utilizing the following formula:

$$p=\sum_{i=1}^{N}\frac{|Pleasantness(c_i)|+|Attention(c_i)|+|Sensitivity(c_i)|+|Aptitude(c_i)|}{3N} \tag{2.5}$$

where c_i is an input concept, N the total number of concepts, and 3 is the normalization factor (as the Hourglass dimensions are defined as a float between -1 and +1).

2.5.2 A Patient-Reported Outcome Measures

Patient-reported outcome measures are useful to evaluate patients' health status and their experiences by documenting the impact of a disease on functional performance as well as

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[14] a biologically-inspired and psychologically motivated model for the representation and the analysis of human emotions.

the effectiveness of medical and rehabilitation interventions. Sentic Computing is mainly used for improving patient-reported outcome measures (PROMs) for health-related quality of life (HRQoL), which is to record the level of each patient's physical and mental symptoms, limitations, and dependency. It bridges the gap between structured data (patient records, questionnaire) and unstructured data (natural language from social network), which though different at structure level are similar at the concept level. Sentic PROMs is one of the good examples provided in this and exploits the ensemble application of standard PROMs and sentic computing to allow patients to evaluate their health status and experience in a semi-structured way, i.e., both through a fixed questionnaire and through free text.

Nowadays, online social networks have emerged as a new platform that provides an arena for people to share their views and perspectives on different issues and subjects with their friends, family, relatives, etc. Because of the emergence of deep learning techniques, the use of Twitter data has become valuable and popular in analyzing sentimental attitudes and measuring patient-reported outcomes in recent years.

2.6 Deep Associative memory for Unsupervised Learning

The success of learning algorithms generally depends on data representation (Bengio et al., 2013). However, adopting an existing lexicon for sentiment analysis in the context of medicine provides inadequate classification precision, which uses less useful feature sets and therefore lacks discriminatory potential (Nikfarjam et al., 2015b). In addition, the frequent use of informal medical language, non-standard format, poor spelling and abbreviation forms, as well as typos in social media posts prevent understanding patient intents and experiences on social networks. There has been limited progress in addressing these challenges, and so far advanced machine learning-based entity recognition and NLP techniques have been underutilized, especially for the huge textual challenges of medication-related texts. Unsupervised methods have received less attention and there is less work on automatic labeling of medical components and sentiment for given aspects. It is widely believed that end-to-end training with the backpropagation algorithm helps to solve most of these challenges, and plays the main role to retrieve informative feature detectors, with reference to (Krotov and Hopfield, 2019). These detectors are useful for the task performed by the upper layers of that neural network. Additional unsupervised parameters are achieved by calculating hidden units or by convolving complementary neural components by following particular learning rules. To conclude, the generalized version of the well-known Hopfield model and its extensions are considered good example that inhibit the early feature detector in a completely unsupervised manner.

The deep associative memory is one of the most successful approaches which greatly increases the modelling and abstraction capabilities of networks, although training a deep network is much more difficult (Demircigil et al., 2017). In this thesis, we aim at investigating deep associative neural networks based on learning unsupervised representations, which is primarily devoted to learning features from large-scale unstructured data in conjunction with pre-trained biomedical embeddings. This family corresponds to the modeling associative memory for pattern recognition by taking advantage of the greatest computational properties of deep learning. Refers to (Liu et al., 2019), we could categorize them into two main subset algorithms: (1) Probability-based associative memory. (2) Neural associative memory. Probability-based associative memory consists of a multilayer array of processing elements (PEs)(Palm, 2013), where neural associative memory stores patterns in-memory storage matrix (Krotov and Hopfield, 2016).

We argue that, while associative learning models often assume an arbitrary connectionist architecture to define relationships, deep networks learn representations of local patterns that may be less efficient at defining a pattern of unobserved entities. Recent distributions have followed this line and have implemented acceptable solutions by improving learning ability using hierarchical representations of learning (Liu et al., 2019), convolutional and ultimately more precise predictive learning models (Krotov and Hopfield, 2019; Demircigil et al., 2017), although there is an on-going debate on the explanatory power of associative learning theory. For this we were inspired by the process of learning (Liu et al., 2019) and learning from errors (Palm, 2013), and we proved the role of deep associative learning in the definition of definitions of biomedical concepts. The main point of the controversy, however, does not call into question the experimental evidence, of which there is abundance, but whether this evidence is proven by recent models within the framework of the traditional theory of associative learning.

2.7 Transfer Learning

One of the most powerful ideas in deep learning is that sometimes you can take the knowledge that the neural network has learned from one task and apply it to a separate task. This process is called transfer learning. Transfer learning makes sense when you have a large amount of data for the problem you are transferring from and usually relatively less data for the problem you are transferring to. Transfer learning is widespread in deep learning, given the enormous resources required to train deep learning models or the vast and challenging datasets on which deep learning models are trained. Transfer learning can be categorized under one of three subcategories: inductive transfer learning, transductive transfer learning, and unsupervised transfer learning. Each subcategory is based on different situations between the source and target domains and tasks (Weiss et al., 2016). Many contributions have been made in this scope. Instance transfer approaches aim to reweight some labeled data in the source domain for use in the target domain (Dai et al., 2007; Adams, 2009; Jiang and Zhai, 2007). Feature representation transfer approaches have been used to find a good and reliable feature representation that reduces the difference between the source and the target domains and the error of classification and regression models (Ando and Zhang, 2005; Blitzer et al., 2006). Relational knowledge transfer builds a map of the relational knowledge between the source domain and the target domains (Davis and Domingos, 2009; Mihalkova et al., 2007), with both areas being relational domains and the independent and identically distributed (i.i.d.) assumption being relaxed in each field.

In the past few years, deep learning has seen incredible progress and has largely removed the requirement of strong domain knowledge. However, existing approaches in natural language processing still require task-specific modifications and training from scratch (Howard and Ruder, 2018). Knowledge transfer with deep neural networks offers vast improvements to many challenging tasks, e.g., language understanding, word embedding, and sentiment classification. Sentiment classification has seen full applications because of its transfer learning capability to transfer knowledge or lexicons from one domain to other domains. It has played a vital role in improving various meta-word dictionaries by expanding pretrained word embedding vectors such as Word2Vec and GloVe. In our study, we apply a semisupervised feature representation transfer approach to the inductive transfer learning mechanism, whereby we aim to find distributional feature representations under medical settings that minimize domain divergence and classification model error. Technically, the source and target domains are different, but they are dedicated to the same task. Indeed, no labeled sentiment dictionaries in the medical context data are available; thus, we adopted a massive amount of labeled data in a general context. To this end, the source domain is represented under the following settings:

$\mathscr{D} = \{\ \mathscr{F}_S, P(\mathscr{F}_S)\ \}$; where $\mathscr{F}_S : \mathscr{F}eature\ Space$ and $P(\mathscr{F}_S)$: distribution over the feature space.

Transductive transfer learning must satisfy the following criteria:

$Rule(i)$: the feature spaces between the source and target domains are different, $\mathscr{F}_S \neq \mathscr{F}_T$

$Rule(ii)$: The marginal probability distributions of the input data are different, $P(\mathscr{X}_S) \neq P(\mathscr{X}_T)$

$Rule(iii)$: The label prediction tasks between two tasks are different, $\mathscr{Y}_S \neq \mathscr{Y}_T$

$Rule(iv)$: Data imbalance exists with regard to the positive and negative classes for the source and target domains, $P(\mathscr{Y}_S|\mathscr{X}_S) \neq P(\mathscr{Y}_T|\mathscr{X}_T)$

$\mathscr{Y}$ is the label space, and $P(\mathscr{Y}|\mathscr{X})$ is the conditional probability distribution over the feature space.

This setting concerns domain adaptation for knowledge transfer in medication-related processing and sample selection bias or covariate shift, which we want to imitate positive/negative polar facts in given social assumptions. Many low-level features learned from enlarged datasets might help our learning to better understand meta-words and make sense of medication-related semantics and affective levels from well-understood patterns and to recalculate new multi-word expression semantics and contextual patterns.

2.8 Evaluation Metrics

In order to evaluate our methods proposed in this thesis, the evaluation was performed on two levels: (1) automatic biomedical annotation and (2) sentiment classifiers, using the metrics below.

Classification Metrics

Precision - The number of definitional sentences correctly labeled by our model divided by the number of sentences marked by our model as definitional.

Recall - The number of definitional sentences correctly labeled by our model divided by the number of definitional sentences.

F1-measure - $2PR/P+R$, where (P) is the precision, and (R) the recall.

Medical Annotation Evaluation

We conduct a sentence-level medical annotation evaluation for clinical sentence pair similarity tasks. MedSTS[15] and BIOSSES[16] are two benchmark datasets and resources for determining clinical semantic textual similarity and are widely used for medical annotation evaluation tasks. Table 4.5 highlights the statistics of these datasets. Alternatively, a method that is widely used for evaluating multiword concept normalization, such as drug reactions,

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[15] https://github.com/ncbi-nlp/BLUE_Benchmark

[16] https://tabilab.cmpe.boun.edu.tr/BIOSSES/DataSet.html

is to compare the number of correctly normalized drug reactions against the ground-truth value. We adopt this method to evaluate our drug reaction normalizer, defined as follows:

$$Accuracy = \frac{N_{correct}}{N_{T_k}} \tag{2.6}$$

where $N_{correct}$ is the number of correctly normalized drug reactions and N_{T_k} is the length of drug annotations that are true samples.

2.9 Conclusion

Medical sentiment concerns a patient's health status, the effect of medical event, a medical condition, medical procedure and diagnosis or treatment. Conceptual embeddings and biomedical language models produce meaningful concept representations that show that the contextualized language models (e.g. BioBERT, BioELMo) possess tremendous representational power and are able to achieve impressive accuracy gains. However, these models are still unable to learn high-quality representations for concepts with low context information (i.e. rare words). Infusing the complementary information from knowledge bases is likely to be helpful when the corpus-specific information is insufficient to learn robust representations. Moreover, as the biomedical domain contains numerous knowledge bases, it is imperative to develop approaches that can integrate the knowledge bases in a continual fashion. In the next chapters, we will investigate which manners and settings are the best at creating a knowledge combination from biomedical literature that enhance performance of feature learning.

Chapter 3

Literature review

> *"If you want to have good ideas, you must have many ideas."*
>
> —Linus Pauling

3.1 Introduction

This chapter offers an updated literature review of sentiment analysis research and focuses the main key challenges involved in sentiment analysis in the biomedical domain. In particular, the chapter proposes insights on the evolution of sentiment analysis research in the field of medical information whereby seeking the importance of extracting aspects in the context of medicine and bio-medical entities for enhancing models performance. Subsequently, a comprehensive introductory review explains transfer learning theory adaptation for transferable characteristics of semantic models applied to biomedical sentiment annotation, together with a discussion on how the deep associative learning for unsupervised representations recognition can enhance the understanding of patient language. The chapter ends with an introduction of biomedical distributed representation as an imperative step for concept-level sentiment analysis and the explanation of its key shifts, which highly differentiate it from standard embedding algorithms.

3.2 Biomedical Sentiment Analysis

3.2.1 Affective Computing & Sentiment Analysis

The basic tasks of affective computing and sentiment analysis are emotion recognition and polarity detection (Satapathy et al., 2017). These two tasks are highly interrelated. Indeed, (Han et al., 2019) stated that " both the terms of affective computing and sentiment analysis relate to the computational interpretation and generation of human emotion or affect. Whereas the former mainly relates to instantaneous emotional expressions and is more commonly associated with speech or image/video processing, the later mainly relates to longer-term opinions or attitudes and is more commonly associated with natural language processing.".

Bio-medical Sentiment Analysis

Sentiment Analysis (SA) has witnessed huge contributions in recent years. Healthcare organizations and pharmaceutical companies have already used this potential of SA techniques applied to narratives and stories generated on social media in many tasks: capturing adverse drug reactions, detecting product problems, categorizing patients' status, and therefore building interpretable sentiment analysis models for personalization of various patient statements, etc. Technically, SA is the task that aims to automatically quantifying the sentiment expressed towards a giving entity, usually by given predefined sentiment assumptions. Exploring the methods used for sentiment analysis in healthcare research may help us better understand the options available for future research in this growing field.

Social networks are increasingly popular as a platform for sharing personal health information (Nikfarjam et al., 2015b). This information can be used for public health surveillance tasks, in particular for extracting and tracking drug-related data, such as drug efficacy or drug abuse incidents. Patients narratives on social media can reveal critical public health issues (Giustini et al., 2018). In particular, sentiment is a commonly used metric to investigate the positive or negative reports contained in these messages. For example, authors in (Hu et al., 2018) analyzed a tweet of risky behavior related to drug abuse as a positive tweet, or a tweet of safe behavior as a negative tweet. A rich variety of techniques have been proposed in this context ranging from dictionary-based methods using annotated knowledge, supervised machine learning methods to fully unsupervised methods, in conjunction with statistical methods such as affinity analysis and cluster occurrences of words, thereby inducing word sentiment intensities. Among these, supervised learning approaches have been the most successful algorithms to date.

In the bio-medical contexts, the lack of meaning of words, the inability to properly match the medical context and the clarification of medical entities are the most crucial challenges in bio-medical SA. Deep learning techniques for sentiment analysis have become very popular, in particular, they provide automatic feature extraction and both richer representation capabilities and better performance than traditional feature-based techniques (Araque et al., 2017). In particular, they are widely used to build distributed vocabulary and to overcome the limitations of manually labeled lexicons. Nevertheless, most of existing deep learning-based SA approaches largely focus on grammar directions such as semantic direction or focus only on extracting sentiment words. They have widely adopted pre-trained incorporations to exploit semantics as much as possible and contextual information, especially pre-trained contextualized word vector representations have been widely used to create contextual and semantic vocabularies (Bengio et al., 2013), and therefore used to induce sentiment-related information by deploying these representations and their attributes. Two main approaches involved in this case, (i) Supervised methods applying an induction update based on lexicons. For example, count positive and negative term scores to determine sentiment direction, and improvement is presented by creating a data set of relevant features using predefined sources such as SentiWordNet (Baccianella et al., 2010). Unsupervised methods, in particular neural network based approaches exploit unstructured data to generate and retrieve hidden sentiment information by identifying the constraints of conjunctions on the positive or negative semantic orientations (Mohamad Beigi and Moattar, 2021; Wang et al., 2021). The latter have also been used to expand the size of sentiment lexicons and learn from new raw data, which further succeeded in the accuracy of many tasks of disambiguating the meaning of words, analyzing sentiment, and find out new knowledge.

Aspect-based Sentiment Analysis

An important part of research effort focuses on Aspect-based SA. It provides more detailed information than general SA (Nazir et al., 2020), which allows to formulate interactions, contextual dependencies, semantics, and relationships of different data objects, e.g., aspect, event, person, target.etc. Refers to (Schouten and Frasincar, 2016), three processing steps can be distinguished when performing AbSA: identification, classification, and aggregation. In bio-medical domain, supervised AbSA methods are the most accurate approaches (Satapathy et al., 2017), especially lexicon-based approaches, but many unseen entities still appeared regarding the social networks dynamicity. Although their effectiveness in selecting relevant and original features, they still remain not well-adapted to unlabeled examples. Owing to the limited availability of lexicons that specifically offer medical contextual definitions and sentimental correlations between varied medical concepts, they fail to address affective aspects regarding biomedical contexts. Unsupervised AbSA methods are also used to discover medical patterns from real-time examples. The problem is that these methods might result in redundant and irrelevant features leading to a serious loss of biomedical data (Li et al., 2019a). Aspect Extraction (AE) is the most challenging task for biomedical analysis. Numerous contributions only consider explicit aspects such as drugs or disease where implicit aspects have been neglected. For example, (Jiménez-Zafra et al., 2019) used two aspects: drugs and doctors over two different corpora extracted from the social web. Authors in (Rodrigues et al., 2014), focused on detecting the mood of patients with cancer by analyzing their messages in online communities.

Despite multiple attempts, existing unsupervised approaches generally suffer from suboptimal entity recognition methods due to the frequent use of informal medical language, non-standard format, poor spelling and biomedical abbreviation forms, as well as typos in social media. Two main research questions have been involved: (i) how to perform the process of AE effectively regarding these unique characteristics of social networks towards specific biomedical targets ? and (ii) how to map relationships between different data objects for improved biomedical aspect-based sentiment analysis ?

The extraction of explicit/implicit aspects, medical entities, aspect categories of multi-word medical concepts may require involvement of external controlled medical knowledge and vocabularies. Refers to many studies (Garcia-Pelaez et al., 2019; Patel et al., 2015; Kwon et al., 2018), this knowledge-based integration ensures and enhances the credibility and transparency of analysis conveyed toward these medical concepts patterns. Since it relies on sufficiently large biomedical training corpora to define the appropriate medical definitions, a deeper understanding of transfer learning and semisupervised learning becomes apparent.

Semisupervised learning is a fundamental solution that allows learning from heterogeneous unlabeled examples spread via social network in combination with typically sets of labeled data. In this sense, several studies used semisupervised techniques to primarily develop automated corpora (Zhang et al., 2018) by utilizing word representation capabilities in two ways: (1) generating context-depend embeddings (2) transferring knowledge from pretrained embeddings or fusing weighted distributed features (Canales et al., 2020; Usama et al., 2019; Gupta et al., 2018). The ultimate problem is that these corpora result in low medical entities recognition recall due to the failure of recognizing drug-related components and their aspects such as drug reactions, indications,etc.

Extracting drug-related explicit aspects may be failed due to the existence of adverse drug reaction (ADR) multi-word expressions, leading to a higher accumulation of false positives and negatives. Few studies have been carried out to consider side effects in raw text, i.e., annotation of ADR lexicons and corpora. Table 4.1 shows a list of baselines models used for drug reactions lexicons with relevant details. The problems with these lexicons are as follows: (1) They are annotated for local context and target. For example, (Dietrich et al., 2020) considered an adverse drug events benchmark reference dataset consisting of 5,645,336 English-language articles, but it regarded to specific targets that mentioned at least one of six medicinal products of interest such as insulin glargine, levetiracetam, methylphenidate, sorafenib, terbinafine, and zolpidem. (2) The major limits are concerned with the data. Twitter data are unbalanced regarding time, where there is no relationship with other drug-related concepts, such as indications from formal medical language. Word embedding features created from a large non-domain-specific Twitter dataset have been proposed as a solution that may disambiguate medical-sense directions. (3) Another significant problem is how efficiently retrieve formal formats of drug reaction (combinations of words) from imbalanced and unstructured text. This explains why sentiment analysis systems are able to perform reasonably well towards given entities and events but far poorly on clarifying sentiment towards biomedical subjects. To overcome these limitations, a medical normalization step (Chen et al., 2020; Tutubalina et al., 2018; Wei et al., 2013) is carried out by our system for efficient meaning disambiguation as a whole, then extract and define medical entities and aspects.

3.2.2 Biomedical Sentiment Analysis on Social Networks

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.

Patient-reported outcome measures are useful to evaluate patients health status and their experiences by documenting the impact of a disease on functional performance as well as the effectiveness of medical and rehabilitation interventions (Bradet-Levesque et al., 2021; Pérez-Alfonso and Sánchez-Martínez, 2021; Hansen et al., 2021; Sultan et al., 2021; Cambria et al., 2012). Nowadays, online social networks have emerged as a new platform that provides an arena for people to share their views and perspectives on different issues and subjects with their friends, family, relatives, etc (Sailunaz and Alhajj, 2019). Because of the emergence of deep learning techniques, the use of Twitter data has become valuable and popular in analyzing the sentimental attitudes and measuring patient-reported outcomes in recent years. Traditional approaches, including dictionary-based and machine learning tools, are less efficient in terms of learning for biomedical sentiment analysis on Twitter. Supervised algorithms are commonly used including naive Bayes, K-Nearest Neighbors (KNN), logistic regression, Support Vector Machine (SVM), and Artificial Neural Networks (ANNs). For example, (Ruz et al., 2020) used Bayesian network classifier to perform Twitter Sentiment Analysis (TSA) on critical events such as natural disasters or social movements. The latter used the Bayes factor measure that improved the classification performance better than SVM and random forests, given a sufficient number of training examples. The most significant challenge for the machine learning approaches is feature selection, which is often domain dependent. They often result in a highly sparse input matrix and produce low accuracy measures in biomedical sub-tasks. To reduce sparsity, authors in (Ghiassi and Lee, 2018) provided a novel supervised learning technique that identifies a lexicon set unique to the TSA. This identification process generates a collection of vectorized tweets for input to machine learning tools, which is further reduced into a small set of seven meta-features, but they lose word orders and long-term dependencies.

Deep learning methods have increased the accuracy of several sentiment analysis tasks, which offer a rich representation that allows identifying the relations among words, offering interesting qualitative information to historically, semantically, and contextually consider the main features. While these methods have been considered as state-of-the-art solutions, there still remain several challenges and limitations confronting their use on medication-related text analysis. Various contributions rely on combining techniques and fusing datasets to conquer most of these limitations and boost models performance (Dietrich et al., 2020; Hutto and Gilbert, 2014; Pasupa and Seneewong Na Ayutthaya, 2019; Ghiassi and Lee, 2018).

Moreover, Twitter data exhibit depend-platform properties or features, and many additional features have been considered in the literature. Prior studies propose to develop hybrid features regarding Twitter data particularities, which proves its subjectivity and effectiveness for polarity detection with regard to linguistic features such as stylistic part-of-speech (Bravo-Marquez et al., 2014). (Crannell et al., 2016) presented a pattern-matched Twitter analysis of US cancer-patient sentiments that mainly characterizes the content of tweets authored by patients with cancer in the United States. Indeed, they utilize patient tweets to compute the average happiness of patients with cancer for each cancer diagnosis. A large sample of English tweets was used and the tweets were filtered by the cancer diagnosis. The patients' Twitter identification numbers were used to gather all the tweets for each patient where happiness values for the patients' tweets were calculated using a quantitative hedonometric analysis. Others proposed other salients such as (Hassan et al., 2020) that used the citation count as the dependent variable (number of unique Twitter users), with 6,482,260 dependent tweets linked to 1,083,535 publications, which was considered an indicator of the regression model. It improved the adjusted R-squared value of regression analysis in several disciplines.

3.2.3 Sentic Computing and Biomedical Sentiment Annotation

There are currently numerous English-language sentiment knowledge bases and state-of-practice benchmarks such as SenticNet (Cambria et al., 2020) and SentiWordNet (Baccianella et al., 2010), ANEW (Nielsen, 2011), and VADER (Hutto and Gilbert, 2014),etc. Few medical sentiment-annotated lexicons are trained on medication-related examples with regard to crossdomain and cross-lingual measures, such as unprecedented shifts in patient attitudes (Zhong et al., 2020). In particular, biomedical sentiment analysis requires particular attention to be paid to the sentiment annotation scale regarding biomedical natural entities and aspects (Han et al., 2020). Indeed, limited labeled training data fails to cover the entire input space.

Automatic sentiment lexicon annotation techniques involve other substantial requirements such as aspect extraction and medical entity normalization, especially, to bridge the gap between patients' language and formal medical language. The multidimensional way of mining their feelings and their sufferings concerning treatments and symptoms is of critical importance. This task is extremely difficult, as it involves a deep understanding of most of the explicit and implicit meanings. It mainly relies on parts of the text and context in which sentiment aspects are explicitly expressed, such as polar terms, emotion words, and co-occurrence frequencies. Indeed, patient opinions are not just reviews of a product/service but more like small donations of experience (Cambria et al., 2012, 2010). In addition, the implicit meanings are important. Referring to many studies (Zuo et al., 2020), opinions and sentiments are often conveyed implicitly through latent semantics, which makes purely syntactical approaches ineffective, especially when aiming to find new exciting outcomes hidden in the unstructured narratives on social networks. Sentic computing is one of the most crucial techniques used for this purpose (Cambria and Hussain, 2015; Satapathy et al., 2017) and has been exploiting in many patient-centred applications (Ji et al., 2021; Zucco et al., 2018; Ofek et al., 2013; Jelodar et al., 2020; Sanglerdsinlapachai et al., 2021; Singh and Singh, 2021), which exploits semantics and their sentics based on the relation dependency, and linguistics properties to annotate automatically concept-level sentiment of an input phrase. Where semantics are concepts that are most semantically-related to the input concept, and sentics are emotion categorization values expressed in terms of varied affective dimensions such as pleasantness, attention, sensitivity, and aptitude.

Since polarity is strongly connected to attitudes and feelings and involves quantifying the affective reaction of a human to a document, a media item or an event, we proposed to use sentic computing to encode contextual semantics and sentics to synthesize the full range of emotional medication experiences in terms of pleasantness, attention, sensitivity, and aptitude. Then after, these generated former sentics is efficiently deployed using our extreme learning machine model, and therefore a better understanding of the contextual role of each concept within a sentence is achieved in this study. Indeed, the proposed model leverages semantic and contextual relatedness to deeply understand the world and social aspects, extract medical components, and define cultural awareness and common-sense knowledge.

3.3 Biomedical Distributed Representations

Embeddings have received substantial attention because of their capabilities to capture the semantics of biomedical concepts. To date, methods have rapidly adopted word embeddings and combined different types of medical dictionaries from controlled biomedical ontologies, vocabularies and medical resources, such as PubMed[1]and MedLine[2] databases. Many studies have contributed to revolutionizing the use of word embedding techniques to represent biomedical text as a reduced dimensional vector. Primary methods trained the embeddings based on (1) the average surrounding context words, such as the continuous bag-of-words (CBOW) model in Word2Vec (Mikolov et al., 2013b), (2) weighted context words, such as the Skip-Gram model in Word2Vec, (3) global cooccurrence statistics, such as GloVe (Pennington et al., 2014a), and (4) word n-grams, such as fastText (Mikolov et al., 2017). For example, authors in (Zhang et al., 2019a) applied Word2Vec to a corpus of 10,876,004 English abstracts of biomedical articles from PubMed to estimate the relatedness of two words. Also, authors in (Kosmopoulos et al., 2015) provided biomedical word embeddings that combine subword information from unlabeled biomedical text with a widely-used biomedical controlled vocabulary called medical subject headings (MeSH). However, word embeddings are traditionally computed at the word level from a large corpus of unlabeled text, ignoring the information present in the internal structure of words or any information available in domain-specific structured resources such as ontologies. Where these knowledges hold the potential for significantly improving the quality of word representations, as suggested in some recent studies in the public domain.

Recently, the use of embedding with advanced computational linguistics techniques has shown promising performance in biomedical concept extraction and tagging (Chen et al., 2020), which employed other tools such as PubTator (Wei et al., 2013) (a state-of-the-art named entity recognition system), N-gram counts, word sequence occurrences, word sequence probabilities (Jing and Xu, 2019), and medical patterns of word semantics. Many pre-trained embeddings require no human-labeled data but they make use of resources for weak supervision (e.g., UMLS semantic types). They have been shown to speed up manual data curation by providing human annotators with automated pre-annotations generated by rules or machine learning models. Authors in (Chen et al., 2020) deployed PubTator via four different word embedding techniques on 30 million PubMed abstracts. It is the largest among the publicly available biomedical concept embeddings to date. It covers over 400,000 biomedical concepts mentioned in the literature and journal life pharma sciences. Additionally, many researchers have built continuous vectors space by using a training set of

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[1] https://PubMed.ncbi.nlm.nih.gov/

[2] https primarily://www.nlm.nih.gov/bsd/pmresources.html

sentence embeddings with over 30 million documents from both scholarly articles in PubMed and clinical notes from MIMIC-III clinical Database (Chen et al., 2019). Their purpose is to prove the effectiveness of discriminating expression features by employing pair similarity tasks in different biomedical text genres. For example, in (Wei et al., 2012), resources were derived from the combination of all publication abstracts from PubMed and all full-text documents from the PubMed Central [3] (PMC) open access subset and others. Our method is implemented on the top of training samples as a combination from PubMed and MIMIC-III clinical Notes.

Patient narratives on social network might contain different spellings of varied bio-medical entities such as genes, drug-interactions, and diseases. The capture of the semantic relatedness and contextual visibility of these bio-medical entities plays a vital role in retrieving hidden information and clarifying meanings and their attached sentiments. Various contributions have been done in this context: (1) bag of meta-words (Fu et al., 2018), (2) improved embeddings (Shuang et al., 2018), (3) and one-hot character vectors for aspect-based sentiment analysis(Pham and Le, 2018). Deep learning models have slightly improved these representations performance. For example, authors in (Pham and Le, 2018) joined multiple convolutions to generate suitable word representation for typical settings and tasks. Other distributions have combined unbiased representations from CNN with semantics from multiple BiLSTMs for generating contextual vectors (Rezaeinia et al., 2019). Even if most of them got good accuracy, they are not robust because (i) medication-related texts require learning from real-world data, (ii) they present additional language challenges that may require processing by a word-expert annotation system for efficient meaning disambiguation, especially for reducing biomedical data loss. To conquer these limitations, we attempt to define suitable transfer learning setting over the biomedical resource combination assessed through the experiments, and therefore this setting fit our extreme learning machines to define biomedical patterns on social networks.

3.4 Conclusion

This chapter described sentiment analysis methods in the context of medicine. Our focus was on the philosophy and trends in the generation of sentiment conveyed towards a medical target and the use of bio-medical vocabularies and datasets. We described the creation of several popular aspect-based sentiment methods and their failure in capturing sentiment and analyzing medication-related texts. We then discussed different computing methods to automatically annotate unstructured data, and also presented a list of available bio-medical

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[3] https://www.ncbi.nlm.nih.gov/pmc/

knowledge that helps to derive category information and context information. Finally, we believe that the diversity in goals, approaches, and uses of sentiment generation methods and resources of medical information determines the value of good quality algorithms to sentiment analysis in the context of medical information. In the next chapter, we will highlight some of critical points in the context of depend-domain distributed representations, especially for detecting drug-related knowledge: how a resource in one medical language can be mapped to another, and what settings and rules should be followed.

Chapter 4

Affective Concept-Based Encoding of Patient Narratives via Sentic Computing and Neural Networks

"Everything is theoretically impossible, until it is done."
—Robert A. Heinlein

4.1 Introduction

The automatic generation of features without human intervention is the most critical task for biomedical sentiment analysis. Regarding the high dynamicity of shared patient narrative data, the lack of formal medical language sentiment dictionaries prevents retrieval of the appropriate sentiment, which is unapproachable and can be prone to annotator bias.

We propose a novel affective biomedical concept-based encoding via sentic computing and neural networks. The main contributions include four aspects. First, a biomedical embedding, in which a medical entity is defined, normalized, and synthesized from a text, is built using online patient narratives after being combined with label propagation from a widely used comprehensive biomedical vocabulary. Second, considering the dependence on biomedical definitions, drug reaction sample selection based on general matching is suggested. These feature settings are then used to build and recognize affective semantics and sentics based on an extreme learning machine. Finally, a semisupervised LSTM-BiLSTM model for biomedical sentiment analysis is constructed.

There was a massive influx of patient self-reports related to the COVID-19 pandemic.

A study was conducted in this direction, and we tested the validity, medical language familiarity, and transferability of our approach by analyzing millions of COVID-19 tweets. Comparisons to affective lexicons also indicate that integrating extreme learning machine cognitive capabilities has advantages over biomedical sentiment analysis. By considering sentics vectors on top of the formed embeddings, our semisupervised LSTM-BiLSTM achieved an accuracy of 87.5%. The evaluations of unsupervised learning approximated the results of the previous model when dealing with a serious loss of biomedical data.

In this chapter, we demonstrate the effectiveness of integrating deep-learning-based cognitive capabilities for both enhancing distributed biomedical definitions and inferring sentiment compositions from many patient self-reports on social networks. The relevant encoding of affective information conveyed regarding medication subjects clearly reveals defined roles and expectations that can have a positive impact on public health.

Table 4.1 An overview of baselines models used for drug reactions lexicon construction regarding varied benchmarks algorithms

ADR Lexicon	**corpus**	**Algorithm**	**Accuracy (%)**
(Sarker et al., 2018a)	Twitter	Multinomial logistic regression	69 %
		Bidirectional GRU + GoogleNews embedding	55 %
		hierarchical based-Character LSTM (Char-LSTM)	47 %
		hierarchical based-Character CNN (Char-CNN)	77 %
(Limsopatham and Collier, 2016a)	AskPatient	CNN	78 %
		DNorm	73 %
		RNN	68 %
		Multi-class logistic regression	57 %

4.2 Proposed Approach

As illustrated in the introduction section, our main goal is to consider, extract, and exploit biomedical data for efficient biomedical sentiment analysis. Fig. 4.1 shows the overall architecture of the proposed system. It allows the contextual semantics of a given entity, its data-object properties and its relationships to be exploited in order to compute the attached sentiment based on the formed sentics. The subsections below give more details about each component.

Table 4.2 A summary of pre-trained embeddings for biomedical words and phrases using medical databases such as PubMed (abstracts,concepts...etc.) and MIMIC-III clinical notes

Biomedical Word Embedding	Embedding	Parameter settings	Text Copora
BioWordVec[1] (Zhang et al., 2019a)	FastText	200-dimensional word embeddings, where BioWordVec vector 13GB in Word2Vec bin format and BioWordVec model 26GB.	PubMed and clinical note from MIMIC-III clinical Database
BioSentVec[2] (Chen et al., 2019)	Sent2Vec	700-dimensional sentence embeddings. We used the bigram model and set window size to be 20 and negative examples 10.	PubMed
BioASQ3[3] (Kosmopoulos et al., 2015)	Word2Vec	1,701,632 distinct word vectors and biomedical types	10,876,004 English abstracts of biomedical articles from PubMed.
BioConceptVec[4] (Chen et al., 2020)	CBOW skip-gram glove fastText	It covers genes, mutations, chemicals, diseases and cellines. The trained embeddings contain over 400,000 concepts.	The entire PubMed biomedical concepts. PubTator to annotate biomedical concepts in the PubMed.

4.2.1 Biomedical Embedding Method

The embedding strategy followed at this point in the process is designed to create a contextual embedding for biomedical concept dependencies on very large shared data. We use semisupervised learning, which uses label propagation to automatically label unlabeled data. As described in Fig. 4.2, an embedding strategy is defined to represent the entire sentential context representation and is primarily constructed on two levels as follows:

1. **Enrich the training use case:** This is a straightforward technique for mutating predefined knowledge to draw upon pretrained word embeddings (Table 4.2). An embedding strategy with metaword features is used to support the large vocabularies of social networks. Three main biomedical components were considered: (i) the MeSH relationship network, (ii) distributed representations, and (iii) biomedical concepts and their data-object attributes. Behind the biomedical embedding strategy, a universal metaword dictionary is used by employing GloVe vectors that are trained on very large general-scope data. Glove vectors are incorporated to adjust the general context of some biased medical concepts and biased words, e.g., oils, love, and cancer.

2. **Transfer learning use case:** We followed the setting described in section 2.7, which concerns the domain adaptation of knowledge transfer for medication-related pro-

cessing and sample selection. The main objectives are to (i) extract medical entities from social network content, (ii) define their correspondence on formal vocabularies, (iii) adjust the medical training contexts to reduce serious biomedical data loss, and (iv) consider the long-term dependencies of n-gram medical components from highly defined abstracts, such as entries referring to the side effects of a given drug.

This method assigns a weight to each entry based on Eq. 5.1. The context embeddings are computed using the weighted sum of the embeddings of the neighbor words of the target word w_i and thereby sequentially generate the augmented embedding for representing the entire sentential context.

$$e(i) = \sum_{j=i-t;\, j\neq i}^{j=i+t} e(j)\frac{t-|i-j|}{t} \tag{4.1}$$

The performance of transfer knowledge depends mainly on how the sufficient and adequate training corpus is used. Table 4.2 summarizes the statistics of the distributed vectors we use in this study, which are used for constructing both models and evaluations. They represent an open set of biomedical word vectors (embeddings) that combines subword information from PubMed and MIMIC-III clinical notes with a widely used controlled biomedical vocabulary. Table 2.1 provides statistics on the different medical language systems and corpora used for training our system. This combination provides well-learned vectors for unseen entries. For each entry that appears in the corpus for the first time, we define dependency vectors that capture semantic and biomedical concept connections and contexts, as described in Fig.4.2 ; this is not necessarily training with additional formal data but retraining in a new model with a corpus that has the same vocabulary properties as those previously employed. By considering the MeSH relationship network, the embedding gain greatly improves the performance of the downstream computational prediction models (Guo et al., 2020). Indeed, this mechanism enhances the accuracy of our model in comparison with other biomedical embedding baselines in the literature, as we will discuss in section 4.3.1.

For a better generalization performance, we choose to let the training of the new model propagate back to these word vectors to gain understanding of the intrinsic semantic and conceptual connections. Consequently, we can achieve a valid and substantial embedding generation. Then, the underlying transfer is deployed sequentially to generate augmented embeddings that leverage adequate contextual biomedical representations for biomedical sentiment analysis.

As shown in Table 4.4, a given patient narrative may represent a side effect citation, which can be detected as a drug reaction subword that may be neglected or not considered. In the next section, we aim to define a drug reaction normalization component to embed drug-related entries from given shared contents.

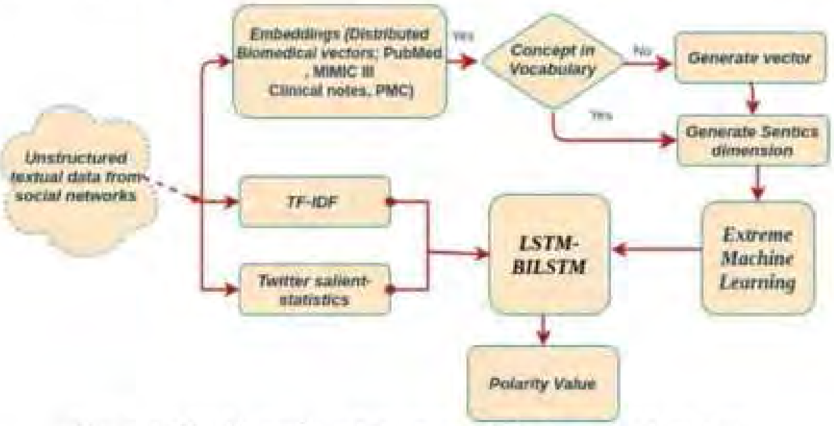


Fig. 4.1 The Overall architecture of the proposed system

4.2.2 Drug Reaction Normalization Component

The strong motivations behind adding the drug reaction normalization component are (i) obtaining a distinct set of words that refer to drug reactions and (ii) clearly negotiating the negativity of these elements to reduce the number of false positives and false negatives obtained by our classifier, which are caused mostly by mistaken categorization of ADRs (e.g., headache) and beneficial effects (e.g., hair loss reversal) (which are also known as medical events). We consider the aspect-based sentiments of these medical events by exploring embedding characteristics through groups of drug reactions, where the subgroups consist of the defined elements of a group for which the group events with regard to a given event are commutative (common drug interactions).

Drug reaction normalization is the task of retrieving and mapping word combinations that represent drug reactions and finding their corresponding formats from external drug knowledge such as the side effect resource (SIDER). This task frequently requires analysis at the feature extraction level, which can be difficult without sufficient background knowledge of the formal medical context. For this purpose, we have deployed external multicorpus drug reaction knowledge from a state-of-the-art design for adverse drug reaction normalization (Sarker et al., 2018a) and the (SMM4H) 2017 shared task (Nikfarjam et al., 2015a), data and systems for medication-related text classification and concept normalization from Twitter. The automatic construction of the annotated drug reaction dataset explores many learning algorithms through groups for drug reaction detection (25678 annotated tweets and 9150 ADR phrases and identifiers). Ensembles of system combinations obtained the best score of

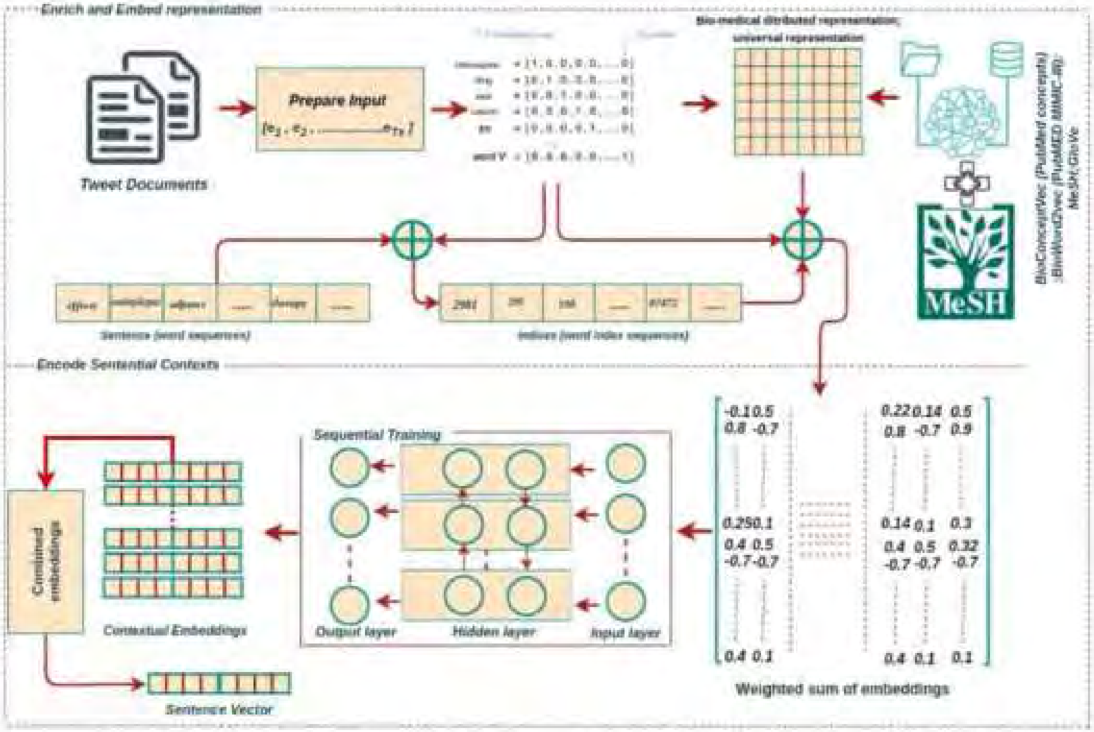


Fig. 4.2 The process designed to Deploy the feature-based setting to generate the appropriate sentiment ((Grissette and Nfaoui, 2021b))

88.7%, outperforming individual systems for the normalization of ADR expressions on social networks. The problems are that (1) the systems frequently misclassify rarely occurring ADRs due to suboptimal entity recognition methods in drug reaction detection, and (2) the lack of context in length-limited posts prevents explicit drug reaction formats from being defined. With the dependence on biomedical definitions described in section 4.2.1, drug reaction sample selection based on general matching and neural networks is developed. We have paired the drugs and side effects as samples, thereby modeling the problem by using a neural network component that serves to extract related drug reaction contextual semantics, as described in Fig.4.5. Indeed, this component consists of the shared layers with the previous construction embedding model. We aim to add related side effect semantics to our weight matrix (embedded biomedical definitions) by using an annotated dataset primarily to seek the possible side effect semantics of unknown words such as those described in Table 4.4. This component also allows the long-term dependencies of drug reactions on large patient reports and their related attributes to be defined, such as indications, diseases, and drugs.

Each tweet is a candidate for reporting a drug reaction or medical event reaction that can be translated into formal medical language using our neural-network-based detector. The drug reaction detector takes as input a set of n-grams and the corresponding medical format,

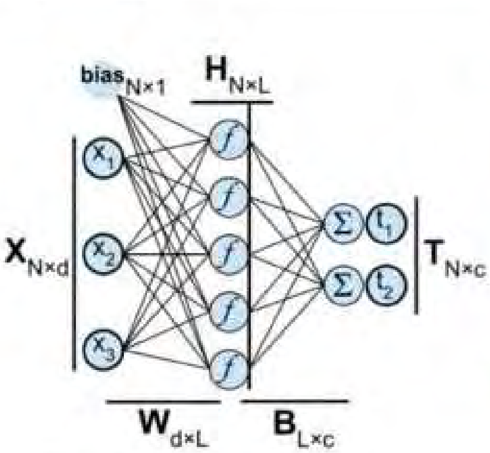


Fig. 4.3 Multiple hidden layer Extreme Learning Machine network

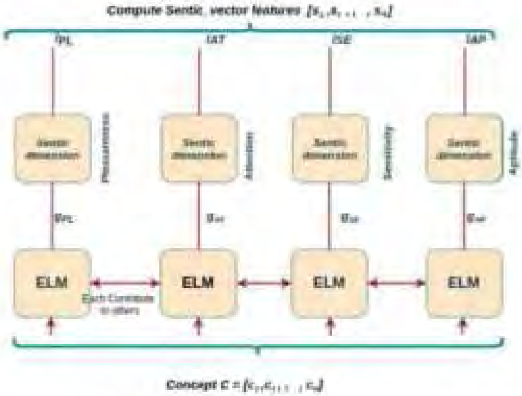
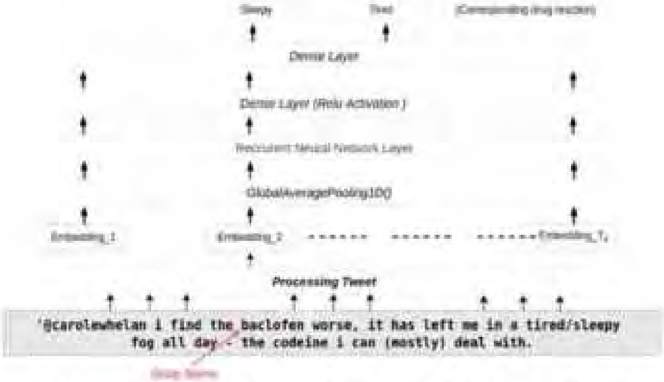


Fig. 4.4 ELM-based network to generate sentic vectors by specifying compound emotion into four sentic dimensions.



'@carolewhelan i find the baclofen worse, it has left me in a tired/sleepy fog all day - the codeine i can (mostly) deal with.

Fig. 4.5 Neural Network-based drug reaction normalizer process

and it is trained principally with our proposed model to obtain automatic connections with positive and negative medical facts. The model learns the weights via the portable multi-corpus training defined earlier. Indeed, a simple recurrent neural network is used on top of the augmented embedding from the previous component and achieves stable accuracy in detecting drug reaction references in a given raw text.

4.2.3 Inductive Sentiment Method

This section presents a novel method to deduce sentiment from unlabeled data obtained from social networks. We describe the core steps of the proposed analogical affective reasoning method as follows: (1) We first describe in detail how we adapt the sentic computing approach for the task of encoding the affective information conveyed towards medication-related targets. Then, (2) we propose leveraging TF-IDF statistical features in our proposed

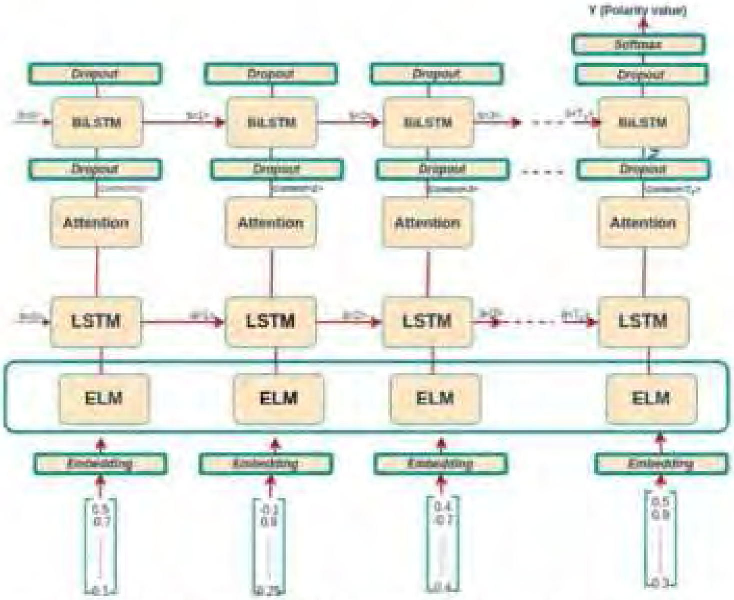


Fig. 4.6 ELM-based network for computing sentimental outputs

feature framework. Finally, (3) we create an LSTM-BiLSTM sentiment computing component based on the proposed feature framework.

By adding an extreme learning machine algorithm into our neural network model, the proposed method obtains a good understanding of medication-related affective aspects and generates suitable sentics. Furthermore, we address the question raised in section 1.1.1 regarding how the deficiency of recognition tasks for word combinations (large medical concepts) in the text may fail to provide relevant insight. By convolving the [1-4] gram training setting, it is estimated that accurate recognition capabilities can be achieved for efficient affective reasoning tasks.

Encoding Sentics and Semantics via a Neural Network

Owing to the need to analyze large volume of patient narratives and extract medication-related concepts, we consider two levels of abstraction: a single entry and a set of entries under various learning problems as the context and target formalization. In particular, we explain the sentic computing approach to clarify common-sense cognitive aspects and affect-related information, especially for medication-related natural language concepts. Human emotions and their modeling are increasingly understood to be crucial tasks, especially under particular circumstances, e.g., patients with particular health conditions.

According to the hourglass of emotions model that is used to form the full spectrum of human emotional experiences, the mind is to a large extent emotionally controlled to obtain independent resources. Moreover, shared information can be relatively quantified to generate affective vectors by specifying emotion compounds through four sentic dimensions that measure the degree to which (i) the user is amused by interaction modalities (pleasantness); (ii) the user is interested in the interaction content (attention), (iii) the user is comfortable with the interaction dynamics (sensitivity), and (iv) the user is confident in the interaction benefits (aptitude). In particular, sentic computing-based encoding is used to synthesize the full range of emotions conveyed towards medication-related experiences and to make sense of medical facts. The model's output is in terms of the polarity, which is a floating number between -1 and +1 (where -1 is extreme negativity and +1 is extreme positivity) (Satapathy et al., 2017), and is calculated according to the following formula:

$$p = \sum_{i=1}^{10} \frac{Pl(c_i)| + |At(c_i)| - |Se(c_i)| + |Ap(c_i)|}{3N} \tag{4.2}$$

where c_i is an input concept, N is the total number of concepts, and 3 is the normalization factor.

Each concept may appear in a negative context (negative intensity) or in a positive context (positive intensity). Therefore, we consider the absolute value; for example, in terms of the attention dimension, "surprise" is negative in the sense of lack of attention but positive in terms of the point of view.

The existing sentiment generation approaches discussed in section 3.2.1 are mainly focused on the identification of parts of the text that express sentiment as polar terms, expressions, and statements that express emotions. In our proposal, we attempt to build analogy-based sentics and semantics within a neural network learning strategy that strives to provide an understanding of a clear connection between different affective aspects. Indeed, a semantic configuration is first used to deconstruct medical natural language text into concepts. Second, linguistic patterns are used in conjunction with sentic dimensions to infer polarity from sentences. If no match is found in the vocabulary or in the linguistic patterns, the neural network model is used.

The large number of patient narratives discussed on social networks spread large amounts of information citing a large number of medication-related concepts. Indeed, they are contextually and semantically associated in different contexts, which further require a higher entity recognition performance to better capture conceptual and sentimental patterns in a sparse dynamic affective space. Moreover, a large social network solution requires particular computing characteristics that allow shared relevant information insights to be captured. First, the process should have low computational complexity, and fast affective learner aspects are required regarding varied targets. In particular, the sentic vector encoding is computed every time for various entries, and multiword expressions are also considered. Otherwise, multiple neural network learning with numerous parameters in each time step will lead to issues in backpropagation network training, while ordinary backpropagation-based neural networks have to deal with the local minima problem, including retraining strategies, convergence rates, etc.

All these features are examples of good extreme learning machine (ELM) training points. Extreme learning machine algorithm training shows appreciable results with very low computational cost, which is especially relevant when dealing with many patterns defined in a high-dimensional space, where it always converges to the global optimal solution. In this study, we proceed by feedforward neural networks with multiple hidden layers that powerfully identify affective patterns as well as those associated with medication-related conceptual sentics as a function approximation. As depicted in Fig. 4.3, for a coactivated unsupervised learning problem, each concept (target) is first learned or explained by general concept matching, the semantic and sentic dimensions of which are well explained. Otherwise, concept associations regarding specific biomedical contexts are recalculated every time a new multiword expression is inserted into the vocabulary in Fig. 4.1, which is further designed to be the input to the LSTM-BiLSTM sentiment inductive model, received as a training set X of N labeled pairs, where (x_i, y_i) is the input.

- $x_i \in \mathbb{R}^{T_x}$: Input embedding vector. Here, T_x is the maximum length of the inputs.

- $y_i \in \mathbb{R}$: The expected target polarity value p is calculated according to four sentics dimensions (pleasantness, attention, sensitivity, and aptitude).

The input layer has T_x time steps and is connected to N_h neurons of the hidden layer through a set of weights $\{\hat{W}_j \in \mathbb{R}^{T_x}\ j = 1, \ldots\ldots, N_h\}$, which is initialized arbitrarily. The jth hidden neuron embeds a bias term b_j that is activated using a nonlinear activation function g(.).

The coactivation of different affective levels allows different compound emotions to be captured in varied medication-related discussions. Effectively, Fig. 4.4 highlights the ELM-based network that generates the sentic vectors, where the use of a scalar output implies that the network has one output unit, without loss of generality. The sentic vectors are recalculated independently into four predefined levels, allowing us to deductively propagate the long-term affective dependencies of each concept in each dimension and then measure how each sentic level contributes to the others. Many performance evaluations (Huang et al., 2004) have been carried out on various inference problems, and ELM has demonstrated learning abilities leading to crucial results. The random weights in the hidden layer endow a

network with a notable representation ability that embeds the compound emotions of non sentimental expressions such as medical concepts.
The overall output function, f(x), of the network is:

$$f(x) = \sum_{j=1}^{N_h} \bar{W}_j g(\hat{W}_j.x + \hat{b}_j) \tag{4.3}$$

where $\bar{W}_j$ is a vector of weighted links, $\bar{W}_j \in \mathbb{R}^{N_h}$.

TF-IDF Component

After expanding the sentic vectors with the aim of leveraging the seminal affective meaning of medical concepts, related bag-of-sentimental-concepts features are formed that are similar to bag-of-concepts features. Each dimension in the feature vector represents a concept, and each concept is assigned a value by multiplying the TF-IDF and the polarity value of the concept. The theoretical foundations are considered to be less than firm by information theory experts. The inverse document frequency for any given term is defined as:

$$tf(term,tweet) = \frac{f_{tweet}(term)}{\max_{word \in tweet} f_{tweet}(word)} \tag{4.4}$$

$f_d(t) : frequency\, of\, term\, t\, in\, tweet\, d$

$$idf(term) = \log(\frac{n_{tweet}}{n_{allTweets}}) \tag{4.5}$$

The $n_{allTweets}$ are tweets that contain term. The Twitter TF-IDF matrix is defined as:

$$W_{term_j,tweet_i} = tf(term_i,tweet_j) * Idf(term_i) \tag{4.6}$$

Each coefficient $W_{i,j}$ associated with term i in tweet j describes and quantifies how important various terms are in a tweet that is part of a Twitter corpus in a slice of time.

Sentiment Computing Component

In this step, we leverage our feature framework from different core steps and bidirectionally propagate them to efficiently compute sentiment-related information towards a particular target t_i in a given context c_j. The overall sentiment inductive method is shown in Fig. 5.2. The proposed architecture is designed to receive as an input a large number of tweets represented according to an m-dimensional contextual embedding space and to predict the corresponding overall sentiment with regard to the various affective dimensions involved, i.e., pleasantness, attention, sensitivity, and aptitude, as discussed in the last section. For the outputs, in principle, the inductive polarity covers three main salient features derived from minute Twitter data and is characterized by an analog value in the range $[-1, 1]$, which represents the intensity of the expressed or received emotion under a medical policy, which is synthesized every time through learning procedures.

However, two important aspects should be taken into consideration. (1) The architecture relies on an embedding strategy that aims to transfer embeddings from large medical ontologies already adopted for social network data (section 4.2.1) and to learn connections between new multiword expressions that may refer to medical concepts such as drugs, symptoms, and ADRs. The design of a reliable sentiment predictor regarding biomedical contexts is important, especially when considering that few alternative schemata have been provided in the literature without clearly adopted medication-related concept features or a target of analysis. (2) The affective reasoning model discussed previously is considered an input to the sentiment sequential model. Indeed, the values from each sentic dimension are ultimately remapped to obtain the expected concept polarity. Neural computing spans each affective dimension separately, where various dimensions contribute to each other. More complex emotions can be synthesized by using three or even four other sentic levels, e.g., $joy + trust + anger = jealousy$, as discussed by the authors of (Cambria et al., 2020). Conceivably, each affective dimension may be handled by a dedicated ELM, which addresses learning and explains semantics for a given sentic dimension independently, and then, by using formula 4.2, the semantic associations of attitudes and feelings are defined as polarity values. These polarity values are joined to another feature $\hat{y}$. Then, these values are fed into a BiLSTM sentiment classifier that is designed primarily to learn efficient connections and long-term dependencies using the policies from previous steps and to loop them into a network, as shown in Fig. 5.2, which provides the overall scheme of the proposed approach. It yields as output the analog polarity value that will eventually lead to the corresponding sentiment insight.

The problem definition should also state what kind of performance is desired. In this study, automatic sentiment induction of biomedical concepts based on sentic computing and neural networks is carried out to principally clarify truly affective information regarding given medication-related aspects to better fit the medical conceptual aspect and affective associations to detect the "fakeness" or "genuineness" of a given medical fact. Indeed, the ultimate motivation behind the choice of BiLSTM was to learn long-term dependencies, especially those for medication-related terms. Another reason is that multiple BiLSTM layers

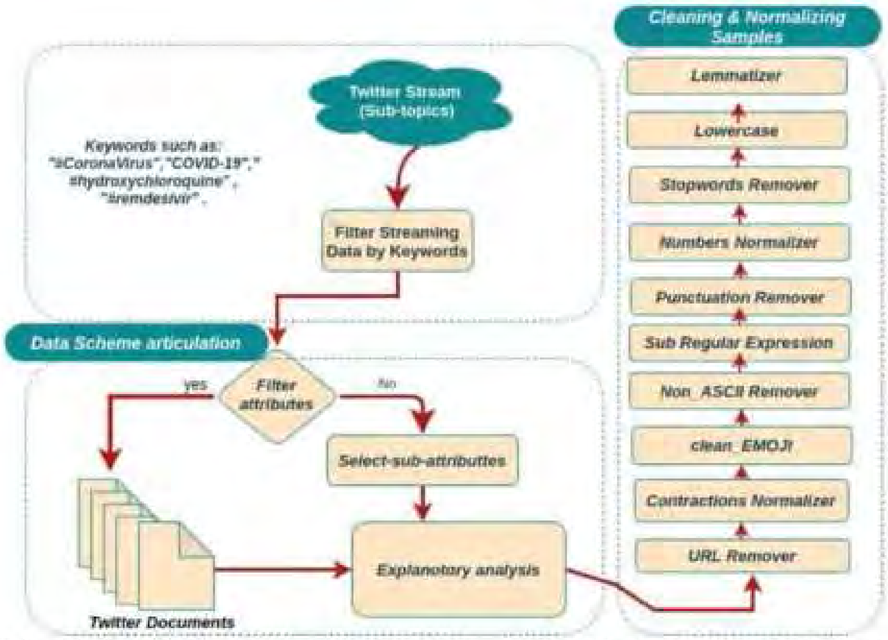


Fig. 4.7 The process of gathering Tweets from '2020-03-16' to '2020-05-02' and preparation process

allow the exploitation of sentic semantics under medical vector dependency at the same time steps and the collection of affective common-sense knowledge through sequential computing, designing the computation of the four affective sentic levels. Moreover, we employ the attention mechanism to help memorize long normalized term dependencies and identify how much attention should be given to particular medication-related concepts through the proposed neural networks. Attention is arguably one of the most powerful concepts in deep learning. The attention layer is a component of memory networks, which focuses their attention on external memory storage rather than a sequence of hidden states.

4.3 Validation and Results

In this section, we first present the relevant COVID-19 problem for this study. Afterwards, we conduct experiments in the following directions: (1) we respond to the questions raised and formulated in this study; (2) we perform a sentence-level evaluation with the clinical semantic textual similarity benchmarking resource to prove model transferability; and (3) we discuss the model performance over the embedding levels, where it is compared with BioSentVec (a sentence-level biomedical distributed representation (Chen et al., 2019)) in combination with general-scope embeddings. We then evaluate the models using a set of

Table 4.3 The Overall sentiment (polarity value) of some tweets from dataset groups collected through this study

Twitter document	**Medical components**	**Polarity value**
@singleuesguy hydroxychloroquine ninety percent chance help covid19 patient with chronic disease state association	hydroxychloroquine, covid19, patient,chronic disease	0.4
@thekjohnston remember trump amp blowhard fox wouldnat shut hydroxychloroquine miracle covid cure makina	covid,hydroxychloroquine	-0.2
@channelstv bauchi governor mandate use chloroquine treat covid19	chloroquine, covid19,	-0.02
@jamestodaromd fda need randomize controlled trial hydroxychloroquine treatment covid19 also fda discourage	trial, hydroxychloroquine treatment covid19	-0.4
@tedlieu anyone read tweet @realdonaldtrump say hydroxychloroquine amp azithromycin game changer #covid	hydroxychloroquine, amp, azithromycin	0.1
@ingrahamangle hyperglycemia hydroxychloroquine covida19 pandemic drop brufsky journal medical virology wiley online lia	hyperglycemia, hydroxychloroquine, covida19, medical virology	-0.3

Table 4.4 Samples of annotated tweets and their drug reaction detected

Twitter document	**Drug reaction detected**
@carolewhelan i find this drug worse, it has left me in a tired/sleepy fog all day - the codeine i can (mostly) deal with.	Sleepy
@shipmom cipro is awful makes me sick as a dog too	Sick
@jameetmiller i didn't have side effects when i started taking cymbalta. after about 6 mths had to stop because it raised my blood pressure.	raised my blood pressure
brisdelle dangerous. paxil is supposed to treat depression and suicidal thoughts. i took paxil and got depressed. went off & ok in 2 wk.	depression
09.26 day 12 rivaroxaban diary: headache, right shoulder and neck ache, lower back pain, weak knees, limping when walking.taken paracetamol	headache

deep learning algorithms based on our proposed feature framework in comparison with other sentiment dictionary baselines. Furthermore, as discussed in section 1.1.1, the biomedical knowledge combination advantages in improving the system accuracy are assessed through various experiments. In addition, we demonstrate the use of additional features, e.g., the frequency weighting feature for providing significant gains in accuracy and recall over the corpus-based classifier. Finally, (4) we present and discuss different medication-related short text perspectives and the evaluation results.

4.3.1 Experiment Design

COVID-19 Case Study

The current pandemic is widely known owing to the large number of patient narratives on social networks, which are characterized by vigorous activity and dynamism in terms of global pandemic combat. Many platforms, such as Twitter, are becoming inundated with information and misinformation and are used to share serious side effects of vaccinations and drugs, which might disturb public health.
To validate the proposed case study, the social network Twitter was used. Twitter is a microblogging site that generates a constant stream of communication, some of which concerns events of general topics. In the design of the experiments, a large number of narratives on the COVID-19 crisis are extracted using a set of relevant keywords dedicated to the filtering of information (the most-used drug data groups are used in section 4.3.3). Hence, by posting a tweet, it is possible to analyze the information behavior and then synthesize the affective components (sentics) in the sense of judgments or intentions according to a specific target.

Twitter-Specific Corpus

This contribution also addresses medical domain transferability challenges for biomedical sentiment analysis on Twitter. Due to the limited annotated data, we built our Twitter-based corpus to efficiently define adequate features to generate sentiment semantics and sentics. COVID-19 tweets were collected from January 2020 to May 2020 regarding three properties: (i) the time axis, (ii) drug-related keywords, and (iii) medication-related evidence. We collected tweets and replies in COVID-19-related discussions. The methods of gathering and preprocessing data are described in Fig. 4.7. First, we streamed data related to a set of keywords, and we built a data scheme with regard to two types of attributes:

- **Attributes from Twitter:** ['id', 'created_at', 'source', 'original_text', 'lang', 'favorite_count', 'retweet_count', 'original_author', 'hashtags', 'user_mentions', 'place', 'place_coord_boundaries'].
- **Encoded attributes :** ['cleaned_text', 'Sentics', 'polarity', 'medical concepts', 'Bag_of_ADRs'].

The "Sentics" attribute represents affective dimensions including sentiment intensity, semantics, and subjectivity; the "polarity" attribute stands for a polarity value, which is a floating number between -1 and +1 (where -1 is extreme negativity and +1 is extreme positivity); "medical concepts" indicates the set of defined medical entities within a text; and

'Bag_of_ADRs' concerns drug effects or indications stated in the Twitter document.
Second, we have stored tweets in a set of files (dataset groups) regarding drugs vs. disease components and a time axis, allowing more conceptual personalization in the same semantic configuration subspace. We applied an explanatory analysis to filter the relevant data into drug-related groups to make sense of medication-related semantics and affective levels from well-understood contextual concept associations. Finally, these tweet samples were passed through a set of normalization and processing steps. Ultimately, we kept 9 M COVID-19 related tweets. Based on the previous settings of the prepared and encoded attributes, we computed the attached polarities and affective dimensions of each tweet and its replies. Then, they were annotated automatically using the former sentics, and we used them for training and testing purposes.

Additional Twitter Salience

Real-time Twitter-based documents present typical particularities, including limited text size, noise, informal language, and hashtags, which must be taken into consideration. Owing to the character limit, the authors of tweets are usually straightforward. The shortness and lack of biomedical context of length-limited posts cause problems in defining complicated medical components such as drug reactions or events.

Due to the high level of communication rates regarding the urgent COVID-19 pandemic, people spend much time sharing the same ideas about a given drug or committed drug reaction. Observing the three tweets below, each was repeated more or less than the average of 596,730 times (in 9 million tweets). Certain narratives have received much attention and have been frequently retweeted.

Tweet 1: Take #hydroxychroloquine followed by a 500ml glass of Dettol. (As per Presidential Instructions) Lie down in a comfortable position and cover..

Tweet 2:#Hydroxychroloquine in #COVID_19 . The drug is untested the benefits unknown, and the risks not negligible, especially at the mass prophylaxis level of use.

Tweet 3: Im at a complete loss for words. Fox joined by Geraldo Rivera are still PUSHING hydroxychroloquine as a magic bullet for Covid_19 The FDA issued a WARNING
I ve taken the drug for Lupus for 6 years. It has side-effects. ENOUGH!

To determine the appropriate boundary of the affinity of each term, we define the average affinity value as an additional feature to adjust the polarity with regard to how many representatives are in the corpora by the formula:

$$Affinity(P) = \frac{f(P)}{min_{\forall w_i \in P}(f(W_i))} \tag{4.7}$$

The $f(P)$ is the frequency of phrase P and $min(f(w_i))$ is the minimum frequency across the words in phrase P. Referring to (Ghiassi and Lee, 2018), the application of the affinity method allows us to select a set of n-grams that have "higher collocation frequencies relative to the individual occurrence frequencies of the constituent unigrams."

Table 4.5 Two banchmarking datasets used for medical annotation evaluation tasks.

Dataset	**Description**	**settings**	**Accuracy**
MedSTS[5]	Resource for clinical Semantic Textual Similarity	MedSTS (MedSTS_ann) containing 1,068 sentence pairs was annotated by two medical experts with semantic similarity scores of 0-5 (low to high similarity).	0.81
BIOSSES[6]	Semantic Sentence Similarity Estimation System for the bio-medical domain	The BIOSSES data set comprises total 100 sentence pairs all of which were selected from the TAC2 biomedical Summarization Track Training Data Set .	0.79

4.3.2 Parameter setting

This precomputation strategy allows a nice compromise between GPU (NVIDIA (R) CUDA compiler driver) and implementation simplicity. For the ELM, the wide lower layer and each of the 4 bidirectional-LSTM layers, we used the Adam optimizer with 128 units for both the LSTM and BiLSTM folds. In addition, we trained the model from 1-30 epochs, computed on the GPU[7], and then moved the precomputed hidden weights to the CPU for the prediction task. This makes many things much easier. To boost our model performance, we train a sufficiently large neural network in terms of parameters and connections to take advantage of the very large number of shared experiences on social networks in a matter of seconds.

4.3.3 Results

The experiments conducted assess the performance of our model. We mainly compare our model with other methods in three aspects: (1) We compare the performance of our proposed feature framework with biomedical embedding baselines. (2) We explore the performance of

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[7] https://www.marwan.ma/hpc

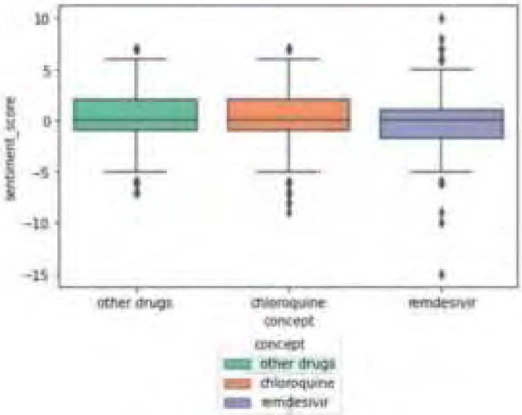

Fig. 4.8 Box plot of the performances provided on each medical component

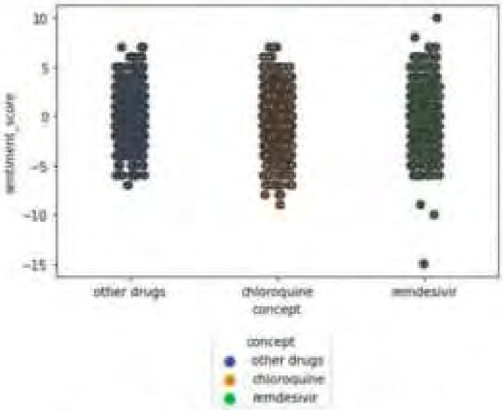

Fig. 4.9 The dispersity of sentimental polarities vs. Training Data over three medical components

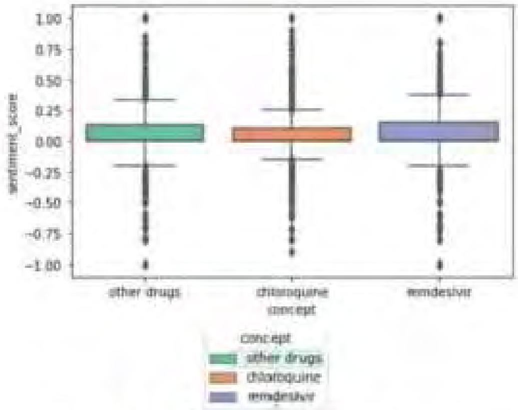

Fig. 4.10 Box plot of the performances provided on each medical component

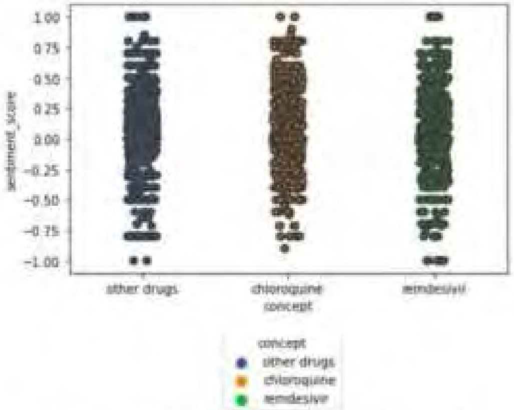

Fig. 4.11 The dispersity of sentimental polarities vs. training data over three medical components

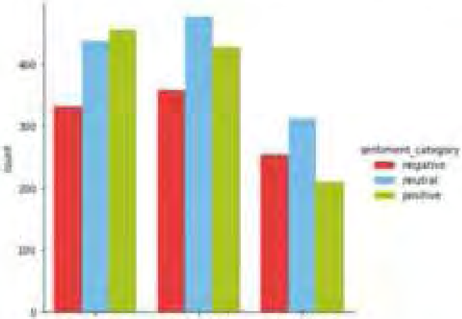

Fig. 4.12 Positives vs. Negatives of three most visible medication-related components

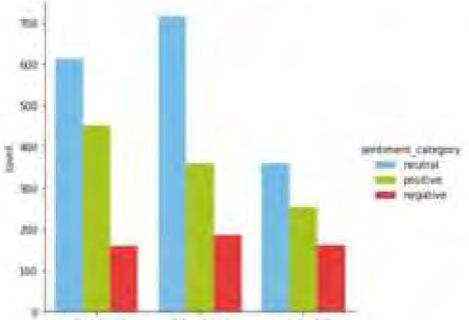

Fig. 4.13 Positives vs. Negatives of three most visible medication-related components

Table 4.6 Statistics of proposed sentiment inductive model on first Twitter corpus regarding two frequently releated-drugs components narratives (Chloroquine and Remdesivir) with other drugs

	sentiment score							
	count	mean	std	min	25%	50%	75%	max
concept								
Chloroquine	1261.0	0.051449	0.234630	-0.9	0.0	0.0	0.100	1.0
Other drugs	1224.0	0.058930	0.248925	-1.0	0.0	0.0	0.136	1.0
Remdesivir	774.0	0.043039	0.302643	-1.0	0.0	0.0	0.150	1.0

Table 4.7 Statistics of other lexicons such as AFINN for sentiment inductive model on first Twitter corpus regarding two frequently releated-drugs components narratives (Chloroquine and Remdesivir) with other drugs

	sentiment score							
	count	mean	std	min	25%	50%	75%	max
concept								
Chloroquine	1261.0	0.002379	2.185993	-9.0	-1.00	0.0	2.0	7.0
Other drugs	1224.0	0.261438	2.067610	-7.0	-1.00	0.0	2.0	7.0
Remdesivir	774.0	−0.114987	2.398460	-15.0	-1.75	0.0	1.0	10.0

our approach in a biomedical sentiment analysis case study. (3) We compare different ways to encode sentiment regarding medical aspects and related components. The most crucial challenge of this study is the lack of a labeled training dataset including medication-related concepts since the drug reaction detector model requires much label training data. However, with word embeddings, the model can build good classifiers even with only modestly sized label training sets. We cover large-scale biomedical semantic indexing and map medical concepts to natural language expressions citepd in patient narratives on social networks, especially drug reaction expressions and PubMed concepts.

In fact, we have a potent biomedical continuous space of $10,876,004$ English abstracts of biomedical articles from PubMed, 400,000 concepts, and $15,677$ resulting vectors of $1,701,632$ distinct words that form drug reaction expressions, PubMed abstracts, symptoms, drugs, etc. All words were converted to lowercase, the embedding was converted to the same dimension, and the vector dimension was 300. Our sequential model considers tweets as a sequence of tokens, and the outputs are floating numbers in $[-1,1]$ with clear medical concept tagging. The settings of the features used in the model are as follows:

1. The biomedical distributed representation, which shuffles pad vectors into the same dimension.
2. GloVe vectors, which define universal words and adjust the general context of some biased medical concepts and biased words, e.g., oils, love, and cancer.

Table 4.8 Comparison of proposed feature framework with different ensemble classifiers using other sentiment benchmark dictionaries ((Grissette and Nfaoui, 2021b))

Corpus	Sentiment dictionary	Algorithm	Accuracy
Twitter datasets	Our proposed feature framework	LSTM-BiLSTM	**0.87**
		LSTM	0.72
		Multiple RNN	0.72
		CNN	0.68
		SVM	0.58
	SenticNet (Cambria et al., 2020)	BiLSTM	0.79
		LSTM	0.73
		Multiple RNN	0.66
		CNN	0.72
		SVM	0.60
	AFINN (Nielsen, 2011)	BiLSTM	0.72
		LSTM	0.71
		Multiple RNN	0.62
		CNN	0.68
		SVM	0.45
	VADER (Hutto and Gilbert, 2014)	BiLSTM	0.67
		LSTM	0.68
		Multiple RNN	0.65
		CNN	0.63
		SVM	0.52
	TextBlob (Knuth, 2020)	BiLSTM	0.67
		LSTM	0.62
		Multiple RNN	0.70
		CNN	0.66
		SVM	0.45

3. Sentic vectors, which define sentimental semantics and recontribute to the affective dimensions every time, namely, the sentics.

4. The LSTM, which learns embeddings for new multiword expressions and represents long-term dependencies in the very large vocabulary of medication-related concepts, e.g., drug names, symptoms, pandemics, and diseases.

5. The BiLSTM, which deploys precomputed features and learns long-term sentiment dependencies regarding medication aspects and contexts.

6. The attention mechanism, which defines attention parameters that propagate the amount of attention that should be given to those features of the input sentence.

For each token, we consider an embedding vector hybridizing both a universal format and biomedical information into a 300-dimensional vector. Our baseline model can actually

Table 4.9 Evaluation of proposed sentiment feature framework with existing embedding strategies ((Grissette and Nfaoui, 2021b))

Sentiment dicionary	**Embeddings**	**Accuracy**
Our proposed sentiment inductive model	Our embeddings framework	**0.87**
	BioWordVec +BioConceptVec	0.79
	BioASQ3 +GloVe	0.71
	BioWordVec +GloVe	0.72
	BioSentVec+ Twitter GloVe	0.72
	BioWordVec +FastText	0.76
SenticNet	Our embeddings framework	**0.79**
	BioWordVec +BioConceptVec	0.75
	BioASQ3 +GloVe	0.76
	BioWordVec +GloVe	0.69
	BioSentVec+ Twitter GloVe	0.73
	BioWordVec +FastText	0.70
AFINN	Our embeddings framework	**0.74**
	Twitter GloVe +BioWordVec	0.70
	BioSentVec + GloVe	0.67
VADER	Our embeddings framework	0.81
	GloVe +BioWordVec	0.77
	BioSentVec + GloVe	0.73
TextBlob	Our embeddings framework	0.71
	GloVe +BioWordVe	0.69
	BioSentVec + GloVe	0.67

work fairly well using only biomedical vectors but leaves out universal and concept-related contexts such as drugs or symptoms. Therefore, we developed dynamic medical corpora, which are further dedicated to learning deeper representations under target medical settings, and we collected 8,593,940 examples. The first version of our model used 9 million COVID-19-related tweets learned by the BiLSTM and our sentic computing-based sentiment architecture. This gain is sometimes not significant regarding the generalization aspect. Moreover, these deep architectures work significantly better than the classical approaches. We have obtained degrees of error from approximately 8% to 5% when we used n-grams with TF-IDF. This number of Twitter examples can be addressed efficiently by learning from scratch based on the literature, which works best for large datasets, where our method beats classical approaches such as the bag of words and part-of-speech feature selection techniques. To convert our input sequence into a vector of fixed size, we apply some dense layers. We apply a multilayer positron on top of the 300 features and train them using a long-term memory algorithm that uses GloVe vectors to ensure that universal words are defined in connection with the biomedical expressions.

Table 4.10 Benchmarking sentiment dictionaries used for evaluation tasks

Lexicon	**Description**	**Level of automation**
VADER (Hutto and Gilbert, 2014)	A sentiment dictionary, it attuned to sentiment in micro-blog. It combined various lexical features with consideration for five general rules that embody grammatical and syntactical conventions for expressing and emphasizing sentiment intensity. Thus, It has been found to be quite successful when dealing with social media texts e.g. used by Amazon's Mechanical Turk for sentiment ratings.	Semi-automated
AFINN (Nielsen, 2011)	A sentiment Dictionary (over than 3300)rated for valence with an integer between minus five (negative) and plus five (positive), though not as good as the more elaborate approach found in SentiStrength.	Manual
TextBlob (Knuth, 2020)	Sentiment Lexicon goes along finding words and phrases it can assign polarity and subjectivity to, and it averages them all together for longer text. The scores from TextBlob are normalised scale as compare to AFINN.	Automated
SenticNet (Cambria et al., 2020, 2014; Cambria and Hussain, 2015)	The knowledge base which the sentic computing framework leverages on for concept-level sentiment analysis. SenticNet is automatically constructed by clustering the vector space model of affective commonsense knowledge extracted from varied lexical resources.	Automated

We apply neural networks at different architecture levels, and we prove how we can embed our medication-related concepts efficiently, especially unlabeled examples. We propose analyzing two-grams and three-grams using the ELM neural network to propagate the sentiment aspects for new multiword medication 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 may be selected as possible drug reactions. They are used to define embeddings and may still perform this correctly and generalize much better. The activation step of the predicted sentics has approximately four levels but concomitant dimensions. Theoretically, the model synthesizes the full range of emotional experiences in terms of pleasantness, attention, sensitivity, and aptitude, as the different combined values of the four affective dimensions can also model the affective states. In this way, we trained our model to achieve good performance and obtain a deep sense of concepts.

Additionally, popular non-domain-specific sentiment lexicons as well as state-of-the-art machine-learning and deep-learning models are chosen as benchmarks, and the experimental results show that our sentiment feature framework outperforms the benchmarks with statistically significant differences, thus proving the effectiveness of the proposed approach. An input sequence was first processed for embedding generation to train the specific features that this neural network needs to classify the conveyed sentiment. The LSTM and Bi-LSTM had different operational learning procedures, which were learned, memorized, and hybridized outputs that served as the inputs of the next level (Fig. 5.2). Indeed, the weight matrix of each level was stored for evaluation. Deep learning models have slightly different results regarding the embedding strategy offered in this study vs sentiment dictionaries; we also evaluated the models in our model groups based on comparisons with Deep Learning algorithms (LSTM, BiLSTM, multiple RNNs, and CNN) and SVM on COVID-19 Twitter datasets, as described in Table 6.2.

The BiLSTM algorithm on one- and two-grams, in conjunction with the SenticNet prior sentiment knowledge, achieves an accuracy range of [83-85]%. Particularly, when we merge [1-4]-grams through the proposed architecture with BiLSTM on top of those that depend on features, we obtain an accuracy of 8.2 bumps, which gives us an almost 87.5% accuracy with the potential for clarifying the corresponding medical concepts as targets. Then, we ensure that false positives and negatives are avoided. We train the model for 1-30 epochs, and then we choose a set of optimal parameters from the trained model under this setting. Subsequently, we choose the optimal settings that yield the minimum loss. Therefore, we can capture the information about three-, four-, and five-grams, and for each n-gram, new multiword expressions are inserted into the vocabulary.

Observing sentiment information regarding three pertinent drug names reveals their high rate of appearance in our experimentation. A statistical analysis was performed on the inference results for three drug components to visually show the distribution of numerical data and skewness by displaying the data quartiles (or percentiles) and averages. However, for a different time, Fig. 4.10 shows a box plot of the performances provided for each component. The number of positive examples was the highest due to the highly recommended use of these drugs to avoid COVID-19 contamination. In particular, we obtained many tweets from US President Trump discussing chloroquine treatment. Thus, we tracked many chloroquine treatment use cases and/or drug effects since we captured drug effects in the text, turning the target of the analysis towards no emotion. Before regenerating sentics-related vectors, the neutrality in the results was explained. Fig. 4.11 shows the dispersion of sentimental polarities over the three medical components, which helps in seeking the extreme positive values and extreme negatives, which can be used to manually verify whether false positives or negatives occur. The histogram in Fig. 4.12 shows the positivity and negativity of each component.

Experiments with different distributed biomedical methods and sentiment prediction DL-based algorithms were carried out. Our method shows the effectiveness of considering medication concepts in various situations. An exploratory data analysis is also offered for comparison lexicons. Here, we plot the statistical results for the AFINN model. The box plot in Fig. 4.8 shows higher inference positivity, while Fig. 4.9 presents a histogram showing the sentiment discrepancy over three drug-related discussions.

In addition, we visualize the positive and negative numbers in Fig. 4.13 and a clear indication of the variance behavior. For comparison, we applied literature baseline sentiment lexicons based on the embedding vectors we created. We have used five benchmark sentiment lexicons for the evaluation: (i) SenticNet: we aimed to evaluate our connotated vocabulary with both SenticNet 3 (Cambria et al., 2014), to evaluate the model ability to learn affective information of out-of-vocabulary terms, and SenticNet 6 (Cambria et al., 2020), to compare the overall polarities with a sentiment lexicon that considers other dimensions; (ii) AFINN: a word list for sentiment analysis for short microblog text; (iii) the TextBlob dictionary, and (iv) the valence aware dictionary and sentiment reasoner (VADER): a second rule-based benchmark sentiment analysis lexicon that is specifically attuned to sentiments expressed via social media and works well on texts from other domains. Table 4.10 summarizes these word-level benchmark datasets in detail. Although they are very effective, these methods have several limitations and need to be improved regarding sentiments for biomedical text. Indeed, the AFINN lexicon gives the largest absolute values, with high positive values. We find similar differences between the methods when looking at other metrics; the proposed sentic computing-based sentiment model is high and has more variance than AFINN and VADER. Table 4.6 presents all sentiments that appeared various times in finding long stretches of similar text, but all three methods agree roughly on the overall trends in the sentiments through the common shared narratives we obtained through our analysis. An explanatory summary is given in Table 4.7.

Furthermore, to ensure the effectiveness of our embedding generation, we conducted other experiments using two different sentiment lexicons, where three basic feature embedding strategies were used. As described in Table 4.9, each embedding feature plays a different role in sentiment determination. GloVe Twitter with a combined biomedical embedding generally performed much better than BioSentVec, which helped resolve noisy Twitter data and further gave meaning to the classification task. However, the proposed biomedical-based embedding clearly enhanced the sentiment inference, outperforming the evaluation techniques. Table 4.3 presents the polarity value of some tweets from the dataset groups collected.

Table 4.11 Statistics on over 9 Millions Tweets vs. Distributed representation of general scope data(Word2Vec-GloVe) and biomedical datasets

Emebeddings	setting of embedding		words analysis	
	Corpus	statistics	defined words	undefined words
Google Word2Vec model	google news	300dim	48931(12%)	331557(76%)
GloVe model	wikipedia	840B tokens, 2.2M vocab, cased, 300d vectors	79096(18%)	301392(69%)
BioWordVec model	PubMed+MIMIC-III	200dim Word2Vec bin format	87810(19%)	292678(66%)
BioConceptVec with CBOW model	PubMed and Pubtator auto-tagger	contain over 400,000 concepts 100dim	77853(17.6%	302635(68.5%)
BioConceptVec with Skip-Gram model	PubMed and Pubtator auto-tagger	contain over 400,000 concepts 100dim	77853(17.6%	302635(68.5%)
BioConceptVec with fastText model	PubMed and Pubtator auto-tagger	contain over 400,000 concepts 100dim	77853(17.6%	302635(68.5%)
BioConceptVec with GloVe model	PubMed and Pubtator auto-tagger	contain over 400,000 concepts 100dim	77853(17.6%	302635(68.5%)

4.4 Linguistic Gap Discussion

In this section, we discuss the importance of distinguishing biomedical components, their aspects, and their relationships in detecting sentiment orientation regarding social network dynamicity and the rapid progress of biomedical language. The poor performance of biomedical sentiment analysis on Twitter may be attributed to many challenging particularities of both tweets and bio-medical entities. Approximately twenty billion tweets are typed every day on varied topics. Distilling the hidden information faces many difficulties and challenges, including language diversity, brevity, shortness, acronyms, named entities, hashtags, emoticons, the frequent use of informal (nontechnical) medical language, nonstandard formats, and abbreviation forms, as well as typos in social network messages. Specifically, the brevity of tweets results in relatively few terms, which contributes to increasing the biomedical disambiguation complexity. The massive bio-medical entity citations, such as drug names, diseases, symptoms, and adverse drug reactions, remain unconsidered by existing tagging and entity recognition methods (Grissette and Nfaoui, 2019), which hinders understanding of patient assessments. Therefore, this may necessitate a level of biomedical text comprehension. Numerous learning approaches have recently been considered to overcome these limitations (as discussed in section 3.2).

Most supervised learning approaches are trained on a limited set of word features that result in traditional feature representation and typically diminish the model performance by ignoring other significant insights. Thus, these approaches focus on an individual word's

Table 4.12 Example of two different undefined words showing the weakness of BioWordVec to detecting related-drug information

Medical term	**Description**	**Other names**	**reference**
Creatine[8]	Creatine [9] is a chemical that is found in the body. an effective therapy for cancer, which in samples obtained by the NCI and the FDA consisted of creatine monohydrate in mineral oil.	Acetic acid, Cr, Creatin, Creatina, Créatine, Créatine Anhydre, Creatine Anhydrous, Creatine Citrate, Créatine Citrate, Creatine Ethyl Ester, Créatine Ethyl Ester...etc.	FDA[10](U.S. Food and Drug Administration) and NCI[11](National Cancer Institute).
Attenta[12]	Attenta belongs to a group of medicines called central nervous system stimulants. Attenta is thought to work by regulating certain chemicals in the brain, which affect behaviour and sleep.	Piperidine acetic acid, α-phenyl-, Ritalina, Rilatine, Attenta, Medikinet, Metadate, Methylin, Penid, Tranquilyn, and Rubifen ...etc.	Medicines [13]

sentiment value, which is independent of the context and insufficient in yielding a better feature subset and hence affects the classification accuracy. The performance of supervised learning depends on the quality data annotation or makes use of resources for weak supervision (Grissette and Nfaoui, 2020b) and results in a further lack of discriminatory tasks. In the bio-medical domain, these models result in inaccurate sentiment prediction performance. Unsupervised learning approaches result in irrelevant and redundant features. Additional techniques have been considered, such as N-gram techniques, to efficiently leverage language properties. Such techniques include (1) unigram methods used for corpus-based approaches, (2) n-grams for tracking syntactical aspects, (3) parts of speech, (4) POS tags, and (5) the information gain method, which is mostly used to reduce the number of features. These methods mostly result in a sparse feature representation with ambiguous polarity since some words may have different polarities regarding several contextual aspects. Some researchers have assembled various features from different methods to enhance the accuracy and recall performance (Gamon, 2004). For example, the authors of (Pang et al., 2002) merged various numbers of features, ranging from 3,066 features (a simple collection of unigrams from the General Inquirer) to 34,718 features (unigrams and bigrams), to boost system performance. However, they made their features completely independent of each other, and features beyond sentences are often corpus dependent, while this may not be the case for online corpora. For this reason, many contributions focus on extracting features from a sentence only by leveraging its definitional structure. Indeed, many previous methods generate features from sentence-based dependency parsing, which can reflect only part of the structure feature. Thus, in comparison with benchmark machine learning algorithms such as SVM, the SVM classifier performed worse than unigrams when using all bigrams as features instead of just the unigrams. The authors of (Elfaik et al., 2020) proposed selecting specific bigrams to improve the unigram baseline. The selection mechanism of unigrams, bigrams, and even 3-, 4-, and 5-grams can greatly improve sentiment analysis performance while reducing the modeling complexity, as noted by (Ghiassi and Lee, 2018). At the sentence level, most studies that use unigrams yielded better classification results than those of n-grams for domain-dependent use cases.

N-gram-based techniques have recently achieved remarkable progress in terms of enhancing representation features using neural networks. The most successful type of method is embedding. One possible solution is that we are most likely to focus on ways to improve embeddings of cognitive capabilities, as discussed in section 4.2.1. Indeed, we demonstrated the importance of processing and selecting n-grams in enhancing affective reasoning. In this section, we discuss some linguistic gaps confronted through bio-medical entity identification. For this purpose, we perform biomedical embedding comparisons in two cases: (i) a small dataset and (ii) a large dataset.

On a small dataset, utilizing BioWordVec as a large distributional biomedical space in the literature, more than 18 drug names in each dataset group were unrecognized. Approximately the same filtering rate was obtained using a Google Word2Vec pretrained embedding. Thus, the BioConceptVec model resulted in poor performance in detecting multiword medical components, and similar results were obtained for all the embedding versions used (CBOW, Skip-Gram, fastText, and GloVe). Otherwise, the GloVe model performed better; in this case, only 9 drugs were undefined because GloVe was trained on Wikipedia corpora.

On a large dataset, the evaluation was performed on 441,228 original tweets (with repeated tweets filtered out) from 9 million tweets collected in this study, with 407,578 total words. Table 4.11 summarizes the results we obtained after generating embeddings using various biomedical models. These models only captured some general medical concepts (such as cancer and tumor) because of the very large general-scope corpora they were trained on, such as Google News and Wikipedia. After the first filtering attempt, we identified 292,358 words ignored by the GloVe model. We found 79,096 (18%) words defined by the GloVe model and 301,392 (69%) undefined terms. We performed the same process using the Google model to identify general-scope words, and we obtained only 12% of the terms in the vocabulary. After a second filtering with the GloVe model, we identified 282,430 ignored words. A mean of 380,480 undefined medical bigrams was found, and in terms of medical unigrams, only 25.8% of all words were defined, with 74.17% of all words lacking embedding vectors. Even though we enriched the data and retrained the word embeddings, the semantically rich knowledge, contexts, and medical senses were lost.

The nonidentification of the full range of words is made completely clear by all the embeddings that we evaluated. BioConceptVec defined only 77,853 (17.6%) concepts, whereas 302,635 (68.5%) concepts were ignored. Although BioWordVec was trained on PubMed abstracts and the MIMIC-III clinical Database, it neglected much drug-related information, such as ['wcco', 'partnera', 'warna', 'unimelb', 'mcswan', 'creatina', 'ncdca', 'asu per', 'attenta', and 'tidak'], which were subsequently identified using BioConceptVec vectors. This inability is due to the multiple name types. Another significant challenge in terms of related word names is that a medical concept may be known by its commercial name and reported by its chemical name or vice versa. Each concept may have many names ranging from natural language concepts, commercial names (generic brand names), and chemical names to other spellings depending on the region or speaking culture. For example, methylphenidate drugs are referred to by many names, including Ritalin, attenta, Medikinet, and metadata, as discussed in Table4.12.

The semisupervised approach has great adaptability to domain-dependent challenges, offers more portable solutions across various domains and significantly allows domain transferability (Ghiassi and Lee, 2018) due to reusable feature-sentiment correlation across domains. Therefore, we deployed a transfer mechanism to obtain generalization benefits from corpora trained on very large datasets to obtain various biomedical components. Indeed, this setting is convolved to leverage knowledge from both the bio-medical domain and general-scope domains to overcome the constraints of limited training data in biomedical contexts.

4.5 Conclusion

Sentiment analysis is widely used for analyzing online patient-generated narratives. In this chapter, we developed an affective concept-based encoding method via neural networks and sentic computing. It relies mainly on biomedical semantic identification, which is investigated at three levels: (1) a contextual neural network, (2) an embedding matrix, and (3) a biomedical distributed representation obtained from comprehensive and controlled medical databases such as PubMed. Then, the natural medical concept semantic and sentic vectors are calculated. In addition, this chapter summarized a comprehensive state-of-the-art methods of the studies performed in various areas of biomedical sentiment analysis.

During the worldwide fight against COVID-19, we have suggested validating the proposed approach by analyzing COVID-19 narratives shared on social networks. Experiments have shown the effectiveness of considering biomedical concepts in analyzing medication-related texts. Indeed, the results have proved that integrating deep-learning-based cognitive capabilities enhances the biomedical sentiment analysis performance. In particular, our affective encoding approach outperforms benchmarks with statistically significant differences. Furthermore, the current work can provide meaningful support for biomedical sentiment analysis applications in social networks and can truly track patient status. It may also help researchers and professionals in many related discovery tasks, such as (1) inferring unknown side effects of possible drugs and treatments based on the formed embeddings, (2) clarifying the relationships among sets of drugs and conditions and situations to better clarify the "fakeness" or "genuineness" of a given medical fact, and (3) analyzing changes in health status or unexpected situations. In the next chapter, we will present a different manner to efficiently incorporate biomedical knowledge regarding online settings and learn and discover new patterns for unseen medical items.

Chapter 5

Deep Associative Learning Approach for Bio-Medical Sentiment Analysis Utilizing Unsupervised Representation From Large Scale Patients' Narratives

> *"The common question that gets asked in business is, 'why?'*
> *That's a good question, but an equally valid question is,*
> *'why not?'. "*
> —Jeff Bezos

5.1 Introduction

Owing to the quick spread of minute health-related experiences, the distillation of knowledge from such unstructured narratives is an extremely challenging task. In spite of the success of neural networks methods in improving learning structural reliability, they result in inadequate accuracy of the bio-medical sentiment classification when employing less useful features sets. Therefore, they lack discriminatory potential. In this study, we propose to add a deep associative memory into neural networks for an effective sentiment decomposition, which emphasizes correctly on bio-medical entities related to the extraction of different data-object properties, and contextual-semantics dependencies for a given aspect. The underlying trust of these measures is behind the ability to compute the completion of unseen medical patterns, where comprehensive bio-medical distributed representations are used for representing the formal medical connections from PubMed databases. Experiments on a biomedical sentiment analysis task show that the model provides comprehensive embeddings with meaningful medical patterns. It achieved an average performance of 87% on varied large online datasets. It also outperforms baselines in discovering and identifying medical natural concepts. We provide meaningful support to bio-medical sentiment analysis applications in social networks. Indeed, the facets of this study might be used in many health concerns such as: analyzing change in health status or unexpected situations.

5.2 Proposed Approach

A key problem in sentiment analysis is its sensitivity to the domain from which the training data originates or on which a sentiment lexicon is built. Existing pre-formed world knowledge provides insufficient context to reliably, determines the sentiment polarity and builds upon personal knowledge and understanding.

The design principle of our approach is to add approximate associative reasoning into neural network model for medication-related sentiment decomposition task. Let D be a collection patient narratives made up of N documents d_k, $k \in \{1:N\}$, heuristic sentiment intensity v_k which would be projected into the target space of three class labels, entitled **"POSITIVE"**, **"NEGATIVE"** or **" NEUTRAL"**. A given patient report d_k, $d_k \in D$ is formed by a set of m sentences $p_1, p_2, ..., p_m$. Each sentence p_j is a sequence of words $p_j = w_{j1}w_{j2}...w_{jl}$, where l is the size of p_j, the goal is to **(i)** extract medical patterns,**(ii)** project medical sentences into the distributional medical target space, and **(iii)** calculate their attached sentiments.

Meaningful learning involves in-depth knowledge of the context of the facts learned. This is particularly important for understanding the patients' experiences in the many contexts sampled in text. In particular, we ensure the credibility of our model comprehension by incorporating knowledge from formal biomedical ontologies and journals of life science. In different word-level abstractions, as depicted in Fig.5.3, we explore a basic knowledge transfer mechanism that studies both biomedical distributed representation and universal word representation. The system has been initialized in addition to the following predefined basic knowledge used to represent the connections of basic medical patterns connections, including Clinical Notes MIMIC III and PubMed database (Zhang et al., 2019b) Central PubMed resources (Chen et al., 2020) (More details are described in Section 2.4).

The proposed medical semantic network allows bidirectional associative memory to complement cognitive structures with sufficient meaning and drug-related semantics, as well as the sentential context in which it occurs. Thus, the combined word representation captures both distributional and compositional semantics to calculate attached sentiment. To formalize a medical new pattern, an input vector x_k associated with pattern vector y_k is used to calculate the corresponding associative memory by summing the total related pattern experiences of learning W_k (depend weights matrix). Second, a convolutional component is used to deploy associate features and leverage properties of data objects effectively complete patterns. The entire architecture is illustrated in Fig. 5.2. To sum up, our approach attempts to create a related medical configuration space that focuses on harnessing both sentimental and biomedical associations through unsupervised neural network associative memories.

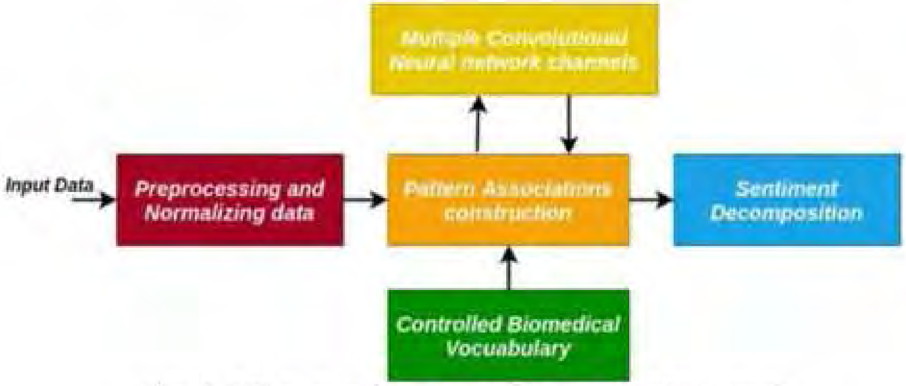

Fig. 5.1 The overall process of the proposed approach

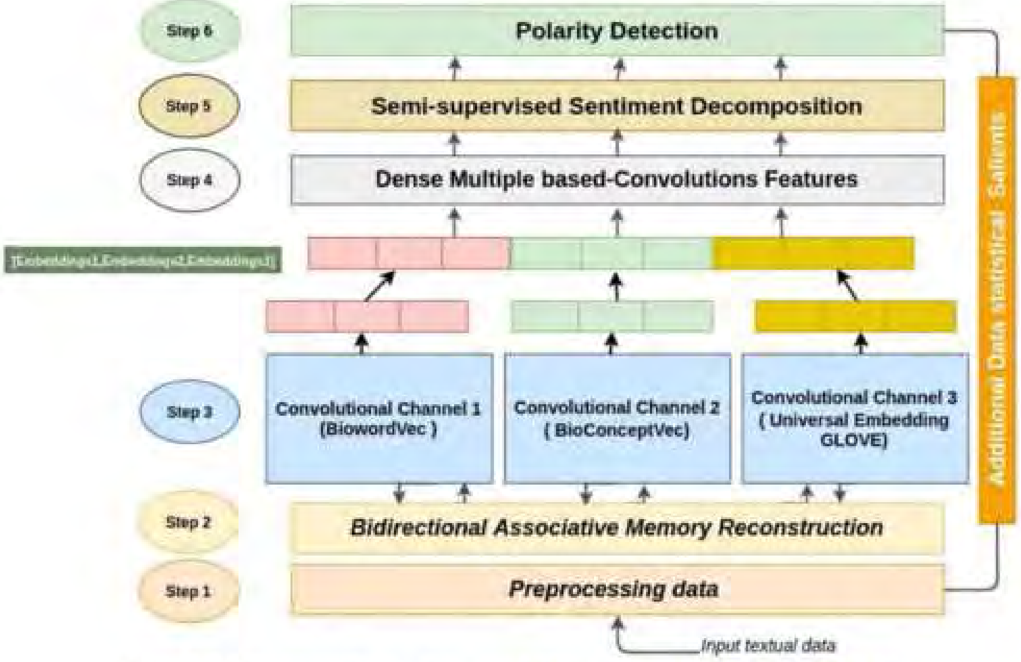

Fig. 5.2 The overall architecture ((Grissette and Nfaoui, 2021a))

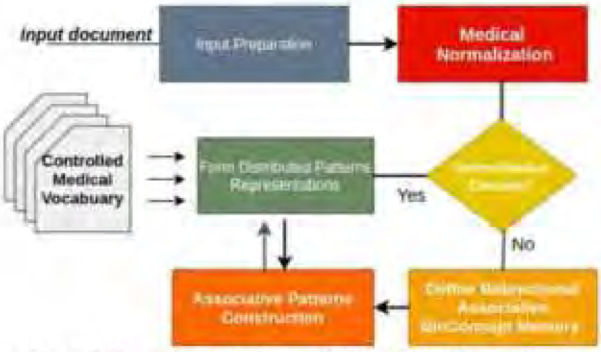

Fig. 5.3 Illustration of the construction of distributed patterns representations

5.2.1 Deep associative neural network model

Deep learning typically uses non-dynamic feedforward neural networks[1]. Truly distributed representation methods can capture various arbitrary aspects of the word depending on certain contexts as well as the semantics on the words. But, they are limited in relating and defining domain-dependent models and neglect incomplete (ambiguous) definitions and concepts such as the definition of drug reaction. Thus, standard embedding representations can lead to huge and deeper memory, as well as simultaneous and repeated recall of similar memory contents.

This article examines these questions by deploying neural associative memories and additional theory of collective memory, including generalization ability, familiarity recognition, categorization, error correction, and temporal sequence retention (**?**).Our motivation behind using associative memory is that it allows us to store a much larger number of pattern and memory associations. In this work, we aim to add other salient points to (i) address the relationship between different properties of data objects and medical concepts and (ii) define the two models that link one model to another (hetero-associative memory) through bidirectional memory and also associates a pattern with itself (auto-associative memory) or by convolution with the corresponding medical pattern. This philosophy provides a model with the ability to recover missing medical models. When it comes to the huge shared patient experiences, a simple neural associative memory model fails to meet the text requirements of drugs, and dealing with complex data at scale on social media has been crucial because most associative models are not reported. Since the Convolutional Neural Network (CNN) is a feedforward neural network with convolutions and parameterizable targets, it has a special spatial-local correlation by enforcing a model of local connectivity of pattern between neurons in adjacent layers, where associative memory algorithm retrieves patterns more than the number of neurons (Zhang et al., 2018).

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[1] http://meetings.aps.org/link/BAPS.2017.MAR.P5.9

The algorithm 1 illustrates the typical computational goals discussed above. Associative memory is distributed in nature, this assumption is at the origin of the execution of storage mechanisms for a large number of models. A normal associative memory task is to test participants on their recall of pairs of unrelated items. Given an input vector x_k associated with pattern vector y_k, we build memory space formalism by summing the total pattern experiences of learning W_k(weights matrix). Each pattern structure is convolving m-neurons that are associated with the synoptic weights matrix to define the exact retrieval pattern, where m is the number of defined patterns fed to the network. Indeed, the exact retrieval aspect from the pool of memories, as shown in the algorithm 2, is calculated in the recursive form of the associative memory, and the associated weights concerning the pattern itself are strongly estimated. This means that we involve data entry and exit to retrieve the associated weight matrix, which each time passes to recalculate the output of unrelated medical phrases or correct associative links.

Algorithm 1: Auto-associative neural network algorithm

```
Result: Set of associated patterns $x_i : c_i$
Initialize the weights $i = 1$ to $n$ and $j = 1$ to $n$; $W_{i,j} = 0$ ;
for Each vector $x_i$( to be stored) do
    Set activation for each input Unit and Output unit respectively:
    for $i = 1$ and to $n$ do
        $x_i = s_i$
    end
    for $j = 1$ and to $n$ do
        $y_i = s_i$
    end
    for $i = 1$ and to $n$ and $j = 1$ and to $n$ do
        W = $\sum_{p=1}^{n} S^T_{(p)} S_{(p)}$ ;
        activation vectors following Eq5.1;
        $W_{new} = W_{old} + x_{i,j}$(Adjust the weights)
    end
    ;
end
```

$$x_i = \begin{cases} 1 & \text{if } \sum_{p=1}^{n} w_i x_i > 0 \\ x_i & \text{if } \sum_{p=1}^{n} w_i x_i = 0 \\ -1 & \text{if } \sum_{p=1}^{n} w_i x_i < 0 \end{cases} \tag{5.1}$$

Algorithm 2: Testing and recorrecting associative neural network algorithm

```
Result: Set of associated patterns $x_i : x_i$
for input $x_i = s_i$ do
    $W = S.S^T$ (Find the weight Matrix);
end
while well activated do
    - Test the I/P vector with one mistake in the input vector.
    - Test the network with one missing in the input vector.
    - Test the network with two mistake in the input vector.
    - activation vectors following Eq5.1
end
```

As shown in the Fig.5.2, we propose to design a related concept abstraction through multiple convolution channels that mainly deploy a distributed biomedical representation. Each channel generates a feature vector in which the powerful properties are summarized, and also stores and completes ambiguous patterns. This joint model used the potential of CNN in patterns extraction to powerfully create local and deeper dense associative representation maps, and help process/memorize data at scale. Where the components of convolutions manage scarcity and reduce dimensionality through the downsampling step.

As deep learning increases learning ability with massive layer parameters, training difficulty and error rate increase respectively. Many contributions have been proposed to reduce errors and effectively build deeper networks with regard to the associative property of patterns. To this end, (Krotov and Hopfield, 2016) has provided reliable storage and definition of many more models through dense associative memory learning techniques. We explore this method which consists of feedforward neural networks with one hidden layer and various activation functions to analyze the computational properties of neural networks.

5.2.2 Modelling Sentiment Decomposition

Neural network methods have seen huge distributions, where they have mainly deployed embeddings features to track sentiment information. But, by taking these approaches to getting sentiment insight from patient self-reports on social media, get as slow as desired accuracy as the model has no knowledge of medical entities. We propose to deploy both the approximate modeling obtained in the previous steps and the approximate reasoning for the composition of feelings, this improved our chances of clarifying the intensity of sentiments from large complex data. We have developed a semi-supervised sentiment scale which consists both in exploiting associations of embeddings and in incorporating lexical and semantic relationships between SentiWordNet[2] and SenticNet[3]. Table 5.3 summarizes the statistics and the level of automation of these.

In addition, SenticNet has also been adopted to improve the accuracy of sentiment classification on Twitter by extracting sentiment indicators from natural language texts at the syntactic and semantic levels, is called Sentic Computing, which aims to bridge the gap between statistical processing of natural language and many other disciplines. necessary to understand human languages, such as linguistics, common sense reasoning, and affective computing. Where Sentiwordnet has been used for the sake of disambiguation of meaning, which explores the semantic knowledge of WordNet (Fellbaum, 2010), WordNet can therefore be seen as a combination of dictionary and thesaurus.

As Algorithm 3 highlights, the generation of an adequate sentiment lexicon consists in defining the sentimental aspects integrated in three stages:

- **Step(i):** Reassemble the embeddings in two organized groups using K-means, typically, we group the vectors in two separate contexts and semantics according to the definition of embeddings.
    - group(1): Positive or positively connected semantics.
    - group(2): Negative semantics.
- **Step(ii):** Inspect the sentiment coefficient by approaching the minimum proximity distance through positive or negative semantics. At each sentiment dimension, each sentiment word will take value between -1 and $+1$ (-1 is extreme negativity and $+1$ is extreme positivity) by element-by-element multiplication as follows: $sentiment_{coef}*Cluster_{polarity}$. Where the cluster of positive semantics has a polarity value equal to $+1$, otherwise, negatives -1.
- **Step(iii)**: The words of sentiment composed note the average of the lexicons summarized in the Table 5.3 to the formalism's initial sentiment rate matrix. we used the internal product of the rate matrix and the elementary vectors from step (ii) to define the sentiment score at the word level.
- **Step(iv)** : Define a sentiment scale between the words for each semantic group and matrix composed by simple element-by-element multiplication.

---

[2] http://SentiWordNet.isti.cnr.it/

[3] https://sentic.net/

Algorithm 3: Semi-supervised sentiment lexicon generation algorithm

```
Data: dictionary of words and their indices
Result:  Dense Embedd Sentiment value of combined vectors([Cluster])
Input:
$n_x$: Size of vocabulary
$l$: embedding dimension
$W \in \mathbb{R}^{l*n_x}$: embedding Matrix
$n$: refers to positive and negative classes.
iter:max iterations of Kmeans.
init:Method for kmeans initialization.
polarity: +1 positive semantics, - 1 negative semantics.
distances: a set of value between 0 and 1 resumes distances from each class centroids.
$coef_s$: sentiment coefficient from semantics induction. Compound Matrix: Matrix
  $C \in \mathbb{R}^{m*n_x}$
m: max length of predefined lexicons
model: KMEANS model $\langle n, iter, init \rangle$ that fit defined embeddings.
for Each vector $x_i \in W$ do
    if $x_i$ in $cluster_0$ then
        polarity = +1;
        distances = $\frac{1}{\min_{words,cluster_0} distances(x_i)}$;
        $coef_s$=polarity*distances;
    else
        polarity =-1;
        distances = $\frac{1}{\min_{words,cluster_1} distances(x_i)}$;
        $coef_s$=polarity*distances;
    end
end
for $i=0$ to $n_x$ do
    $O_i$= OneHotEncoding(Data.indices[i]);
    $compound = O_i$*C;
end
return $[coef_c, compound]$
```

Table 5.1 Statistics of Twitter data sets regarding main aspects used for the development and evaluation

Main aspects	**Number of tweets**
Epilepsy	20192
Parkinson's Disease	208419
COVID-19 pandemic	489302
Heart Attack Disease	390291

Table 5.2 Baselines models for Medical Sentiment Analysis

Model	**Vocabulary**	**Trainable params**	**Accuracy**
BiLSTM	Universal Emebddings (Free-context)	22112	[0.6 - 0.75]
LSTM	Universal Emebddings (Free-context)	12932	[0.6 - 0.72]
RNN	Universal Emebddings (Free-context)	11932	[0.5 - 0.68]
CNN	Embeddings with GlobalAveragePooling1D	68573	[0.5 - 0.7]
SVM	Universal Emebddings		0.638

5.3 Experiments and Output Result

5.3.1 Data sets

In our exploration system, raw tweets are collected through the Twitter APIs. For the collection of targeted Twitter data we use a list of keywords, e.g. epilepsy, Parkinson's disease and HeartAttack. Table. 5.1 summarizes the statistics of tweets based on the context of a medical concept. However, the data is very noisy, as social media posts relieve various natural language concepts such as the spelling of many related medical concepts, everyday expressions, excessive use of abbreviations, acronyms and alternatives, and incorrect medical spellings. The main most crucial challenges are as follows: (1) There was no guidance on how to distinguish between various related drugs meanings such as drug misuse or abuse and legitimate use in collected tweets, (2) patient reports may refer to an unsuspected drug reaction, which deserves great awareness to detect, and (3) the intentions of users when they report problems.

Textual data may require a credible annotated system to clarify medical knowledge and cover the truth about the patient's status. The standardization of the medical concept required massive efforts to cover important aspects. It should be noted that there are many recent distributions offering annotated benchmark data sets for analyzing medical sentiment, but it had been built into the local window of the predefined set of drugs or diseases, for example, eDisease (Carrillo-de Albornoz et al., 2018) Annotated a set of over 3,500 posts on online health forums about breast cancer, Crohn's and different allergies, respectively. Each sentence in a message is manually labeled as "experience", "fact" or "opinion", and as "positive", "negative" and "neutral". In this study, we proceed through word processing steps which

Table 5.3 Summary of two a priori benchmark dictionaries used for sentiment lexicon generation algorithm

Lexicon	Description	Statistics	Automation level
SentiWordNet (Baccianella et al., 2010)	SentiWordNet is an opinion lexicon derived from the WordNet database where each term is associated with numerical scores indicating positive and negative sentiment information.	117 000 synsets are linked to other synsets according to their degrees of positivity, negativity, and neutrality.	Automated
SenticNet (Cambria et al., 2014)	Common-Sense-Based knowledge for concept-level Sentiment Analysis, which is automatically constructed by applying graph-mining and multi-dimensional scaling techniques.	It associated with more than 50,000 natural language concepts through a multi-disciplinary approach.	Automated

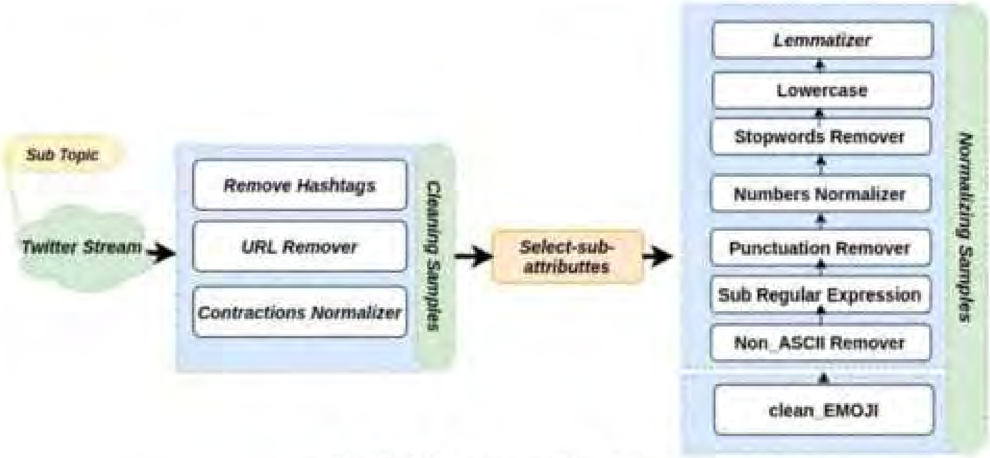

Fig. 5.4 Preprocessing steps

consist of tokenizing, cleaning and normalizing the data in relation to the identification of the biomedical concept to enter into our neural network architecture, as illustrated in Fig.5.4.

5.3.2 Implementation and Output Results

In this section, we go through the steps and parameters for implementing the architecture. The proposed joint model of multiple CNN channels joins both concrete biomedical definitions and a deep dive into the downstream task of associative memory processes to define new associations from real-time medical patterns. Therefore, these features will be input into the sentiment generation algorithm to derive an aspect-based sentiment decomposition with an additional statistical salients to accurately approach sentiment. We aim to prove how we embed our own from a large-scale unsupervised representation for learning affective associations related with these embeddings on top to analyzing two grams or three grams using convolutions. It works even faster than traditional word-bag and part-speech representation techniques.

Our use case scenarios focus on how a large amount of unstructured data from online health forums characterized by the details of patient treatment. This study has been validated on many crucial bed cases: epilepsy, Parkinson's disease, heart attack, etc. It consists of an automatic online method that generates efficient sentiment-related features, identifies and stores natural patterns of drugs linked to various patient spaces. So far, our sentiment analysis model uses the encapsulated sentiment, context, and semantics information differently to parameterize new drug concepts by downstream deep associative memory methodology.

The results of our experiment show that the improvement of joint biomedical distributed vectorization helps to identify formal associations of medical structures from real-time data. These abstractions range from lower level nodes representing the building blocks of discrete word associations to complex data such as concepts of multi-word medical associations. Pattern associations and representations would be learned through multiple convolutional connections between hidden layers, backpropagation, and a set of concatenated feature layers running on learning rules and other processes used in classical conditioning.

In terms of embeddings, as described in section 3. we seek to transfer the formal format of biomedical controlled vocabulary from pre-trained distributed. Biomedical ontologies and formal medical resources, such as PubMed, the MIMIC III clinical database and Central PubMed. it is mainly consulted in the processing of medical concepts distributed in natural language to better correspond to the formal semantics of a widely used controlled biomedical vocabulary. For each input sequence $[x_1, x_2, .., x_m]$, we propose to imitate embedding vectors for a predefined configuration. Another slightly better approach is to use 1D convolutions to update and recalculate the embeddings we described in section 3.1. Each CNN channel formed separately, in particular, the deep neural associative memory model, we further use backpropagation, inspired by (Liu et al., 2019), and form the corresponding convolutions, to define patterns of related concepts, which the neural network needs to store the matrix of related concepts in the memories Matrix for each concept, respectively.

Our proposed model involves three different convolutional components. Each component consists of a flatten layer and a global average pooling 1D. The reason is the size of the output vector introduced into the dense. Or, we used a 1D Global Average Pooling, which averages over the vector to flatten it. Over 15 epochs with an overall average pooling, we got an accuracy of 0.738 on training and 0.81 on test, which takes about 5 seconds on average per epoch. With many convolutions, my precision is 0.83 and my validation is about 0.43. We use the varied size of the filters so that we can capture the optimal parameter, and we also use unigrams, three, four, and five grams, and for each n-gram. We're obviously applying denser layers and actually applying multilayer positron on top of those 300 embeddings and forming it.

we use convolutional networks not only on words, but also on multi-word expressions inserted in the vocabulary each time. As known in the literature, this mechanism works best for large datasets where it beats traditional approaches like a bag of words. And surprisingly, sometimes it even beats LSTM which works at the word level. Finally, we exploit the embedding scheme for sentiment scale generation to use additional statistical highlights. Our statistic-based sentimental scale is formed for each distinct word on a corpus by incorporating lexical dictionaries discussed in section 3.2. both for the gain of disambiguation annotated by the senses and the imitation of natural medical concepts. We also tend to improve our above n-gram training with the TFIDF matrix regarding social media data. Additional functionality, most of the time, requires additional statistical features to credibly re-weight the weights of the social media regarding associated sentiment.

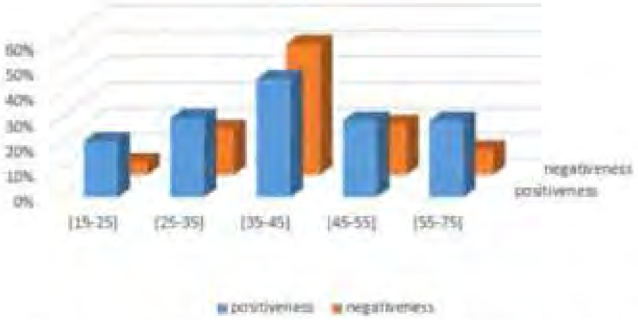

Fig. 5.5 Positive and negative statistics with regard to different ages living medical conditions

5.3.3 Evaluation and Assessment of the Quality of Patient Messages on Twitter

We present and discuss, from several different perspectives, the evaluation results of state-of-the-art deep learning algorithms (LSTM, BiLSTM, SVM, simple RNN, linear regression) utilizing our embeddings-based model for bio-medical sentiment analysis task. These models have slightly different results from Twitter models, where SVM does well in this case. The model based on stacked-LSTM and BiLSTM has consistently improved

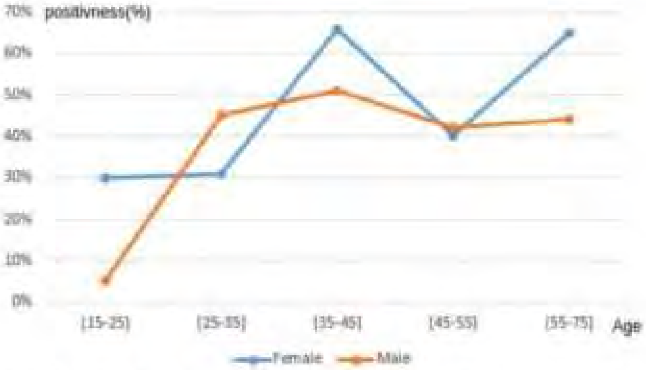

Fig. 5.6 Female/Male switch positiveness and negativeness distribution in various experiments datasets (regarding age axis)

Table 5.4 Embedding evaluation using two Bio-medical pretrained embeddings. (1) Hybrid convolutions from [16] and [19] (2) Joint convolutions from [16] and [19]

Dataset	Embedding strategy	Accuracy(%)
Small dataset	**Proposed strategy**	**84%**
	Hybrid Convolutions of biomedical distributed from (Zhang et al., 2019b) and Bioconcept(Chen et al., 2020)	73%
	Joint Convolutions of biomedical distributed from (Zhang et al., 2019b) and Bioconcept(Chen et al., 2020)	81%
Big dataset	**Proposed strategy**	**87%**
	Hybrid biomedical distributed from (Zhang et al., 2019b) and Bioconcept(Chen et al., 2020)	77%
	Joint biomedical distributed from (Zhang et al., 2019b) and Bioconcept(Chen et al., 2020)	79%

sentiment classification performance, but is effective when we leverage the proposed setup on a large online dataset.

However, it should be noted that if we replace tokens with n-grams and train on small datasets, which is 1D convolutions architecture with MLP in addition to these features, then we could get a huge 3.8 bumps in accuracy and this increases accuracy to over 87 percent. we end up learning deeper representations. Table 5.4 provides an overview of the results obtained and classical models, and on a small training set, then it makes sense to use classical approaches. As much as we fed more data, we assume to associate deeper representations.

Evaluating the sentimental process involves using different sets of data in different contexts. we compared the LSTM and the convolutional architecture that we presented in the section 3.1. In addition, we make a comparison of different datasets, the statistics of Twitter datasets were made in the table .5.1, the approach actually beats BiLSTM on huge datasets and performs great on all datasets. This gain is slowly established in terms of the definition

Table 5.5 The experiments results and comparison of our proposed sentiment generation approach with the baselines SVM, Simple RNN, Bi-LSTM, and Stacked LSTM ((Grissette and Nfaoui, 2021a))

Dataset	Algorithms	Positiveness(%)	Negativeness(%)	Accuracy
Epilepsy	SVM	31 %	26%	0.66
	Simple RNN	45 %	16%	71.3
	BiLSTM	63 %	31%	**0.83**
	Stacked-LSTM	33 %	27%	0.80
Parkinson's Disease	SVM	31 %	26%	0.61
	Simple RNN	45 %	16%	71.3
	BiLSTM	63 %	31%	**0.84**
	Stacked-LSTM	33 %	27%	0.75
COVID-19 pandemic	SVM	31 %	46%	0.69
	Simple RNN	36 %	26%	70.9
	BiLSTM	33 %	**61%**	**0.81**
	Stacked-LSTM	41 %	37%	0.79
Heart Attack Disease	SVM	31 %	26%	0.68
	Simple RNN	31 %	16%	72
	BiLSTM	63 %	29%	**0.87**
	Stacked-LSTM	41 %	37%	**0.83**

of medical regimens, the convolutional approach is in fact very surprising. These deep approaches work much better than traditional approaches. we have degrees by mistake of about 12% to 7%. Another important result, as highlighted in Table.5.5, is that the percentage of positivity and negativity changes from algorithm to algorithm, meaning that context and semantics potentially control the orientation of sentiment in a given plain text. Where **pandemic related-posts** got huge negativeness quantification most times due to the living crisis, where the pandemic period is widely known by tremendous patients 'narratives on social networks, characterized by vigorous activities.

though testing model, we observe the necessity of multi-properties analysis, it is been proceeded by an explanatory analysis. Those observations hold when controlling for age, income, education, ethnicity, and overall health status through all of which are also associated with doing health-related activities online. Especially, varied linked concepts are fortunately dependent on other conditions and properties such as non-SUDEP, SUDEP, SUDI (Sudden unexpected death in infancy (SUDI) is the name for the sudden and unexpected death of a baby), DUDC (Sudden unexplained death in childhood). Fig.5.5 shows an explanatory analysis that has been done regarding age property, where Fig.5.6 illustrates how results change with regard to sexual property.

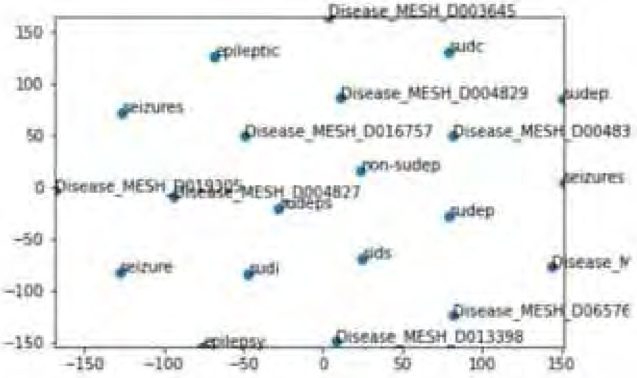

Fig. 5.7 SUDEP Related-concept in the configuration space ((Grissette and Nfaoui, 2021a))

Table 5.6 Statistics in term of various sudep significant senses, and positivity and/or negativity appearance in the configuration space

Concept	Sense	Description	freq	#pos	#neg
SUDEP	Medical complication	sudden unexpected death in epilepsy.	550	350	110
	Epilepsy SUDEP awareness	sets healthcare services and Benefits	208	120	66
	SUDEP Institute	Awareness and education services	115	88	5
	SUDEP Action	for raising awareness of epilepsy risks and deaths	298	104	58

5.4 Discussion

Refers to Fig.5.7, it shows related-medical concepts of SUDEP (sudden unexpected death in epilepsy) concept through configuration space we proposed earlier. We notice that SUDEP appears three times in different positions or configurations. Each time, this concept has different embedding that clearly resumes such semantics and contextual information, but disambiguate reference and associations with real-world namely entities or medical concepts. Moreover, Table 5.6 summarizes results regarding various SUDEP significant senses, which is further needed to be taken into consideration.

In general context, current accuracy is difficult to state without a host of medical concept abstraction caveats accuracy. Sentiment Analysis model consists of many folds, accuracy at supervised sentiment classification for both binary and fine-grained level is routinely above 90%, especially, with neural networks algorithms on particular benchmarking datasets achieving over 96%. On finer-grained sense distinctions, top accuracy range from 59.1% to 79.0% have been reported in recent evaluations from SemEval and Senseval, where the baseline accuracy of the simplest possible algorithm of always choosing the most frequent sense was 51.4% and 65%, respectively. Comparison has done on very large patient narratives datasets, as explained in the dataset's section, between a model with Naive Bayes on top of one and two grams, and those classical model gave 86.3 accuracies. The proposed neural network associative memory estimated current value based on linked patterns values, we are ambitiously aiming at defining deep associations regarding the combination of features-sentiment, in order to showcase the flexibility of the neural word sense disambiguation, and further improve its performance.

Although very effective, these results have several limits and need to be improved, regarding the daily massive shared patients experiences, a dynamism property must be considered respectively to time property. It is substantially very important at time-dependent detecting the minute sentiment information relationship covered towards a set of drugs or events, e.g., Drug reaction, persons, medical adverse events.etc. Thus, it would be interesting to consider other attributes such as user credibility, harmness rate, and helpfulness rate for accurate patients personalisation and high responsiveness.

5.5 Conclusion

Online conversations are becoming huge, especially patients or their families are mostly wading through vast amounts of "social noise" looking for treatment second options, disease groups, patient/doctor insights, and more. This distillation of knowledge due to the massive amounts of unstructured information available, is of considerable importance for bio-medical sentiment analysis tasks. While existing approaches are limited by the fact that they fail to correctly extract bio-medical entities, events, and contextual senses.

In this research, we investigated a distributed associative learning through multiple convolutions to build a dynamic configuration space from unsupervised medical concepts representations. Thus, these embeddings from this joint model are used for accurate sentiment decomposition. Extensive experiments demonstrate the promise of our work. In particular, results showed a significant improvement in bio-medical natural concepts recognition and their attached sentiments.

The findings of this study can be useful for many researchers and health professionals to efficiently analyze patients' narratives in real-world living scenarios. Also, it contributes to a better understanding of patients' experiences and defining the public health status, outcome or effectiveness of a treatment.

One of main model weaknesses is interpretability aspect deficiency regarding patient-centric targets,which make use additional information such as age, sex, psychology status. As a second important aspect in such form of analysis is to consider other attributes (user credibility, harmness rate, helpfulness rate, and time) to further improve the performance of deep learning models for bio-medical sentiment analysis.

Chapter 6

Drug-Related Concept Identification and Drug Reaction Extraction

> *"No amount of experimentation can ever prove me right;*
> *a single experiment can prove me wrong. "*
>
> —Albert Einstein

6.1 Introduction

Every day patients' narratives on social media can reveal crucial public health issues. Mining those online narratives, that remained so far unconsidered, may mirror further hidden health-related issues such as drug issues. In particular, they are widely used to automatically report treatment issues, drug misuse, new infectious disease symptoms, etc. Few approaches have been proposed in this matter, especially for detecting different drug reactions or drug events descriptions from patients' generated narratives on social networks. Most of them consisted of only classifying adverse drug reactions (ADRs), but may fail to identify other aspects such as untreated indications, improper drug selection, sub-therapeutic dosage or overdose, adverse drug reactions, drug interactions, failure to receive drugs, and drug use without indication, and the beneficial drug reaction or drug retroviral effects such as "relieve intraocular pressure associated with glaucoma" (Grissette and Nfaoui, 2020c,b,a). Thus, the frequent use of informal medical language, non-standard format, wrongly spelled, and abbreviation forms, as well as typos in social media messages prevents the identification of drug-related components. As a result, the inaccurate recognition of drug related entities may seriously fail to retrieve the relevant affect expressed, leading to a lower recall than desired. The first part of this chapter aims to analyze word representation taxonomies in the context of medicine by analyzing word-level distributions. Following the construction and detailed analysis of such a resource, a series of machine learning experiments study the impact of different models, features, and review types on the problem. These experiments examine the applicability of the selected methods to improve model reliability and leverage the different conceptual and contextual distributed insights by incorporating unlabelled data into the training process from online examples. The embedding gain is discussed, compared, and improved regarding phenomena setting which also incorporates data from highly controlled medical vocabularies, leading to a new hybrid model. The second part proposes n-gram convolutions vocabulary scheme, dedicated mainly to featuring text under medical setting and clarifying related sentiment. This vectorization results in highly drug-related data objects extraction, which produces medical concept normalization under distributed dependency. This architecture's layers are a shared neural network between the medical featuring channel and the bidirectional sentiment information detector channel. Fewer approaches proposed in this matter, we evaluate the effectiveness and transferability of this study across five benchmarking datasets and various online medication-related posts (Twitter posts, Parkinson's disease forum discussions), which was significantly better than all other baselines.

6.2 Embedding Techniques Comparison: A Corpus-Based Case Study of COVID-19 Drug-related Reviews

6.2.1 Constructing Embedding in the Case of COVID-19

Social networks become an extensive source used to automatically report treatment and drug issues. Few approaches have been proposed in this matter, namely multi-word medical concepts identification and drug-related descriptions that denoted vast connections for understanding patients shared experiences. In particular, the pandemic period widely known by tremendous online generated patients narratives, characterized by hyperactivity, unprecedented dynamism to the global virus-fighting, and spreading massive medication-related information e.g. commonly drugs used and their minute reactions. Numerous medical entities' citations and medication-related reports are effectively and semantically associated in different contexts. Moreover, the frequent use of informal medical language, non-standard format, wrongly spelled, and abbreviation forms, as well as typos in social media messages prevents to clearly tackle bio-medical entities. Therefore, this chapter explores the problem of mutual forms of drug interactions including beneficial drug effects.

Moreover, as many examples of based-deep learning sentiment services are becoming highly reliable, few approaches succeed to analyze medication-related narratives and seek relevant affect insights towards complex medication components such as drug effectiveness distinction. They broadly focus on grammar directions such as semantic direction or only center on extract sentiment words, which provide both richer representation capabilities and better performance but do not consider the related medication concepts. As a result, the inaccurate recognition of drug related entities may seriously fail to retrieve the relevant affect expressed, leading to a lower recall than desired.

In this chapter, we seek to improve the importance of considering drug related entities that keep appearing in new Unicode versions ranging from drugs' names, Diseases symptoms, drug misuse to potentially adverse effects. The taxonomy of word representation is proposed and discussed, which improves model reliability and leverages the different conceptual and contextual distributed insights by incorporating unlabelled data into the training process from online examples. The embedding gain is discussed, compared, and improved regarding phenomena setting which also incorporates data from highly controlled medical vocabularies, leading to a new hybrid model. This typically requires more attention to the aspects and contexts regarding varied medical targets such as treatments, conditions, symptoms, and drug events. So too we argue that primary natural medical language understanding toward specific aspects has to be considered as intrinsic settings for medical vocabulary development. Indeed, natural medical concepts processing, from online generated narratives; has been a mandatory step to better match formal semantics from a widely used biomedical controlled vocabulary. This is specially provided in the context of semisupervised aspect-based learning for sentiment analysis. In this study, the proposed taxonomy, in conjunction with formal medical definitions and contexts learned from bio-medical knowledge (distributed models from Pubmed such as BioWordVec), improves model reliability and leverages the different conceptual and contextual distributed insights by incorporating unlabelled data into the training process from online examples. We focused on seeking data in real-time that is tailored to considering tweets as documents by inspecting reviews of living medication-related cases, Table 6.1 Summarize online datasets from varied platforms used for both training and model developments. The qualification of the proposed taxonomy for sentiment inference has been examined through many experiments on various datasets groups.

In order to seek unknown medical definitions and normalized terms/names, we used RxNorm [1] to seek differences between drug-related terms that look similar but have different meanings in order to save the correct meaning for a given string from a particular source. It offers normalized entities of a given drug with corresponding attributes such as links and common names predefined in varied pharmacy management and drug interaction software and vocabu-

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[1] https://www.nlm.nih.gov/research/umls/rxnorm/docs/rxnormfiles.html

Table 6.1 Summarize Online Datasets from varied platforms used for both training and model developments

Plateform source	#Posts	keywords used
Twitter	256703	Chloroquine, Corona, Virus, Remdesivir, Disease, infectious, treatements,COVID-19
Facebook	48572	COVID-19,Chloroquine, Corona, Virus, Remdesivir, Disease, infectious, treatements
Quora	3748	Chloroquine,COVID-19 Corona, Virus, Remdesivir, Disease, infectious, treatements

laries. These medical vocabularies are used as additional entity context vectors for clarifying medical semantics on and regular basis. In this context, relationships are created between all concepts and unique names, which are further exploited for each string with multiple meanings. Our distributed medical vocabulary is organized by concept or meaning, which are reconstructed to be semantically associated and assigned at least one semantic type from the Semantic Network.

6.2.2 Evaluation and Comparison

As social networks platforms is used to express and share public experiences, we validate the proposed taxonomy by applying formal representations on sentiment classification fine-tuning tasks using datatsets from Twitter, Facebook, Quora posts. This chapter presents a semi-supervised embedding taxonomy that incorporate a comprehensible medical vocabulary, which improves model reliability. It used for leveraging the different conceptual and contextual distributed sentiment intensities. The experimental results shows the effectiveness of the proposed taxonomy to comprehend useful insights from online medication-related texts. The challenge, however, is to respond to both the requirements needed for developing extensible sentiment analysis model and defining what data should be collected to get enough information for analysis purposes/targets. The finding of this study is that we can derive automatically conclusions from presented data and use for real industry case. The experiments executed consider the language in which the messages are written, emoticons, mentions, and the length of texts.

Collectively, these shared experiences contain highly unstructured data combining medical components, multi-word medication related expressions for drug interactions and events.etc. In addition, the use of informal medical language, descriptive, nontechnical/nonstandard format, and abbreviation forms, as well as misspellings Grissette et al. (2017) requires a level of biomedical text comprehension. The pre-processing is a mandatory step for cleaning different components and help network to recognize them. As depicted in Fig. 6.1, highlights ensemble steps for gathering and pre-processing tweets for COVID-19 case study.

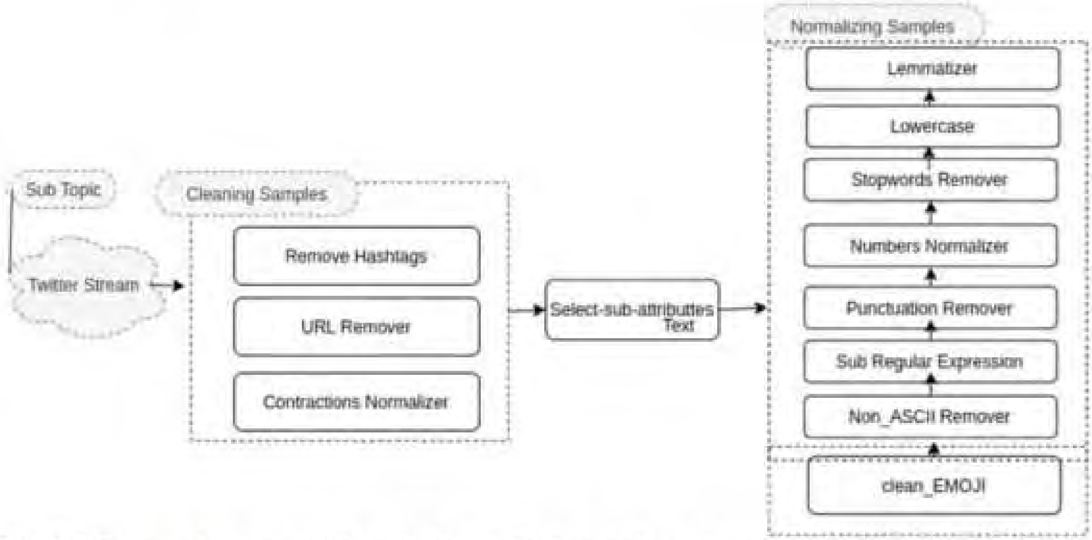

Fig. 6.1 Summarizes ensemble steps for gathering and pre-processing tweets for COVID-19 case study Grissette and Nfaoui (2019)

We streamed data regarding a set of keywords and topics. Then, raw data are stored to a set of files regarding various medical components(keyword) and time axis; we focused on associated criteria of chronic conditions, symptoms and medication-related concepts. Moreover, these samples were passing by a set of normalization and processing steps to be able for our neural sentiment inference model. Indeed, every single post in our dataset consists of a separate document that memories long-established dependencies and semantics of varied medical and pharma data-objects. Table 6.1 presents statistics of each datasets with regard to platform source.

As author in Li et al. (2017) demonstrates the efficacy of integrating a prior sentiment knowledge in the embedding process, in this study, we discuss which the best knowledge, parameters, layers are efficient to boost model ability to learn medication-related affective associations.

We conducted various experimentation originated from the application of the proposed method; a dynamic conceptualization is released. Thus, an aspect-based sentiment assessments has been examined through experiments on three online datasets from various plateforms. An extensive evaluation of different features, including medical corpora, neural network algorithms. Varied deep learning algorithms are used to build sentiment classifier and enhance the distributed representation regarding their attached sentiments. Stacked-LSTM and BiLSTM model are successfully and consistently well-inferred the conveyed sentiment, but it is less efficient when we have exploited drug-related presentations on a big online dataset, as shown in Table 6.2. As discussed before, we conduct development vocabulary scheme to enhance the effectiveness and transferability of embedding vectors across various online medication-related posts, which the obtained representations significantly succeed the sentiment inference model and performs better than all other baselines. In addition, Glove or FastText got in very slow results, where Biomedical distributed vocabularies enhance inference performance. Both combinations shows a clear improvements and additional understanding of medication-related entites, especially BioWordVec vectors and BioConceptVec that helps to cover drug-names and their meanings. Finally, the sentiment contribution leveraged to summarize and generate a sentiment value for each vector. Table6.2 presents experiments results using a real Twitter datasets, comparing these results with the traditional biomedical embedding methods highlighting the benefits and the effectiveness of assumptions considered in this study.

6.3 Enhancing Convolutions based Sentiment Extractor via dubbed N-grams Embedding Drug-related Vocabulary

6.3.1 Proposed Ensemble Models

We propose a deep learning-based architecture dedicated mainly to identifying drug-related concepts from a text on social media and link them with the corresponding UMLs metathesaurus concepts and other medical knowledge. More specifically, we compiled an exhaustive list of ADR/drug Concepts and their corresponding UMLs IDs, including Concepts from DrugBank Dataset. First, we probe the translation-based approach between patient's language used in social media messages and formal medical language used in the descriptions of medical concepts in standard ontologies. Second, medical concept normalization under distributed dependency has convoyed for drug-related conceptualization at the level of sentence pair. This architecture's layers is a shared neural network between the medical featuring channel and the Bidirectional sentiment information detector channel.

Medication Knowledge-related Normalisation and Modelling

Patients and health consumers are storming medication-related experiences intentionally on Social media. A Rich and high dimensional data has a wide variety of medical concepts and medical facts that require well-encoding approaches to exceed sentiment analysis performance successfully. However, the traditional system treats words as discrete atomic symbols linked to sentiment score, and therefore are encoded them as unique representation and provides no useful sentiment-related information to the policy regarding medical concepts,

Table 6.2 Evaluation of proposed sentiment feature framework with existing embedding strategies Grissette and Nfaoui (2021)

corpus-based dictionary	**sentiment dictionary**	**Algorithm**	**Embeddings**	**Accuracy**
Twitter Datasets	Our vocabulary	BiLSTM	Our embeddings framework	**0.85**
		BiLSTM	BioWordVec +BioConceptVec	0.71
			BioWordVec	0.52
			BioWordVec +GloVe	0.69
			BioSentVec+ Twitter GloVe	0.70
			BioWordVec +FastText	0.66
		LSTM	BioWordVec +GloVe	0.62
		CNN	BioASQ3 +GloVe	0.67
		Stacked-LSTMs	BioWordVec +GloVe	0.67
		SVM	BioWordVec +GloVe	0.47
	SenticNet Cambria et al. (2020)	BILSTM	Our embeddings framework	0.68
			BioWordVec +BioConceptVec +GloVe	**0.70**
			BioASQ3 +GloVe	0.56
			BioWordVec +GloVe	0.59
			BioSentVec+ Twitter GloVe	0.65
			BioWordVec +FastText	0.60
		Stacked-LSTM	BioWordVec +GloVe	0.69
		CNN	BioSentVec+ Twitter GloVe	0.62
Quora Forum	Our vocabulary	BiLSTM	Our embeddings framework	**0.86**
			BioWordVec +BioConceptVec	0.69
			BioASQ3 +GloVe	0.62
			BioWordVec +GloVe	0.64
			BioSentVec+ Twitter GloVe	0.65
			BioWordVec +FastText	0.66
	SenticNet Cambria et al. (2020)	BiLSTM	Our embeddings framework	**0.71**
			BioWordVec +BioConceptVec	0.55
			BioASQ3 +GloVe	0.61
			BioWordVec +GloVe	0.60
			BioSentVec+ Twitter GloVe	0.63
			BioWordVec + BioConceptVec +FastText	**0.65**
Facebook	Our vocabulary	BiLSTM	Our embeddings framework	**0.87**
			BioWordVec +BioConceptVec	0.79
			BioASQ3 +GloVe	0.71
			BioWordVec +GloVe	0.72
			BioSentVec+ Twitter GloVe	0.72
			BioWordVec +FastText	0.76
	SenticNet Cambria et al. (2020)	BiLSTM	Our embeddings framework	**0.79**
			BioWordVec +BioConceptVec+Glove	0.70
			BioASQ3 +GloVe	0.66
			BioWordVec +GloVe	0.59
			BioSentVec+ Twitter GloVe	0.53
			BioWordVec +FastText	0.62

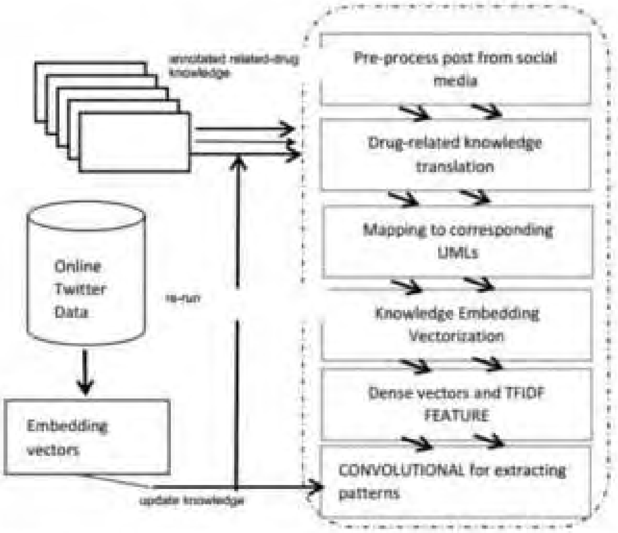

Fig. 6.2 The proposed process to create drug-related vocabulary patterns.

their semantic, and their context. Meaning, SA model is leveraged very little of what it should learn about the sentiment expressed towards medication-related concepts as a target of analysis such as abstracts or drug effects.

More specifically, the frequent use of informal language, non-standard grammar, and abbreviation forms of medical concepts, as well as typos in social media messages, are the most challenging task and have to be taken into account. As illustrated in the Fig. 6.2, we focus on developing a practical and specific batch normalization approach. Though, this task of medical concept normalization aims at mapping a variable features length from social media message to a medical concept in standard external coding of standard ontology regarding the semantic level, which further co-occurs in varied contexts by different manners. Another central idea in this process is constructing online meta-concepts by convolving a convolution to define formal vectors to new concepts.

Drug-related Social Media Corpora

There are few corpora of drug-related knowledge from patients generated narratives on social media; choosing the proper combinations of corpora of drug-related knowledge has a vital role in exceeding sentiment analysis. We choose five benchmarking corpora as the medical resources for both training, evaluating, and testing.

1. The first corpus[2] is for mining drug-related knowledge from Twitter chatter (Sarker and Gonzalez, 2017) consists of 267,215 Twitter posts made during the four months.

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[2] http://diego.asu.edu/Publications/Drugchatter.html.

The posts mention over 250 drug-related keywords. this corpus is used to generate several distributed word representations in this context.

2. The PsyTAR[3] dataset (Zolnoori et al., 2019), ThePsychiatric Treatment Adverse Reactions contains 891 patients' drug reviews. Each review labeled for the presence of Adverse Drug Reaction(ADR), withdrawal Symptoms(WDs), Drug Effectiveness (EF), Drug Indications(DIs), Sign/Symptoms/ Illness(SSIs), Drug Infectiveness(INF), and others.

3. The DrugBank[4] database with 1,440 drugs and 248,146 drug-drug interactions.

4. The SMM4H[5] corpus (Sarker et al., 2018b), social media mining for health monitoring and surveillance(SMM4H) is a large corpus for medication-related text classification and concept normalization. this corpus trained on Twitter data, and deal specifically with many linguistic variations and semantic complexities in various ways people express medication-related concepts and outcomes.

5. The ADRMINE[6] ADR Corpus (Nikfarjam et al., 2015b) from patient drug-related mentions on Twitter, a corpus for Drug concepts and bio-concepts extraction that has been built based on machine learning system which uses conditional random fields (CRFs). the corpus's method utilized a variety of features for modeling words' semantic similarities.

Drug-related Patterns Translator from Social Media

The Existing of an adverse drug reaction(ADR) candidate in-text may seriously fail to retrieve the appropriate sentiment expressed, leading to a lower recall than desired. The problem of ADRs detection on social media is clarified through several specific tasks such as: Searching for related literature on available medical knowledge. The most prior successful ADR detection methods are based on a sequence-labeling approach that mainly employs conditional random field (CRF). Indeed, CRFs limited by the scope of their input, where the model considers only the target word and its neighboring words within a fixed-width window. Therefore, they could exclude important information mentioned more distantly (Cocos et al., 2017). Recently, Deep Learning methods have played an increasing role that exceeds ADRs detection performance from patients generated narratives. Most of these methods have been

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[3] https://sites.google.com/view/pharmacovigilanceinpsychiatry/home.

[4] https://www.drugbank.ca/releases/5-1-5/downloads/ all-full-database

[5] http://dx.doi.org/10.17632/rxwfb3tysd.1

[6] http://diego.asu.edu/Publications/ADRMine.

Table 6.3 Summary of based neural network ADR detection and prediction methods on Social media

Algorithm and Vectorization Scheme	Medical Knowledge Used	F1-measure
Supervised Sequence CRF ADRMine with CNN-RNN model (Nikfarjam et al., 2015b)	Side Effect Resource (SIDER), Consumer health vocabulary(CHV), The Coding Symbols for a Thesaurus of Adverse Reaction Terms (COSTART)	0,72
Bidirectional LSTM for Labeling Adverse Drug Reactions (Cocos et al., 2017)	Twitter ADR Dataset, Twitter Word2vec, and the labeled ADHD dataset	0,75
Social Media Mining for Health monitoring and surveillance(SMM4H) based CNN, and SVM algorithm (Sarker et al., 2018b)	15 717 annotated tweets for adverse drug reactions (ADRs),10 260 for medication consumption, from medication-mentioning tweets, 6650 ADR phrases and identifiers.	subtask-1: 0.435 , 0.693 for subtask-2, and 88.5 % for subtask-3. Ensembles of system combinations obtained best scores of 0.476, 0.702, and 88.7%, outperforming individual systems.
Phrase-based Machine Translation (P-MT) (Limsopatham and Collier, 2016b)	CNN-RNN method that automatically identifies medication-related mentions regarding medical conditions contexts and translates social media text to formal medical language.	0.81% on AskAPatient Dataset,TwADR-S and TwADR-L datasets(0,45).

used Word Embedding Features (Nikfarjam et al., 2015b) as inputs for RNN or CNN model. According to table 6.3, a combination of pre-trained embeddings increases the accuracy of pre-trained word embedding, which further proves their role in mining adverse drug reaction mentions on social media.

As illustrated in section 3.1.1, we focus on creating a hybrid vectorization scheme based on a combination of medical knowledge for better retrieving the correspondence format of drug-related concepts on online posts. we proceed by many steps, as shown in Fig. 2 to enrich the vocabulary by daily life drug or treatment discussions.

The overall process is exhibited in Fig. 6.3. As depicted in this figure, our proposed architecture convolved in many joined channels as follows:

(i) The Main Model is dedicated to translating ADRs and drug-related knowledge from texts, and map them to embedding corpora in order concatenate embedding features for each concept. Then we apply convolutions to learn patterns through the predefined corpora. Technically, the medication-related text is prepared by considering a sequence of individual documents for getting Multiple meanings/context regarding sentiment information. A hybrid vectorization scheme is designed to both struggles with the correct format of the

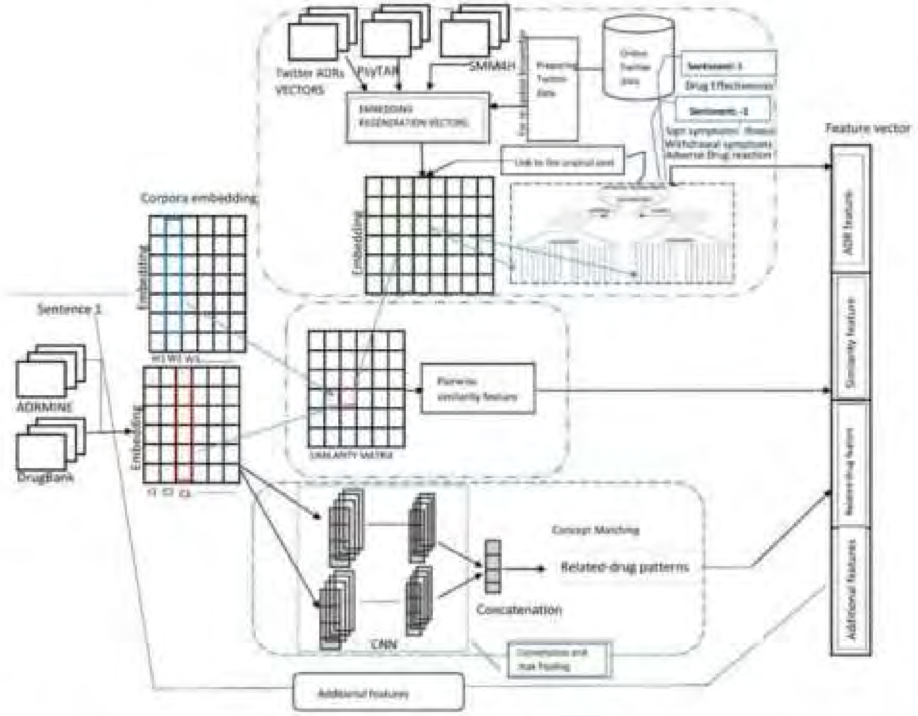

Fig. 6.3 The proposed based-translation model for ADRs and drug-related knowledge from texts.

medical concept based neural network transition approach and embedding regeneration on document-level.

(ii) Online Twitter Data normalization is assessed by incorporating and executing an external medication-related knowledge and data systems to empower our medical concepts recognition model. We extend this point for defining similarity values for undefined medical concepts. Next, the convolutions based transition method for identifying medical expressions on social media texts such as ADRs by learning semantic representations, we approach this step by extending a phrase-based machine translation for ADRs corpora from social media. Meaning, a transition between the patient's language used in social media messages and formal medical language used in the descriptions of medical concepts in a standard ontology. We enrich this step by updating corpora by Learning from online data and correcting format from the first data system.

(iii) On document Level, an Embedding regeneration is performed to track the various possible context of the conceptualized vectors. There are different Embedding approaches.

Fig. 6.4 An Example of Tweet Posted on 2019-05-26 at 13:56:37.864000.

Both are creating documents vectors; one approach would be GLOVE, which works on word-level that we adopt it to work on document-level as a sequence of words by leveraging word vectors. On the other hand, another predictive approach, e.g., doc2vec, is widely used for creating documents vectors.doc2vec presents many disadvantages in our case, is performed unique representation, discrete ids that leads to data sparsity. Both perform similarly well, but Glove trains a little faster, it would be enriched with TFIDF feature that considers the frequency of such medical concept to measure the effectiveness or damage. Another advantage is leveraging the strength of medical concepts literally co-occur in various contexts regarding sentiment information.

The main alternative is constructing meta-words embeddings by initializing the embedding matrix by vectors predefined by GLOVE as a supervised classification problem, the pre-trained count-based method of Twitter GLOVE [7] dataset with vectors of 300 dimensions (Pennington et al., 2014b). Indeed, we imitate the Glove weights of tweets that show up in our training vocabulary and used for tokens in every tweet. We perform the closest vector inside the matrix by measuring the cosine distance of Glove vectors for each token is outside this embedding matrix, which would leverage as an additional feature. This method will improve our network by learning embeddings of documents also when we feed our normalized online twitter data instead. Besides, the input is a set of vocabulary words, which is further sentimentally labeled through the next channel.

Since the number of contexts can be large, it factorizes the matrix to get a lower-dimensional matrix of tweets, which represents words by features. The novelty in this step is the embeddings documents save sentiment information for each context, counts how frequently it sees it in the same context. As shown in Fig. 6.4, possible ADRs expression translated to the formal medical language used in the descriptions of medical concepts in a standard ontology(Sarker et al., 2018b).

The whole process is shared between the medical concept normalization model and the Embedding technique, and the output holds the concatenation of all features vector. We map results down to a small, dense vector for each document. We would mainly be able to identify exact duplicates, unsuspected medical concepts, and facts such as undefined ADRs

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[7] //nlp.stanford.edu/data/glove.twitter.27B.zip

or infectious diseases by making practically online rich information useless for tracking gaps. Given a fake supervised task, predicting sentiment-related information based on their similarities. We assigned sentiment score to each medical concept. A low sentiment value (-1) implies negative autocorrelation because we mapped the expressions of prohibited negative medical facts(such as ADRs mention, WDs mention, DIs mentions, sign, symptom, ILLness(SSIs) mention, or Drug Infectiveness(INF) mentions) with very negative sentiment. The difference between them is relatively small. A high value (1) for a positive flag, for example, sentences contains Drug Effectiveness(EF) mentions. We finally update All entities Linked to the original posts where we assume that tweet contains ADRs firmly classified as a negative post. Technically, after translating medical concepts from the text. We added to previous vectors of labeled datasets we used. In the next step, sentiment scores of each word are extracted from all lexicons and will normalize them. If a word doesn't exist in any dictionary, its score will be calculated from very similar concepts' score. The generated vectors from the last step will be concatenated with other vectors from previous levels.

Pairwise ADR and Drugs Similarity Matching

A pairwise similarity matrix is used to detect whether a given candidate pair of text conveys the same drug-related knowledge. The element-wise difference computed between these semantic representations to get the discrepancy measure. Meaning, convolution is used to learn the patterns of pairwise semantic resemblance and are applied to the similarity matrix to define unit-to-unit similarities. For the given pair of l1-length Sentence S1 and l2-length Sentence S2, S1 and S2 is represented by embeddings vector. The Fig.6.5 illustrates this process.

To compute this semantic discrepancy measure, we define the similarity matrix with the size of l1xl2 via embedding vectors of the pairwise units of our medical knowledge, by computing cosine similarity between the matched-pairs of units. A similar pair of units has to be compared to every unit vector in the matrix with all the unit vectors in another one we use. We approach this step by creating a convolutional neural network that consists of 4-layers. We first define the possible correspondences between corpora vectors, by one-dimensional convolution cross-correlation with n-input channels. The outputs of the last convolution layer are fed into a k-max-pooling layer, which extracts the top k most important features and gives it into Flattened layer to leverage them, which computes a new adapted K value for each iteration.

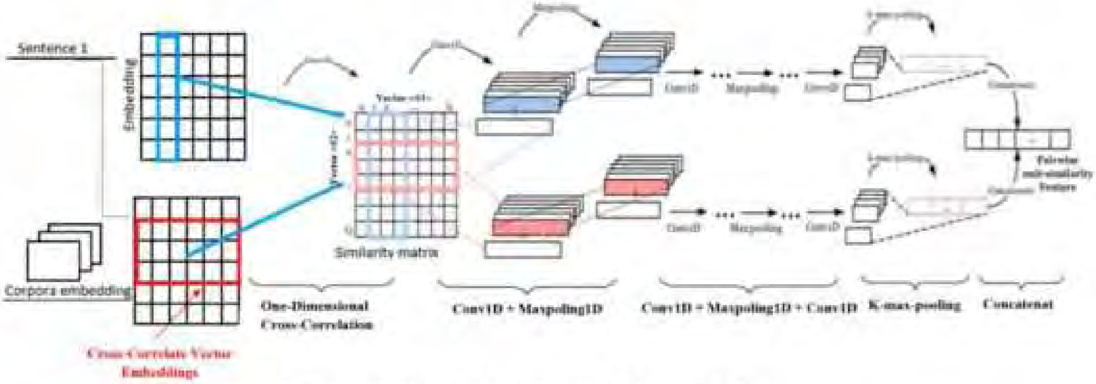

Fig. 6.5 Pairwise Similarity Measure Process

Sentiment Feature Generator for Drug-related Concepts

Despite the abundance of English sentiment lexicons, analyzing sentiment in such depend-domain such as pharmaceutical/medical domain suffer from lack of such resources. Limited progress on automated medical concept extraction approaches from the medication-related text, which relies on sentiment information. Moreover, many based Machine Learning contributions have also resulted in sparse space with no sentiment information insights. As patients, self-report experiences are growing up on social media, describing all incredible details of their treatment procedures, the importance of such semantic and sentimental density does as well. The sentiment modelling problem is at the core of many sentiment analysis tasks that involve a degree of medical language comprehension. Our goal is to dub a dynamic sentiment learning process to identify relevant keys of real emotions expressed toward a specific medical entity regarding daily usages.

It is evident from the above discussion, and we need to dive further deep to comprehend the sentiment, Since sentiment expressed towards drug-related targets rarely observed or not observed at all. In this step, we propose to apply convolutions on online data that rely mainly on the pairwise similarity matrix discussed in section 3.1.2. Meaning, the sentiment is mainly dubbed on the obtained vocabulary, which relies on minute online twitter data to meet the changes which are far higher than of today than ever. An essential task after extracting concepts, and the phrases indicating the drugs is to discover the sentiment-related relations among such concepts and sentences, especially those that characterize ADRs, or the cause of the ADRs.

A third based-cluster model is proposed that derives sentiment features at both sentence-level. Technically, the vocabulary assembles for each new subword, and the subword was assigned a vector containing the standard statistical features overall dimensions and terms of the space, when the term may convey different sentiments in various contexts. Indeed, annotators are usually uncertain about the total sentiment value of a given condition, and we approach this step by incorporating an embedding regeneration that serves to identify sentiment regarding Multiple Meanings or contexts. We construct a large matrix of subwords by the framework that discriminates positive or negative sentiment regarding online shared information, medication-related expressions, and the embedding relationship between all terms in the space.

Existing sentiment lexicons unconsidered many related-medical concepts, that fail to retrieve the real expressed sentiment. In this study, we proceed to clarify and compute the sentiment score, especially for the undefined medical subword. In which we fix the similarity window of a given concept(we randomly choose the size). In the first step, we randomly fix n similar concept in both negative context and respectively for positive class. Then, we proceed with three main steps discussed in section 3.1.4 to retrieve the score based on the medical annotation and semantically matching. The sentiment rate is based on three statistical features:

- TF-IDF weight for each word/phrase in the space.
- sentiment-related embeddings value generated within the translation process.
- pairwise similarity matching between words in the same class.

To assign which class is relatively positive and which is negative. We consider initial quantification in terms of cosine similarity; n-grams sequences are weighted by how they close to each other. Then we properly use TFIDF scores of each word in each sentence to consider the unique every word appear in various contexts; a simple dot product is used to indicate the sentiment average. Next, new coordinates of every class are calculated, as the mean of coordinates of all data points assigned to each centroid, and iterations are repeated till reaching a minimum value of the squared sum of distances between points awarded to classes.

Sentiment Classification Model

The traditional approach used to summarize sentiment intensity is to consider the text as a combination of its words and get the quantity of sentiment with the utilization of additional resources such as sentiment dictionaries or ontologies, thesauri, and multiple-polarities corpora.

Where, sentiment intensity usually quantifies in a binary fashion, which assigned a high score to the positive polarity and low score to negative polarity (GRISSETTE Hanane NFAOUI EL

Habib, 2017). The problem that these resources quantify sentiment in non-depend-context and do not fit with medication-related text. Otherwise, lexicon-based approaches can achieve excellent performance. Still, they often require large amounts of annotated samples, which are expensive to build due to the requirement of domain annotation experts, especially in the medical context due to high knowledgeable surfaces. Otherwise, the hybrid vectorization previously described in section 3.1.2, results with a minute embedding representation tied with overall sentiment orientation of the tweet that leveraging the strength of convolutions-based medical vocabulary regarding sentiment information. That means, our proposed architecture is carrying of sentiment expressed regarding drug-related concepts in the text, and the number of dimensions (emotions) is lexicon-dependent. At the same time, for each size, a given term can be scored either in a different way by using a specific rating scale.

Besides, we aim at sparsely figuring out the way of how people express emotion regarding medication and patient's backgrounds by memorizing how sentiment changes over experiences under varied medical conditions. We also focused on exploring contextual and semantic connections of the previously conceptualized vocabulary, and detect the relevant features saving the relationship between them. There are different ways we can approach this architecture, e.g., Recurrent neural network(RNN), but the problem with Simple Deep learning algorithm is the inability to build long-term dependencies and packageable stories. Indeed, one approach is exploring sentiment-related vocabulary based on the characteristics of bidirectional LSTM. Another essential aspect of learning is the attention mechanism, which allows deciding what the most relevant data to memorize regarding the sentiment value it has is.

We point at summarizing sentiment-related vocabulary regarding relevant components to be computationally efficient for predicting the conveyed sentiment. The model would be divided into two parts: (1) BiLSTM Sentiment Learning and (2) attention mechanism. The contextual sentiment quantity will be effectively leveraged through the BiLSTM Sentiment Learning step when a re-released summarization will be done in the second step. The Embedding sentiment-related Matrix is fed into BiLSTM Sentiment Learning layers to efficiently build a memorable story that able to understand sentiment information regarding various medical concepts and remember the context behind the sequences.

6.3.2 Results and output data of the study

The ensemble Models constructed on two levels: target based-features level and based-sentence embedding Level. Our goal relies on building a meta-concepts vocabulary concerning: (i) internal semantic and sequential properties, (ii) the conceptualized drug-related representation for online posts. Which is considered a bidirectionally mapped of the obtained encoded features map in the sequence that is fed as input into the BiLSTM network. The memorizable long-term dependencies learned by the RNN become the semantic representations regarding expressed sentiment.

Data acquisition

Uncounted gigabytes of information pour into healthcare pages and micro-blogs at a staggering rate. We chose to apply our regeneration vectors strategy on a sample of online-drug-related posts from social media under the proposed medical sittings, which is discussed in Section 6.3.1. More specifically, in this section, we present the results obtained by applying the proposed methods on both Twitter data and patients' self-reported messages on other healthcare forums. The experiments executed consider the language in which the messages are written, the number of texts analyzed. We have created two web crawlers that collect posts involved in cancer, Heart attack, epilepsy, and Parkinson's disease contexts.

Twitter Data: Twitter is the most popular micro-blogging that attracted millions of users to share and disseminate the most up-to-date information; that why we focused on this study to train our ensembles models using twitter data. Every single tweet in our corpora is considered as a separate document that saves the life of correlate information contained regarding medical and pharma objects.

Message from Parkinson's Disease(PD): Most of the PD communities are of public access, where PD's patients and their families pour essential information about their daily problems and treatments. In this chapter, we ingest both Parkinson's related messages from the Michael J. Fox Foundation forum, to prove the efficiency of data on forums that remained more details concerning drug and treatment vs. disease.

Experiments Settings and Training Corpora

To review, in our implementation, the proposed corpora generated on four-phases : (1) Matching Drug-related concepts based on the pairwise measure discussed above. (2) a translation-based conceptualization approach between patient's language used in social media messages and formal medical language used in the descriptions of medical concepts in standard ontologies, as described in Section 2.4. An embedding generation based-phrase performed in this phase. (3) convolutions conveyed to explore and learn the pattern and assign initial sentiment value. In the end, (4) additional statistical features have been added to the last feature vector.
Besides, Each dataset exhibited typical properties of social media-based health-related texts.

For example, the Social Media Mining for Health (SMM4H) corpora mainly provided high annotated and normalized adverse drug reactions (ADRs) expressions from medication-mentioning tweets. In our case, it has been used for large-scale evaluation of automatic medication-related posts for the classification and normalization. We varied several parameters, including training data sizes, vector sizes, context window size, and which sequences occurrences assigned to a positive class or negative class. as Fig.6.6 and Fig.6.7 illustrate. Even Though the training shows better learning of opinionated terms regarding the context in the healthcare sphere, the learning regarding context per sentiment-polar cluster proves the effectiveness of assessing or judging sentiment information properly through features generation as described in Section 3.1.4.

Results

In the following section, we conducted many experiments derived from the application of the proposed hybrid vectorization ensemble models. However, our approach was unique because our training data was automatically created and updated to extract minute related-medical features on fresh communication. It combines both annotated tweets and real-world online polar tweets in the context of medical information. Then a sentiment predictor Model-based-BiLSTM approach is constructed concerning the word usage under medical setting and distributed sentiment.

The proposed architecture achieved good performance regarding the medical, pharmaceutical sphere, and potential use cases. Indeed, the extraction of complex medical concepts automatically encoded with relatively good performance, from informal user-generated content to formal medical settings. Thus, our approach is particularly scalable, suitable for modeling efficient sentiment-related vocabulary from online social media data, as it relies on large volumes of unlabeled data. Thus diminishing the need for large annotated training data sets for training sentiment classification model.

We have tested our approach on five different deep learning and machine learning algorithms, and we conducted an online evaluation. A sample of 2807 drug-related reviews on the online healthcare forum of Parkinson's disease, was collected and prepared to enrich the vocabulary. For twitter, we gathered more than 15000 tweets that fed into the network for updating drug-related knowledge from real-life experiences. We have further conducted many experiments on various twitter datasets at different times.

A comparison is also conducted between our proposed model and other pre-trained embedding vectors. We have created four models based on different Embedding approaches, which both are creating word vectors. Both perform similarly well, but Glove trains a little faster.

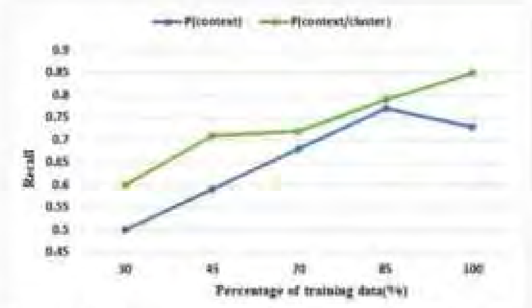

Fig. 6.6 Recall vs. Training Data Percentage regarding context, and context per cluster Respectively

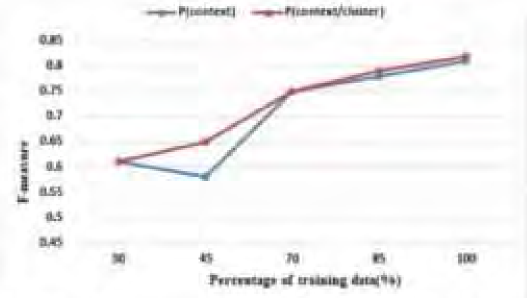

Fig. 6.7 F1-measure vs. Training Data Percentage regarding context, and context per cluster Respectively

Twitter word2vec, in this case, is performed unique representation, discrete ids that lead to data sparsity. The first two models are based on pre-trained distributed vectors such as :

1. Improved pre-trained Glove Twitter embeddings: we trained our model by using another improved Glove Twitter vectors (2B tweets, 27B tokens, 1.2M vocabulary in 200 dimensions vectors) as initial embedding matrix for our dictionary from online Twitter training data. Then we copy all the Glove weights of tweets that show up in our training vocabulary. For every subword outside this embedding matrix, we approach this step by mapping the closest tweet vector.
2. Improved pre-trained Twitter word2vec vectors: is Word2Vec predictive neural language model of 400M Tweets Embedding model. We also extend the pre-trained vectors under the healthcare setting, which apply and identify vectors for complex medical language; this task presents several exciting challenges, including the noisy nature of the data, the informal style of the user posts, misspellings, and data imbalance. It has been shown in past research that frequently underperforms when exposed to medication-related text because of the presence of different medical phrases and misspellings, and frequent use of idiomatic, ambiguous and sarcastic expressions toward specific drugs, treatments, or drug events.

We evaluate the proposed hybrid vectorization scheme on two training modes (1) by context,(2) and by context per sentiment assessment, which further compared with the described word embedding representation schemes above. As proved in Fig.6.8 presents the sentiment-related value of a set of concepts that seem in the closest context of "medication" opinionated terms, and more specifically in terms of drug effectiveness. Feature format showed as $< subword, sentiment\ value >$. We initially compared the sentiment intensity in the three distributed representations. In particular, the proposed hybrid vectorization

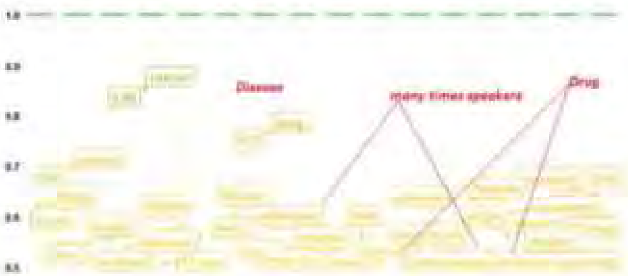

Fig. 6.8 The sentiment-related value of a set of concepts that seem in closest context of "medication" opinionated terms ((Grissette and Nfaoui, 2020b))

Table 6.4 A comparison of 'medication' subword sentiment-related obtained and other baselines (GLOVE,Word2vec) in term of drug effectiveness

Main Model(Proposed Vectorization) $< subword, sentiment\ value >$	**Model-1 (Glove vectorization)** $< subword, sentiment\ value >$	**Model-2(Word2vec vectorization)** $< subword, sentiment\ value >$
$< drug, 0.7703089 >$	$< addiction, 0.057389 >$	$< antidepressant, 0.544389 >$
$< cancer, 0.8507389 >$	$< troubles, 0.007389 >$	$< medication, 0.645889 >$
$< asthma, 0.5700389 >$	$< king, 0.557389 >$	$< cancer, 0.02089 >$
$< dealer, 0.892389 >$	$< web, 0.603885 >$	$< patients, 0.156689 >$
$< treatment, 0.584389 >$	$< weather, 0.604829 >$	$< anticonvulsant, 0.725589 >$
$< vitalin, 0.703389 >$	$< cancer, 0.157389 >$	$< safer, 0.837409 >$
$< cancer, 0.073555 >$	$< traffic, 0.173849 >$	$< trial, 0.603826 >$

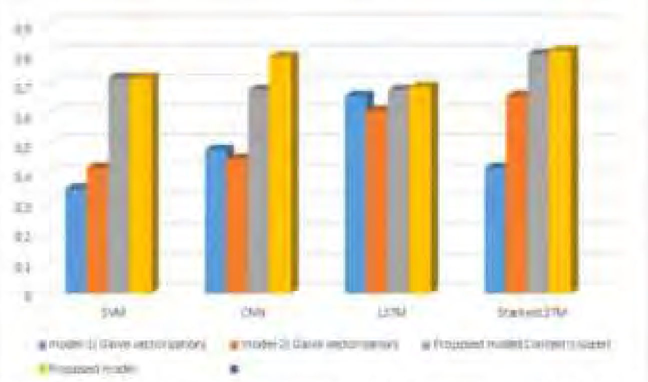

Fig. 6.9 The accuracy(%) comparisons of different models For Twitter Data

proves the ability to perform varied sentiment intensity regarding Multiple contexts about the obtained medical setting.

At Table 6.4, we illustrate how sentiment scores of some typical medical related-words are identified regarding varied medical cases. As noticed vector 'cancer' seem many times with various sentiment's score, especially it appeared in negative polar facts as so as positive facts.

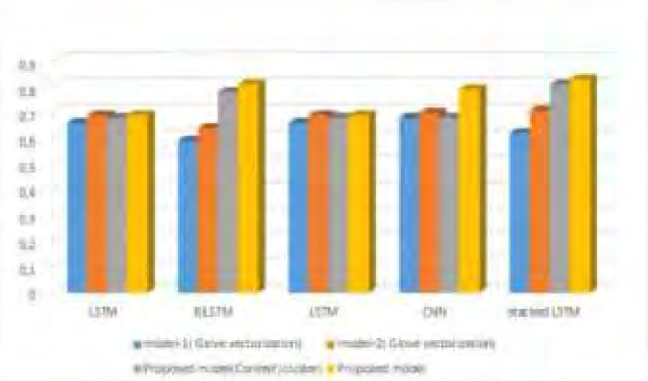

Fig. 6.10 The accuracy(%) comparisons of different models For Forum Parkinson's disease Data

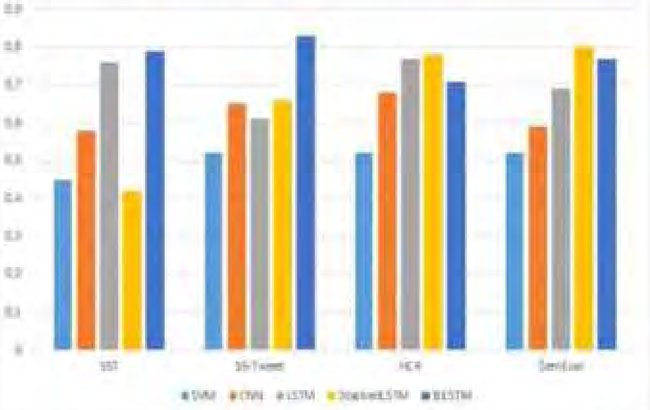

Fig. 6.11 The accuracy(%) comparisons of different datasets For various algorithms

Table 6.5 statistics on four different datasets widely used in the Twitter sentiment analysis

Dataset	#NO Tweets	#Negatives	#Neutral	#Positives
Stanford Twitter Sentiment (SST)	498	177	139	182
Sentiment Strength Twitter Dataset (SS-Tweet)	4,242	1,037	1,953	1,252
SemEval(2017)	13,975	2,186	6,440	5,349
The Health Care Reform (HCR)	2,516	1,381	470	541

Since we generate drug-related vocabulary schemes with regard to sentiment distribution, then we investigate the use of this medical setting to empower our sentiment information learning model. A based-BiLSTM sentiment classification has involved in classifying conveyed Sentiment accurately. Moreover, we examined the effectiveness of five Deep Learning algorithms with deriving embeddings vectors for each model.

First, Experimentation is conducted on Twitter Data, as shown in Fig.6.9. The SVM training

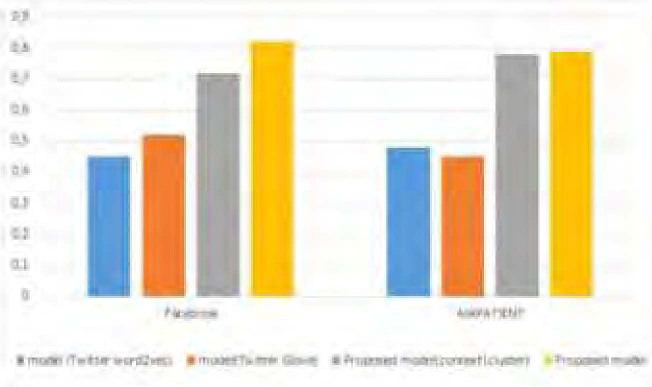

Fig. 6.12 Experiments with differents vectorization methods and Sentiment prediction DL-based Algorithms ((Grissette and Nfaoui, 2020b))

remarkably has excellent performance when a Twitter dataset is tiny and less recall than desired when data grow, which requires (a lot of) training data. But, regarding the medical context as a huge knowledgeable domain, it has many limitations. Especially when the classification model needs to adopt drug/ADRs corpora and efficient sentiment Matching. Our Bidirectional LSTM classifier with both proposed vectorization outperforms existing methods, which significantly explore medical knowledge regarding expressed Sentiment.

Otherwise, both stacked-LSTM and BiLSTM are markedly and consistently outperform all the other algorithms, thus the word2vec based-vectorization model has the lowest accuracy among all models. Conceivably, the fourth model significantly outperforms the third model and confirms the critical role of the existence of changeable Sentiment towards the same drug or treatment regarding the patient's status. it proved the effectiveness of identifying sentiment-related information per window under a dynamic medical setting.

Our use case scenarios focus on how a large amount of unstructured data from varied online healthcare forums fit with the proposed model, which contain more details on different situations from patients generated narratives, doctors, caregiver, and families. They provide very detailed patients' narratives. It considered an automatic online method that generates efficient sentiment-related features regarding drug-related terms from varied patients surfaces. So far, Our sentiment analysis model leverage differently concerning embedding sentiment, contextual, and the semantic information. It supposed to memorize long-term parametrization of drug-related concepts by the downstream methodology and be able to define new unknown terms. Our Experiment results show that improved hybrid vectorization regarding medical concepts such as ADRs is sufficient for the medical Sentiment Analysis task. As illustrated in Fig.6.10, the evaluation models for forum data have slightly differentiated in terms of the algorithm we used for classification. Due to the text setting and parameters for both forums

Table 6.6 Tweets Sentiment classification results by executing the proposed architecture (Asthma and Epilepsy disease case study)

Tweet	**Medical concepts annotation**	**Sentiment Value**
@pharma Asthma plus anexiety plus food is a bad time	asthma:disease	0.094839202
@ furlemate Awe I have asthma so I feel your pain.	asthma:disease	0.49834839202
Major weight loss decreases risk of asthma attacks http://t.oo/6X0NXkH4ij	asthma attacks:disease-type Precaution: Major weight loss	0.7463929202
Fr @MyKembangSepatu Common asthma steroids linked to side effects in adrenal glands: After stopping steroids c ... http://t.co/QmBrVhEzkm	asthma:disease Organ : Adrenal glands Drug : steroids Cures	0.104839202
DanielRadcliffe is one of the God's most unattractive creations since the aardvark	Steroids affects Adrenal Glands : ADE aardvark : Drug	0.2847839202
Nasal vs. throat microbiome diversity with differential risk asthma #AAAAI15	Nasal : microbiome asthma:disease Throat: microbiome	- 0.194839202
Any epilepsy nurses out there using T.E.C to gather data on QUOLIE 10, NDDIE or HADS before a patient attends clini… https://t.co/utnqr6hWZc	Epilepsy:disease: Quolie(translated to QOLIE); NDDIE: treatement tools :	0.663839202
Ironically, while I am attending #AES2019, the meeting of the American Epilepsy Society, this story has just broken. I don't know if this was a SUDEP, since I don't know if he had #epilepsy. But it sure sounds like it might've been.	asthma:disease SUDEP(sudden, unexpected death) : symptoms	0.013299202
Towards Understanding the Phenytoin-like #Antiepileptic Effect of #Cannabidiol and Related Phyto #cannabinoid Metabolites: Insights from Molecular Modeling	Epilepsy:disease cannabinoid: organ Phenytoin: Drug side effects	0.2137384732

Table 6.7 Experiments on various online twitter datasets with varied sizes

twitter data	**positive tweets**	**negative tweets**	**Accuracy**
500 Twitter posts	105 positives	40 negative	0.68
1000 Twitter posts	302 positives	70 negative	0.74
2200 Twitter posts	300 positives	90 negative	0.75
3400 Twitter posts	400 positives	275 negative	0.72
15000 Twitter posts	900 positives	300 negative	**0.81**

and Twitter. For example, SVM does well in the forum case. SVM examined with both simple featuring and word embedding featuring. It usually has excellent performance for sentiment classification, but short-dependencies and small datasets.

Furthermore, the stacked-LSTM and BiLSTM based model consistently outperform all the other methods. The effectiveness of BiLSTM and the possible advantage of the proposed vectorization scheme assessed through these comparisons. Thus sentiment strength model discussed in Section 3.2 for drug-related concepts help to clarify their subjectivity and their role to accommodate the sentiment.

The variations of the evaluation datasets are due to the particularities of the different sentiment analysis tasks. Analyzing drug-related experiences on Twitter spans multiple tasks, such as frequent Hashtags categorization, drug-related polarity detection, sentiment strength detection under the medical setting. As demonstrated above, we probe to perform these tasks either at the tweet level or at the target (entity) level. We conduct comparisons of sentiment strength detection using four different sentiment datasets widely used in the Twitter sentiment analysis literature:

1. **Stanford Twitter Sentiment (SST):** The Stanford Twitter sentiment corpus [8], introduced by Go et al. (Go et al., 2009) consists of two different sets, training, and test. The training set contains 1.6 million tweets automatically labeled as positive or negative based on emotions.

2. **Sentiment Strength Twitter Dataset (SS-Tweet):** This dataset consists of 4,242 tweets manually labeled with their positive and negative sentiment strengths. A negative strength is a number between -1 (not negative) and -5 (extremely negative). The dataset was constructed by (Thelwall et al., 2012) to evaluate SentiStrenth [9] is released under lexicon-based method

3. **SemEval(2017):** This dataset was constructed for the Twitter sentiment analysis task (Task 4) (Rosenthal et al., 2018) in the Semantic Evaluation of Systems challenge. The original SemEval dataset consists of 20K tweets split into training, development, and test sets.

4. **The Health Care Reform (HCR):**The Health Care Reform (HCR) dataset was built by crawling tweets containing the hashtag #hcr (health care reform) (Speriosu et al., 2011). A subset of this corpus was manually annotated by the authors with five labels (positive, negative, neutral, irrelevant, unsure(other)) and split into training (839 tweets), development (838 tweets), and test (839 tweets) sets.

As demonstrated above, these sentiment twitter lexicons have used to re-classify sentiment-related under the proposed medical parametrization. We remain using the N-gram convolutional drug-related vectors. As depicted in Table 6.5, resuming statistics of the SST, SS-Tweet, SemEval an HCR datasets used in this evaluation. Fig. 6.11 shows the accuracy of the four benchmarking sentiment datasets discussed on drug-related distributed vectors

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[8] http://help.sentiment140.com/

[9] http://sentistrength.wlv.ac.uk/

using four Deep Learning methods and SVM. The SST-Tweet with the BiLSTM method has the highest accuracy.
The proposed vocabulary gives clear improvements in using drug-related knowledge mentions for detecting relevant sentiment strength, it pushes the state of the art in a single sentence positive/negative fact prediction from 0.71 up to 0.83 for SS-Tweet dataset evaluation. Among individual Models, based-neural networks showed high performance for detecting sentiment strength under various conditions. The support vector machines have the lowest accuracy due to the size of the dataset used; in contrast, the efficiency has increased for small, cleaned, and with the human-labeled dataset. After checking the model's performance on different benchmark sentiment datasets, we chose to compare the performance of the proposed sentiment-related medical annotation of our model before classifying unseen instances of online data. We compare the extracted drug-related concepts with tweets that have already been annotated tweets by IREMedical Named Entity Recognition Team (NER) Twitter team. Our model seeks new items with various sentiment strength regarding the proposed clusters used in Section 3.1.4, and sentiment strength detection has been made about different medical concepts in sentences as a target of analysis. As can be seen in Table 5 present sample results of positive and negative experiences extracted with drug-related concepts citepd. Finally, the proposed methodology is validated by a series of experiments conducted on five online twitter datasets in a different slice of time. Table 6.7 illustrates a sample of results obtained for some tests, with splitting the number of positive and negative tweets detected.
To prove, the mobility and reliability of the generated vectors concerning the healthcare sitting sphere, we conduct another experimentation on different datasets from Facebook, AskPatient Forums. As shown in Fig.6.12, we compare the classification results with different models discussed above. Both of these dataset has specific characteristics in term of the language used, length, and particular keywords. It can be observed that the proposed vocabulary under sentiment strength cluster distribution has the highest accuracy, and the Glove and Word2vec models have respectively lower accuracy than pertained. Meaning, Glove, and Word2vec vectors are still generic and do not focus on medical concepts citepd in sentences.

6.4 Conclusion

In summary, existing methods for both sentiment analysis and language understanding are generic and require human-labeled data for high sentiment strength detection performance. In this chapter, we explored different aspects of analyzing drug-related texts. Indeed, we examined how efficiently explore different drug-related knowledge for identifying medication-related targets from large daily volumes of unlabeled data. This is about constructing formal meta-concepts embedding representation by incorporating medical knowledge. Most of existing methods 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". The proposed 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. Differently, the gaps of analysis in this study are: we do not assess the model's ability to detect suspected adverse drug reactions, and we do not efficiently distinguish emotional targets. Another limitation is that the poor interpretability aspect for drug issues identification model that can better help observing and understanding patients problems in different conditions and helps provide situational awareness to the bedside in various situations.

Chapter 7

Conclusion & Future Work

> *"There is no real ending. It's just the place where you stop the story."*
>
> — Frank Herbert

7.1 Conclusions

In this chapter, we highlight the major findings and the theoretical contribution of this thesis and identify areas for future research.

With regard to the massive online discussions are sharing and disseminating information, misinformation, and harmful experiences. This thesis aimed at analyzing and revealing typical characteristics of the online patient shared narratives and providing more patient-related background knowledge, as well as assisting downstream knowledge mining and discovery tasks, are more crucial tasks for efficient sentiment analysis in the biomedical domain. Although the huge success of machine learning algorithms, they fail to shape the structure of shared narratives on social networks in a formal medical language. The heart of the effective quantification of aspect-based sentiments relating to drugs/treatments hardly involves a degree of medical language comprehension. Most of the existing research, in this case, assumes the existence of hand-annotated sentiment dictionaries, which is time-consuming and may be subject to annotator/expert bias.

A huge number of biological entities, medication-related natural concepts, bio-medical lexical structures such as genes and mutations, are usually mentioned in a medication-related short text. The identification of the bio-medical entities' contextual semantics has a vital role and being mandatory for succeeding health-related applications performance. For instance, the use of embeddings has shown promising performance in bio-medical concept extraction and tagging (Grissette and Nfaoui, 2020b). However, word embeddings are traditionally computed at the word level from a large body of unlabeled text and exploit grammar directions that only center on extracting semantic-based information, ignoring information present in the internal structure of words or any information available in structured domain-specific resources such as ontologies. Biomedical embedding has brought great for depend-domain entities and their analysis. Many studies aim to perform a skilled and well-learned embedding, especially, health-related communities develop highly defined and comprehensive embedding versions of their databases and ontologies via different word embedding algorithms. Such knowledge has the potential to dramatically improve the quality of word representation. For example, ConceptVec covers more than 400,000 biomedical concepts mentioned in the literature and is to date one of the most important among the biomedical concepts embeddings available to the public. Nevertheless, these vocabularies are obviously not able to distinguish an unseen natural medical concept such as a multi-word phrase indicating undefined drug abuse. In this case, we investigate an associative embedding mechanism that mainly consists of processing distributed medical concepts in natural language to better match the formal semantics of a widely used controlled biomedical vocabulary and contributes to defining unrelated items.

7.2 Main Results & Future Work

A summary of the main conclusions drawn from the data previously discussed in the findings and the cross-analysis is articulated here. First, feature learning representation algorithm is an important issue to consider, especially describing the complex concepts in the context of medicine and yields as output the analog value that would eventually lead to the corresponding acceptable performance in term of extracting sentiments, affects, and interpreting results. The primary focus was to allowing sentiments to flow from concept to concept based on the dependency relation of the input target, in particular, a better understanding of the contextual role of each bio-medical concept and for boosting domain transferability. The relevant encoding of affective information conveyed regarding medication subjects clearly reveals defined roles and expectations that can have a positive impact on public health. A meaningful support to bio-medical sentiment analysis applications in social networks is done and the facets of this study might be used in many health concerns such as: analyzing change in health status or unexpected situations. Finally, we draw upon some important experimental results as follow:

The main experimental results:

Experiments have shown the effectiveness of considering biomedical concepts in analyzing medication-related texts. Indeed, the results proved that integrating deep-learning-based cognitive capabilities enhances the biomedical sentiment analysis performance. In particular, our affective encoding approach outperforms benchmarks with statistically significant differences.

Transfer learning mechanism followed in this thesis has improved model reliability and has leveraged the different conceptual and contextual distributed insights assessed by both (1) incorporating unlabelled data into the training process from online stories and (2) imitating formal English abstracts of biomedical articles from PubMed and other biomedical concept vocabularies to estimate the relatedness of subwords, and whereby combine subword information from unlabeled biomedical text with a widely-used biomedical controlled vocabulary.

The exploitation of such overwhelming unstructured data on social networks through sentiment analysis is of critical importance, however, the general-purpose sentiment analysis methods do not result in the expected performance. This inefficiency is well-rooted in several problems such as the lack of domain-depend annotated resources and deficiency of bio-medical entity recognition techniques.

Using semisupervised learning to unlock new paths towards conquering annotated sentiment lexicons deficiency for biomedical sentiment analysis, building contextual semantics for aspect-based sentiment of a given concept or entity. and finally investigating which way of tackling unstructured medication-related data for enhancing biomedical sentiment analysis training robustness, consistency, and reliability.

The proposed sentic computing-based method meets several requirements, such as the use of large and balanced labeled data for training models, which further yields good sentiment inference results.

The results on real-world stories demonstrate in various qualitative evaluation how shared information in daily patient self-reports absolutely aid to get patient voice and capture unpreventable issues.

Future directions: In the future, we plan to enhance:

The quality of medical entities connotation to establish other polarities within various emotions dimensions defined by emotional theoretical models such as ones in Hourglass model. Thus, we aim at develop our corpus-based model to leverage varied medical components interactions, actions, and patient-centric behaviors. The latter is highly defined to respect the power relation and stereotypes between words and their meanings such cultural meanings e.g. colonization may have heard with negative meanings that may be argued by powerless, voiceless, agency and uncivilized meanings.

The effectiveness of aspect alignment and concept-level aspect-based sentiment analysis that might led to better inferring unknown side effects of possible drugs and treatments based on the formed embeddings, clarifying the relationships among sets of drugs and conditions and situations to better clarify the "fakeness" or "genuineness" of a given medical fact, and therefore analyzing changes in health status or unexpected situations.

The exploitation of common sense, word-class association, and inter-aspect relations have known huge interest for domain-dependent sentiment analysis and for the development of emotion-sensitive systems Aydln and Gungor (2020). In addition, data properties have fair benefits to disambiguate common sense and extract intrinsic relationships. Thus, medication-related narratives including drug issues, events, examination facts may contain many medical relational events and factors that need to be observed collectively.

The vast connections of shared drug reaction assume the existence of a reliable network regarding drug reaction particularities such as the problem of mutual forms of drug interactions including beneficial drug effects, which play a substantial role and potential in defining trust and credibility measurement each time we aim to truly understand and analyze patients shared experiences.

The influencing factors in features identification and relevancy of predefined aspects by detecting non-meaningful (uninformative words) and allowing insertion of pertinent words which share drug-related common semantics.

References

N. Adams. Dataset Shift in Machine Learning. *Journal of the Royal Statistical Society: Series A (Statistics in Society)*, 173(1):274, 2009. doi:$10.1111/j.1467-985x.2009.00624\_10.x$.

D. Anand and D. Naorem. Semi-supervised aspect based sentiment analysis for movies using review filtering. volume 84, pages 86–93. Elsevier B.V., 2016. doi:10.1016/j.procs.2016.04.070.

R. K. Ando and T. Zhang. A high-performance semi-supervised learning method for text chunking. In *ACL-05 - 43rd Annual Meeting of the Association for Computational Linguistics, Proceedings of the Conference*, 2005. ISBN 1932432515. doi:10.3115/1219840.1219841.

R. Antunes and S. Matos. Biomedical word sense disambiguation with word embeddings. In *Advances in Intelligent Systems and Computing*, 2017. ISBN 9783319608150. doi:10.1007/978-3-319-60816-7_33.

O. Araque, I. Corcuera-Platas, J. F. Sánchez-Rada, and C. A. Iglesias. Enhancing deep learning sentiment analysis with ensemble techniques in social applications. *Expert Systems with Applications*, 2017. ISSN 09574174. doi:10.1016/j.eswa.2017.02.002.

C. R. Aydln and T. Gungor. Combination of recursive and recurrent neural networks for aspect-based sentiment analysis using inter-aspect relations. *IEEE Access*, 2020. ISSN 21693536. doi:10.1109/ACCESS.2020.2990306.

S. Baccianella, A. Esuli, and F. Sebastiani. SentiWordNet 3.0: An enhanced lexical resource for sentiment analysis and opinion mining. In *Proceedings of the Seventh International Conference on Language Resources and Evaluation (LREC'10)*, Valletta, Malta, May 2010. European Language Resources Association (ELRA). URL http://www.lrec-conf.org/proceedings/lrec2010/pdf/769_Paper.pdf.

Y. Bengio, A. Courville, and P. Vincent. Representation learning: A review and new perspectives. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 2013. ISSN 01628828. doi:10.1109/TPAMI.2013.50.

J. Blitzer, R. McDonald, and F. Pereira. Domain adaptation with structural correspondence learning. In *COLING/ACL 2006 - EMNLP 2006: 2006 Conference on Empirical Methods in Natural Language Processing, Proceedings of the Conference*, 2006. ISBN 1932432736. doi:10.3115/1610075.1610094.

I. Bradet-Levesque, J. Audet, J.-S. Roy, and V. H. Flamand. Measuring functional outcome in dupuytren's disease: A systematic review of patient-reported outcome measures. *Journal of Hand Therapy*, 2021. ISSN 0894-1130. doi:https://doi.org/10.1016/j.jht.2021.04.010. URL https://www.sciencedirect.com/science/article/pii/S0894113021000570.

F. Bravo-Marquez, M. Mendoza, and B. Poblete. Meta-level sentiment models for big social data analysis. *Knowledge-Based Systems*, 2014. ISSN 09507051. doi:10.1016/j.knosys.2014.05.016.

A. Caliskan, J. J. Bryson, and A. Narayanan. Semantics derived automatically from language corpora contain human-like biases. *Science*, 356(6334):183–186, 2017. ISSN 0036-8075. doi:10.1126/science.aal4230. URL https://science.sciencemag.org/content/356/6334/183.

H. Calvo, A. P. Rocha-Ramirez, M. A. Moreno-Armendariz, and C. A. Duchanoy. Toward Universal Word Sense Disambiguation Using Deep Neural Networks. *IEEE Access*, 2019. ISSN 21693536. doi:10.1109/ACCESS.2019.2914921.

E. Cambria and A. Hussain. *Sentic Computing*. Springer International Publishing., 2015. ISBN 978-3-319-23654-4.

E. Cambria, A. Hussain, T. Durrani, C. Havasi, C. Eckl, and J. Munro. Sentic computing for patient centered applications. In *International Conference on Signal Processing Proceedings, ICSP*, 2010. ISBN 9781424458981. doi:10.1109/ICOSP.2010.5657072.

E. Cambria, T. Benson, C. Eckl, and A. Hussain. Sentic PROMs: Application of sentic computing to the development of a novel unified framework for measuring health-care quality. *Expert Systems with Applications*, 2012. ISSN 09574174. doi:10.1016/j.eswa.2012.02.120.

E. Cambria, D. Olsher, and D. Rajagopal. Senticnet 3: A common and common-sense knowledge base for cognition-driven sentiment analysis. In *Proceedings of the Twenty-Eighth AAAI Conference on Artificial Intelligence*, AAAI'14, page 1515–1521. AAAI Press, 2014. ISBN 9781577356783.

E. Cambria, Y. Li, F. Z. Xing, S. Poria, and K. Kwok. SenticNet 6: Ensemble Application of Symbolic and Subsymbolic AI for Sentiment Analysis. *International Conference on Information and Knowledge Management, Proceedings*, pages 105–114, 2020. doi:10.1145/3340531.3412003.

L. Canales, C. Strapparava, E. Boldrini, and P. Martinez-Barco. Intensional learning to efficiently build up automatically annotated emotion corpora. *IEEE Transactions on Affective Computing*, 2020. ISSN 19493045. doi:10.1109/TAFFC.2017.2764470.

J. Carrillo-de Albornoz, J. R. Vidal, and L. Plaza. Feature engineering for sentiment analysis in e-health forums. *PLoS ONE*, 2018. ISSN 19326203. doi:10.1371/journal.pone.0207996.

Q. Chen, Y. Peng, and Z. Lu. BioSentVec: creating sentence embeddings for biomedical texts. *2019 IEEE International Conference on Healthcare Informatics (ICHI)*, jun 2019. doi:10.1109/ichi.2019.8904728. URL http://dx.doi.org/10.1109/ICHI.2019.8904728.

Q. Chen, K. Lee, S. Yan, S. Kim, C. H. Wei, and Z. Lu. Bioconceptvec: Creating and evaluating literature-based biomedical concept embeddings on a large scale. *PLoS Computational Biology*, 2020. ISSN 15537358. doi:10.1371/journal.pcbi.1007617.

Y. Choi, J. Wiebe, and R. Mihalcea. Coarse-Grained +/-Effect Word Sense Disambiguation for Implicit Sentiment Analysis. *IEEE Transactions on Affective Computing*, 2017. ISSN 19493045. doi:10.1109/TAFFC.2017.2734085.

M. Cinelli, W. Quattrociocchi, A. Galeazzi, C. M. Valensise, E. Brugnoli, A. L. Schmidt, P. Zola, F. Zollo, and A. Scala. The COVID-19 social media infodemic. *Scientific Reports*, 2020. ISSN 20452322. doi:10.1038/s41598-020-73510-5.

A. Cocos, A. G. Fiks, and A. J. Masino. Deep learning for pharmacovigilance: Recurrent neural network architectures for labeling adverse drug reactions in Twitter posts. *Journal of the American Medical Informatics Association*, 2017. ISSN 1527974X. doi:10.1093/jamia/ocw180.

W. C. Crannell, E. Clark, C. Jones, T. A. James, and J. Moore. A pattern-matched Twitter analysis of US cancer-patient sentiments. *Journal of Surgical Research*, 2016. ISSN 10958673. doi:10.1016/j.jss.2016.06.050.

W. Dai, G.-R. Xue, Q. Yang, and Y. Yu. Transferring naive bayes classifiers for text classification. In *Proceedings of the 22nd National Conference on Artificial Intelligence - Volume 1*, AAAI'07, page 540–545. AAAI Press, 2007. ISBN 9781577353232.

J. Davis and P. Domingos. Deep transfer via second-order Markov logic. In *ACM International Conference Proceeding Series*, 2009. ISBN 9781605585161. doi:10.1145/1553374.1553402.

M. Demircigil, J. Heusel, M. Löwe, S. Upgang, and F. Vermet. On a Model of Associative Memory with Huge Storage Capacity. *Journal of Statistical Physics*, 2017. ISSN 00224715. doi:10.1007/s10955-017-1806-y.

K. Denecke and Y. Deng. Sentiment analysis in medical settings: New opportunities and challenges. *Artificial Intelligence in Medicine*, 2015. ISSN 18732860. doi:10.1016/j.artmed.2015.03.006.

J. Devlin, M.-W. Chang, K. Lee, and K. Toutanova. Bert: Pre-training of deep bidirectional transformers for language understanding. In *NAACL-HLT*, 2019.

J. Dietrich, L. M. Gattepaille, B. A. Grum, L. Jiri, M. Lerch, D. Sartori, and A. Wisniewski. Adverse Events in Twitter-Development of a Benchmark Reference Dataset: Results from IMI WEB-RADR. *Drug Safety*, 2020. ISSN 11791942. doi:10.1007/s40264-020-00912-9.

H. Elfaik et al. Deep bidirectional lstm network learning-based sentiment analysis for arabic text. *Journal of Intelligent Systems*, 30(1):395–412, 2020.

M. Enquist, J. Lind, and S. Ghirlanda. The power of associative learning and the ontogeny of optimal behaviour. *Royal Society Open Science*, 2016. ISSN 20545703. doi:10.1098/rsos.160734.

J. Feldman, J. Davison, and A. M. Rush. Commonsense knowledge mining from pretrained models. In *EMNLP-IJCNLP 2019 - 2019 Conference on Empirical Methods in Natural Language Processing and 9th International Joint Conference on Natural Language Processing, Proceedings of the Conference*, 2020. ISBN 9781950737901. doi:10.18653/v1/d19-1109.

C. Fellbaum. WordNet. In *Theory and Applications of Ontology: Computer Applications*. 2010. ISBN 9789048188468. doi:10.1007/978-90-481-8847-5_10.

M. Fu, H. Qu, L. Huang, and L. Lu. Bag of meta-words: A novel method to represent document for the sentiment classification. *Expert Systems with Applications*, 2018. ISSN 09574174. doi:10.1016/j.eswa.2018.06.052.

M. Gamon. Sentiment classification on customer feedback data: noisy data, large feature vectors, and the role of linguistic analysis. *Proceedings of the 20th international conference on Computational Linguistics*, 2004. doi:10.3115/1220355.1220476.

J. Garcia-Pelaez, D. Rodriguez, R. Medina-Molina, G. Garcia-Rivas, C. Jerjes-Sánchez, and V. Trevino. PubTerm: A web tool for organizing, annotating and curating genes, diseases, molecules and other concepts from PubMed records. *Database*, 2019. ISSN 17580463. doi:10.1093/database/bay137.

M. Ghiassi and S. Lee. A domain transferable lexicon set for Twitter sentiment analysis using a supervised machine learning approach. *Expert Systems with Applications*, 2018. ISSN 09574174. doi:10.1016/j.eswa.2018.04.006.

D. M. Giustini, S. M. Ali, M. Fraser, and M. N. K. Boulos. Effective uses of social media in public health and medicine: a systematic review of systematic reviews. *Online Journal of Public Health Informatics*, 2018. ISSN 1947-2579. doi:10.5210/ojphi.v10i2.8270.

A. Go, R. Bhayani, and L. Huang. Twitter Sentiment Classification using Distant Supervision. *Processing*, 2009.

D. A. González-Padilla and L. Tortolero-Blanco. Social media influence in the COVID-19 pandemic, 2020. ISSN 16776119.

H. Grissette and E. H. Nfaoui. A conditional sentiment analysis model for the embedding patient self-report experiences on social media. In *Advances in Intelligent Systems and Computing*, 2019. ISBN 9783030118839. doi:10.1007/978-3-030-11884-6_6.

H. Grissette and E. H. Nfaoui. Drug Reaction Discriminator within Encoder-Decoder Neural Network Model: COVID-19 Pandemic Case Study. In *Proceedings of The IEEE Seventh International Conference on Social Networks Analysis, Management and Security(SNAMS-2020)*, 2020a.

H. Grissette and E. H. Nfaoui. Enhancing convolution-based sentiment extractor via dubbed N-gram embedding-related drug vocabulary. *Network Modeling Analysis in Health Informatics and Bioinformatics*, 9(1):42, 2020b. ISSN 2192-6670. doi:10.1007/s13721-020-00248-5. URL https://doi.org/10.1007/s13721-020-00248-5.

H. Grissette and E. H. Nfaoui. Drug reaction discriminator within encoder-decoder neural network model: Covid-19 pandemic case study. In *2020 Seventh International Conference on Social Networks Analysis, Management and Security (SNAMS)*, pages 1–7, 2020c. doi:10.1109/SNAMS52053.2020.9336561.

H. Grissette and E. H. Nfaoui. Deep associative learning approach for bio-medical sentiment analysis utilizing unsupervised representation from large-scale patients' narratives. *Personal and Ubiquitous Computing*, 2021a. ISSN 1617-4917. doi:10.1007/s00779-021-01595-4. URL https://doi.org/10.1007/s00779-021-01595-4.

H. Grissette and E. H. Nfaoui. Affective Concept-Based Encoding of Patient Narratives via Sentic Computing and Neural Networks. *Cognitive Computation*, 2021b. ISSN 1866-9964. doi:10.1007/s12559-021-09903-z. URL https://doi.org/10.1007/s12559-021-09903-z.

H. Grissette and E. H. Nfaoui. Embedded techniques comparison for bio-medical sentiment analysis: A corpus-based case study of covid19 drug-related reviews. In *2021 International Conference on Embedded Systems and Artificial Intelligence (ESAI2021)*, pages 1–7, 2021.

H. Grissette, E. L. H. Nfaoui, and A. Bahir. Sentiment Analysis Tool for Pharmaceutical Industry & Healthcare. *Transactions on Machine Learning and Artificial Intelligence*, 2017. ISSN 2054-7390. doi:10.14738/tmlai.54.3339.

B. A. GRISSETTE Hanane NFAOUI EL Habib. Sentiment Analysis Tool for Pharmaceutical Industry and Healthcare. Transactions on Machine Learning and Artificial Intelligence, [S.l.], 2017. doi:http://dx.doi.org/10.14738/tmlai.54.3339.

Z.-H. Guo, Z.-H. You, D.-S. Huang, H.-C. Yi, K. Zheng, Z.-H. Chen, and Y.-B. Wang. MeSHHeading2vec: a new method for representing MeSH headings as vectors based on graph embedding algorithm. *Briefings in Bioinformatics*, 2020. ISSN 1477-4054. doi:10.1093/bib/bbaa037. URL https://doi.org/10.1093/bib/bbaa037.

R. Gupta, S. Sahu, C. Espy-Wilson, and S. Narayanan. Semi-Supervised and Transfer Learning Approaches for Low Resource Sentiment Classification. In *ICASSP, IEEE International Conference on Acoustics, Speech and Signal Processing - Proceedings*, 2018. ISBN 9781538646588. doi:10.1109/ICASSP.2018.8461414.

A. Halioui, P. Valtchev, and A. B. Diallo. Bioinformatic Workflow Extraction from Scientific Texts based on Word Sense Disambiguation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2018. ISSN 15579964. doi:10.1109/TCBB.2018.2847336.

J. Han, Z. Zhang, N. Cummins, and B. Schuller. Adversarial Training in Affective Computing and Sentiment Analysis: Recent Advances and Perspectives [Review Article]. *IEEE Computational Intelligence Magazine*, 2019. ISSN 15566048. doi:10.1109/MCI.2019.2901088.

Y. Han, M. Liu, and W. Jing. Aspect-Level Drug Reviews Sentiment Analysis Based on Double BiGRU and Knowledge Transfer. *IEEE Access*, 2020. ISSN 21693536. doi:10.1109/ACCESS.2020.2969473.

C. F. Hansen, K. C. Obionu, J. D. Comins, and M. R. Krogsgaard. Patient reported outcome measures for ankle instability. an analysis of 17 existing questionnaires. *Foot and Ankle Surgery*, 2021. ISSN 1268-7731. doi:https://doi.org/10.1016/j.fas.2021.04.009. URL https://www.sciencedirect.com/science/article/pii/S1268773121000874.

S. U. Hassan, N. R. Aljohani, N. Idrees, R. Sarwar, R. Nawaz, E. Martínez-Cámara, S. Ventura, and F. Herrera. Predicting literature's early impact with sentiment analysis in Twitter. *Knowledge-Based Systems*, 2020. ISSN 09507051. doi:10.1016/j.knosys.2019.105383.

J. Howard and S. Ruder. Universal language model fine-tuning for text classification. In *ACL 2018 - 56th Annual Meeting of the Association for Computational Linguistics, Proceedings of the Conference (Long Papers)*, 2018. ISBN 9781948087322. doi:10.18653/v1/p18-1031.

H. Hu, N. H. Phan, J. Geller, H. Vo, B. Manasi, X. Huang, S. Di Lorio, T. Dinh, and S. A. Chun. Deep self-taught learning for detecting drug abuse risk behavior in tweets. In *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 2018. ISBN 9783030046477. doi:10.1007/978-3-030-04648-4_28.

G. B. Huang, Q. Y. Zhu, and C. K. Siew. Extreme learning machine: A new learning scheme of feedforward neural networks. In *IEEE International Conference on Neural Networks - Conference Proceedings*, 2004. ISBN 0780383591. doi:10.1109/IJCNN.2004.1380068.

C. Hutto and E. Gilbert. Vader: A parsimonious rule-based model for sentiment analysis of social media text. *Proceedings of the International AAAI Conference on Web and Social Media*, 8(1), May 2014. URL https://ojs.aaai.org/index.php/ICWSM/article/view/14550.

H. Jang, E. Rempel, D. Roth, G. Carenini, and N. Z. Janjua. Tracking COVID-19 discourse on twitter in north america: Infodemiology study using topic modeling and aspect-based sentiment analysis. *Journal of Medical Internet Research*, 2021. ISSN 14388871. doi:10.2196/25431.

H. Jelodar, Y. Wang, R. Orji, and S. Huang. Deep sentiment classification and topic discovery on novel coronavirus or covid-19 online discussions: Nlp using lstm recurrent neural network approach. *IEEE Journal of Biomedical and Health Informatics*, 24(10):2733–2742, 2020. doi:10.1109/JBHI.2020.3001216.

S. Ji, S. Pan, X. Li, E. Cambria, G. Long, and Z. Huang. Suicidal ideation detection: A review of machine learning methods and applications. *IEEE Transactions on Computational Social Systems*, 8(1):214–226, 2021. doi:10.1109/TCSS.2020.3021467.

J. Jiang and C. X. Zhai. Instance weighting for domain adaptation in NLP. In *ACL 2007 - Proceedings of the 45th Annual Meeting of the Association for Computational Linguistics*, pages 264–271, 2007. ISBN 9781932432862.

S. M. Jiménez-Zafra, M. T. Martín-Valdivia, M. D. Molina-González, and L. A. Ureña-López. How do we talk about doctors and drugs? Sentiment analysis in forums expressing opinions for medical domain. *Artificial Intelligence in Medicine*, 2019. ISSN 18732860. doi:10.1016/j.artmed.2018.03.007.

A. J. Jimeno-Yepes, B. T. McInnes, and A. R. Aronson. Exploiting MeSH indexing in MEDLINE to generate a data set for word sense disambiguation. *BMC Bioinformatics*, 2011. ISSN 14712105. doi:10.1186/1471-2105-12-223.

K. Jing and J. Xu. A survey on neural network language models, 2019.

Z. Ke, J. Sheng, Z. Li, W. Silamu, and Q. Guo. Knowledge-Guided Sentiment Analysis via Learning From Natural Language Explanations. *IEEE Access*, 2021. ISSN 21693536. doi:10.1109/ACCESS.2020.3048088.

F. K. Khattak, S. Jeblee, C. Pou-Prom, M. Abdalla, C. Meaney, and F. Rudzicz. A survey of word embeddings for clinical text. *Journal of Biomedical Informatics: X*, 4:100057, 2019. ISSN 2590-177X. doi:https://doi.org/10.1016/j.yjbinx.2019.100057. URL http://www.sciencedirect.com/science/article/pii/S2590177X19300563.

D. Knuth. TextBlob Documentation, 2020. URL https://textblob.readthedocs.io/en/dev/.

A. Kosmopoulos, I. Androutsopoulos, and G. Paliouras. Biomedical Semantic Indexing using Dense Word Vectors in BioASQ. *Journal Of Bio-Medical Semantics, Supplement On Bio-Medical Information Retrieval*, 2015.

D. Krotov and J. J. Hopfield. Dense associative memory for pattern recognition. In *Advances in Neural Information Processing Systems*, 2016.

D. Krotov and J. J. Hopfield. Unsupervised learning by competing hidden units. *Proceedings of the National Academy of Sciences of the United States of America*, 2019. ISSN 10916490. doi:10.1073/pnas.1820458116.

T. Kunić. Erik Cambria, Dipankar Das, Sivaji Bandyopadhyay, Antonio Feraco: A Practical Guide to Sentiment Analysis, Springer, 2017. pp. 196. *Medijska istraživanja : znanstveno-stručni časopis za novinarstvo i medije*, 2019. ISSN 1330-6928.

D. Kwon, S. Kim, C. H. Wei, R. Leaman, and Z. Lu. EzTag: Tagging biomedical concepts via interactive learning. *Nucleic Acids Research*, 2018. ISSN 13624962. doi:10.1093/nar/gky428.

Y. Li, Q. Pan, T. Yang, S. Wang, J. Tang, and E. Cambria. Learning Word Representations for Sentiment Analysis. *Cognitive Computation*, 2017. ISSN 18669964. doi:10.1007/s12559-017-9492-2.

Z. Li, F. Yang, and Y. Luo. Context embedding based on bi-lstm in semi-supervised biomedical word sense disambiguation. *IEEE Access*, 7:72928–72935, 2019. ISSN 2169-3536. doi:10.1109/ACCESS.2019.2912584.

Z. Li, F. Yang, and Y. Luo. Context Embedding Based on Bi-LSTM in Semi-Supervised Biomedical Word Sense Disambiguation. *IEEE Access*, 2019a. ISSN 21693536. doi:10.1109/ACCESS.2019.2912584.

Z. Li, F. Yang, and Y. Luo. Context Embedding Based on Bi-LSTM in Semi-Supervised Biomedical Word Sense Disambiguation. *IEEE Access*, 2019b. ISSN 21693536. doi:10.1109/ACCESS.2019.2912584.

N. Limsopatham and N. Collier. Normalising medical concepts in social media texts by learning semantic representation. In *54th Annual Meeting of the Association for Computational Linguistics, ACL 2016 - Long Papers*, 2016a. ISBN 9781510827585. doi:10.18653/v1/p16-1096.

N. Limsopatham and N. Collier. Normalising medical concepts in social media texts by learning semantic representation. In *54th Annual Meeting of the Association for Computational Linguistics, ACL 2016 - Long Papers*, 2016b. ISBN 9781510827585. doi:10.18653/v1/p16-1096.

J. Liu, M. Gong, and H. He. Deep associative neural network for associative memory based on unsupervised representation learning. *Neural Networks*, 113:41–53, 2019. ISSN 0893-6080. doi:10.1016/j.neunet.2019.01.004.

Y. Lu and Q. Zheng. Twitter public sentiment dynamics on cruise tourism during the covid-19 pandemic, 2020. ISSN 13683500.

B. T. McInnes and M. Stevenson. Determining the difficulty of Word Sense Disambiguation. *Journal of Biomedical Informatics*, 2014. ISSN 15320464. doi:10.1016/j.jbi.2013.09.009.

L. Mihalkova, T. Huynh, and R. J. Mooney. Mapping and revising markov logic networks for transfer learning. In *Proceedings of the 22nd National Conference on Artificial Intelligence - Volume 1*, AAAI'07, page 608–614. AAAI Press, 2007. ISBN 9781577353232.

T. Mikolov, K. Chen, G. Corrado, and J. Dean. Efficient estimation of word representations in vector space. In *ICLR*, 2013a.

T. Mikolov, I. Sutskever, K. Chen, G. Corrado, and J. Dean. Distributed representations of words and phrases and their compositionality. *CoRR*, abs/1310.4546, 2013b. URL http://arxiv.org/abs/1310.4546.

T. Mikolov, E. Grave, P. Bojanowski, C. Puhrsch, and A. Joulin. Advances in pre-training distributed word representations. *CoRR*, abs/1712.09405, 2017. URL http://arxiv.org/abs/1712.09405.

O. Mohamad Beigi and M. H. Moattar. Automatic construction of domain-specific sentiment lexicon for unsupervised domain adaptation and sentiment classification. *Knowledge-Based Systems*, 213:106423, 2021. ISSN 0950-7051. doi:https://doi.org/10.1016/j.knosys.2020.106423. URL https://www.sciencedirect.com/science/article/pii/S0950705120305529.

A. Nazir, Y. Rao, L. Wu, and L. Sun. Issues and Challenges of Aspect-based Sentiment Analysis: A Comprehensive Survey. *IEEE Transactions on Affective Computing*, 2020. ISSN 19493045. doi:10.1109/TAFFC.2020.2970399.

S. J. Nelson, K. Zeng, J. Kilbourne, T. Powell, and R. Moore. Normalized names for clinical drugs: RxNorm at 6 years. *Journal of the American Medical Informatics Association*, 2011. ISSN 10675027. doi:10.1136/amiajnl-2011-000116.

F. Å. Nielsen. A new ANEW: evaluation of a word list for sentiment analysis in microblogs. *CoRR*, abs/1103.2903, 2011. URL http://arxiv.org/abs/1103.2903.

A. Nikfarjam, A. Sarker, K. O'Connor, R. Ginn, and G. Gonzalez. Pharmacovigilance from social media: Mining adverse drug reaction mentions using sequence labeling with word embedding cluster features. *Journal of the American Medical Informatics Association*, 2015a. ISSN 1527974X. doi:10.1093/jamia/ocu041.

A. Nikfarjam, A. Sarker, K. O'Connor, R. Ginn, and G. Gonzalez. Pharmacovigilance from social media: Mining adverse drug reaction mentions using sequence labeling with word embedding cluster features. *Journal of the American Medical Informatics Association*, 2015b. ISSN 1527974X. doi:10.1093/jamia/ocu041.

N. Ofek, C. Caragea, L. Rokach, P. Biyani, P. Mitra, J. Yen, K. Portier, and G. Greer. Improving sentiment analysis in an online cancer survivor community using dynamic sentiment lexicon. In *2013 International Conference on Social Intelligence and Technology*, pages 109–113, 2013. doi:10.1109/SOCIETY.2013.20.

G. Palm. Neural associative memories and sparse coding. *Neural Networks*, 2013. ISSN 08936080. doi:10.1016/j.neunet.2012.08.013.

B. Pang, L. Lee, and S. Vaithyanathan. Thumbs up? Sentiment Classification Using Machine Learning Techniques. In *Proceedings of the ACL-02 Conference on Empirical Methods in Natural Language Processing - Volume 10*, EMNLP '02, pages 79–86, USA, 2002. Association for Computational Linguistics. doi:10.3115/1118693.1118704. URL https://doi.org/10.3115/1118693.1118704.

K. Pasupa and T. Seneewong Na Ayutthaya. Thai sentiment analysis with deep learning techniques: A comparative study based on word embedding, POS-tag, and sentic features. *Sustainable Cities and Society*, 50(December 2018):101615, 2019. ISSN 22106707. doi:10.1016/j.scs.2019.101615. URL https://doi.org/10.1016/j.scs.2019.101615.

R. Patel, T. Chang, S. R. Greysen, and V. Chopra. Social media use in chronic disease: A systematic review and novel taxonomy. *American Journal of Medicine*, 2015. ISSN 15557162. doi:10.1016/j.amjmed.2015.06.015.

Q. Peng, L. You, Q. Lu, and X. Li. Mining review unit model for online review analysis. *IEEE Access*, 8:196826–196834, 10 2020. ISSN 2169-3536. doi:10.1109/access.2020.3033820.

J. Pennington, R. Socher, and C. D. Manning. GloVe: Global vectors for word representation. In *EMNLP 2014 - 2014 Conference on Empirical Methods in Natural Language Processing, Proceedings of the Conference*, 2014a. ISBN 9781937284961. doi:10.3115/v1/d14-1162.

J. Pennington, R. Socher, and C. D. Manning. GloVe: Global vectors for word representation. In *EMNLP 2014 - 2014 Conference on Empirical Methods in Natural Language Processing, Proceedings of the Conference*, 2014b. ISBN 9781937284961. doi:10.3115/v1/d14-1162.

A. Pesaranghader, S. Matwin, M. Sokolova, and A. Pesaranghader. DeepBioWSD: Effective deep neural word sense disambiguation of biomedical text data. *Journal of the American Medical Informatics Association*, 2019. ISSN 1527974X. doi:10.1093/jamia/ocy189.

M. E. Peters, M. Neumann, M. Iyyer, M. Gardner, C. Clark, K. Lee, and L. Zettlemoyer. Deep contextualized word representations. In *Proc. of NAACL*, 2018.

F. Petroni, T. Rocktäschel, P. Lewis, A. Bakhtin, Y. Wu, A. H. Miller, and S. Riedel. Language models as knowledge bases?, 2019.

D. H. Pham and A. C. Le. Exploiting multiple word embeddings and one-hot character vectors for aspect-based sentiment analysis. *International Journal of Approximate Reasoning*, 2018. ISSN 0888613X. doi:10.1016/j.ijar.2018.08.003.

N. Poerner, U. Waltinger, and H. Schütze. BERT is Not a Knowledge Base (Yet): Factual Knowledge vs. Name-Based Reasoning in Unsupervised QA. *arXiv preprint arXiv:1911.03681v1*, 2019.

K. E. Pérez-Alfonso and V. Sánchez-Martínez. Electronic patient-reported outcome measures evaluating cancer symptoms: A systematic review. *Seminars in Oncology Nursing*, 37 (2):151145, 2021. ISSN 0749-2081. doi:https://doi.org/10.1016/j.soncn.2021.151145. URL https://www.sciencedirect.com/science/article/pii/S0749208121000280. Oncology Emergencies.

S. M. Rezaeinia, R. Rahmani, A. Ghodsi, and H. Veisi. Sentiment analysis based on improved pre-trained word embeddings. *Expert Systems with Applications*, 2019. ISSN 09574174. doi:10.1016/j.eswa.2018.08.044.

R. G. Rodrigues, R. M. das Dores, C. G. Camilo-Junior, and T. C. Rosa. SentiHealth-Cancer: A sentiment analysis tool to help detecting mood of patients in online social networks. *International Journal of Medical Informatics*, 2014. ISSN 18728243. doi:10.1016/j.ijmedinf.2015.09.007.

S. Rosenthal, N. Farra, and P. Nakov. SemEval-2017 Task 4: Sentiment Analysis in Twitter. 2018. doi:10.18653/v1/s17-2088.

G. A. Ruz, P. A. Henríquez, and A. Mascareño. Sentiment analysis of Twitter data during critical events through Bayesian networks classifiers. *Future Generation Computer Systems*, 2020. ISSN 0167739X. doi:10.1016/j.future.2020.01.005.

A. Sabbir, A. Jimeno-Yepes, and R. Kavuluru. Knowledge-based biomedical word sense disambiguation with neural concept embeddings. In *Proceedings - 2017 IEEE 17th International Conference on Bioinformatics and Bioengineering, BIBE 2017*, 2017. ISBN 9781538613245. doi:10.1109/BIBE.2017.00-61.

A. Sabeeh and R. K. Dewang. Comparison, classification and survey of aspect based sentiment analysis. volume 955, pages 612–629. Springer Verlag, 2019. ISBN 9789811331398. doi:10.1007/978-981-13-3140-4_55.

K. Sailunaz and R. Alhajj. Emotion and sentiment analysis from Twitter text. *Journal of Computational Science*, 2019. ISSN 18777503. doi:10.1016/j.jocs.2019.05.009.

M. D. P. Salas-Zárate, J. Medina-Moreira, K. Lagos-Ortiz, H. Luna-Aveiga, M. Á. Rodríguez-García, and R. Valencia-García. Sentiment Analysis on Tweets about Diabetes: An Aspect-Level Approach. *Computational and Mathematical Methods in Medicine*, 2017. ISSN 17486718. doi:10.1155/2017/5140631.

N. Sanglerdsinlapachai, A. Plangprasopchok, T. B. Ho, and E. Nantajeewarawat. Improving sentiment analysis on clinical narratives by exploiting umls semantic types. *Artificial Intelligence in Medicine*, 113:102033, 2021. ISSN 0933-3657. doi:https://doi.org/10.1016/j.artmed.2021.102033. URL https://www.sciencedirect.com/science/article/pii/S0933365721000269.

A. Sarker and G. Gonzalez. A corpus for mining drug-related knowledge from Twitter chatter: Language models and their utilities. *Data in Brief*, 2017. ISSN 23523409. doi:10.1016/j.dib.2016.11.056.

A. Sarker, M. Belousov, J. Friedrichs, K. Hakala, S. Kiritchenko, F. Mehryary, S. Han, T. Tran, A. Rios, R. Kavuluru, B. De Bruijn, F. Ginter, D. Mahata, S. M. Mohammad, G. Nenadic, and G. Gonzalez-Hernandez. Data and systems for medication-related text classification and concept normalization from Twitter: Insights from the Social Media Mining for Health (SMM4H)-2017 shared task. *Journal of the American Medical Informatics Association*, 2018a. ISSN 1527974X. doi:10.1093/jamia/ocy114.

A. Sarker, M. Belousov, J. Friedrichs, K. Hakala, S. Kiritchenko, F. Mehryary, S. Han, T. Tran, A. Rios, R. Kavuluru, B. De Bruijn, F. Ginter, D. Mahata, S. M. Mohammad, G. Nenadic, and G. Gonzalez-Hernandez. Data and systems for medication-related text classification and concept normalization from Twitter: Insights from the Social Media Mining for Health (SMM4H)-2017 shared task. *Journal of the American Medical Informatics Association*, 2018b. ISSN 1527974X. doi:10.1093/jamia/ocy114.

R. Satapathy, E. Cambria, and H. Amir. *Sentiment Analysis in the Bio-Medical Domain*. Springer International Publishing., 2017. ISBN 978-3-319-68468-0.

K. Schouten and F. Frasincar. Survey on Aspect-Level Sentiment Analysis. *IEEE Transactions on Knowledge and Data Engineering*, 2016. ISSN 10414347. doi:10.1109/TKDE.2015.2485209.

R. R. Shah, Y. Yu, A. Verma, S. Tang, A. D. Shaikh, and R. Zimmermann. Leveraging multimodal information for event summarization and concept-level sentiment analysis. *Knowledge-Based Systems*, 2016. ISSN 09507051. doi:10.1016/j.knosys.2016.05.022.

K. Shuang, Z. Zhang, H. Guo, and J. Loo. A sentiment information Collector–Extractor architecture based neural network for sentiment analysis. *Information Sciences*, 2018. ISSN 00200255. doi:10.1016/j.ins.2018.08.026.

I. Sindhu, S. M. Daudpota, K. Badar, M. Bakhtyar, J. Baber, and M. Nurunnabi. Aspect-based opinion mining on student's feedback for faculty teaching performance evaluation. *IEEE Access*, 7:108729–108741, 2019. ISSN 21693536. doi:10.1109/ACCESS.2019.2928872.

R. Singh and R. Singh. Applications of sentiment analysis and machine learning techniques in disease outbreak prediction – a review. *Materials Today: Proceedings*, 2021. ISSN 2214-7853. doi:https://doi.org/10.1016/j.matpr.2021.04.356. URL https://www.sciencedirect.com/science/article/pii/S2214785321032764.

P. Smith and M. Lee. Cross-discourse Development of Supervised Sentiment Analysis in the Clinical Domain. In *Proceedings of the 3rd Workshop in Computational Approaches to Subjectivity and Sentiment Analysis*, pages 79–83, Jeju, Korea, jul 2012. Association for Computational Linguistics. URL https://aclanthology.org/W12-3712.

M. Speriosu, N. Sudan, S. Upadhyay, and J. Baldridge. Twitter Polarity Classification with Label Propagation over Lexical Links and the Follower Graph. *Proceedings of the Conference on Empirical Methods in Natural Language Processing*, 2011. ISSN 1937284131.

P. Sultan, K. Ando, E. Sultan, J. E. Hawkins, A. Chitneni, N. Sharawi, N. Sadana, L. E. Blake, P. M. Singh, P. Flood, and B. Carvalho. A systematic review of patient-reported outcome measures used to assess postpartum pain using consensus based standards for the selection of health measurement instruments (cosmin) guidelines. *British Journal of Anaesthesia*, 2021. ISSN 0007-0912. doi:https://doi.org/10.1016/j.bja.2021.03.035. URL https://www.sciencedirect.com/science/article/pii/S000709122100235X.

M. Thelwall, K. Buckley, and G. Paltoglou. Sentiment strength detection for the social web. *Journal of the American Society for Information Science and Technology*, 2012. ISSN 15322882. doi:10.1002/asi.21662.

E. Tutubalina, Z. Miftahutdinov, S. Nikolenko, and V. Malykh. Medical concept normalization in social media posts with recurrent neural networks. *Journal of Biomedical Informatics*, 84:93–102, 2018. ISSN 15320464. doi:10.1016/j.jbi.2018.06.006.

M. Usama, W. Xiao, B. Ahmad, J. Wan, M. M. Hassan, and A. Alelaiwi. Deep Learning Based Weighted Feature Fusion Approach for Sentiment Analysis. *IEEE Access*, 7: 140252–140260, 2019. ISSN 21693536. doi:10.1109/ACCESS.2019.2940051.

Y. Wang, G. Huang, J. Li, H. Li, Y. Zhou, and H. Jiang. Refined global word embeddings based on sentiment concept for sentiment analysis. *IEEE Access*, 9:37075–37085, 2021. doi:10.1109/ACCESS.2021.3062654.

C.-H. Wei, B. R. Harris, D. Li, T. Z. Berardini, E. Huala, H.-Y. Kao, and Z. Lu. Accelerating literature curation with text-mining tools: a case study of using PubTator to curate genes in PubMed abstracts. *Database : the journal of biological databases and curation*, 2012:bas041, 2012. ISSN 1758-0463. doi:10.1093/database/bas041. URL http://www.ncbi.nlm.nih.gov/pubmed/23160414http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC3500520.

C. H. Wei, H. Y. Kao, and Z. Lu. PubTator: a web-based text mining tool for assisting biocuration. *Nucleic acids research*, 2013. ISSN 13624962. doi:10.1093/nar/gkt441.

K. Weiss, T. M. Khoshgoftaar, and D. D. Wang. A survey of transfer learning. *Journal of Big Data*, 2016. ISSN 21961115. doi:10.1186/s40537-016-0043-6.

J. Weston, A. Bordes, O. Yakhnenko, and N. Usunier. Connecting language and knowledge bases with embedding models for relation extraction. In *EMNLP 2013 - 2013 Conference on Empirical Methods in Natural Language Processing, Proceedings of the Conference*, 2013. ISBN 9781937284978.

D. S. Wishart, Y. D. Feunang, A. C. Guo, E. J. Lo, A. Marcu, J. R. Grant, T. Sajed, D. Johnson, C. Li, Z. Sayeeda, N. Assempour, I. Iynkkaran, Y. Liu, A. Maclejewski, N. Gale, A. Wilson, L. Chin, R. Cummings, D. Le, A. Pon, C. Knox, and M. Wilson. DrugBank 5.0: A major update to the DrugBank database for 2018. *Nucleic Acids Research*, 2018. ISSN 13624962. doi:10.1093/nar/gkx1037.

Q. Yang, H. Xie, G. Cheng, F. L. Wang, and Y. Rao. Pronunciation-Enhanced Chinese Word Embedding. *Cognitive Computation*, 1:3, feb 2021. ISSN 18669964. doi:10.1007/s12559-021-09850-9. URL https://doi.org/10.1007/s12559-021-09850-9.

J. Yu, J. Jiang, and R. Xia. Entity-sensitive attention and fusion network for entity-level multimodal sentiment classification. *IEEE/ACM Transactions on Audio Speech and Language Processing*, 28:429–439, 2020. ISSN 23299304. doi:10.1109/TASLP.2019.2957872.

Y. Zhang, Q. Chen, Z. Yang, H. Lin, and Z. Lu. BioWordVec, improving biomedical word embeddings with subword information and MeSH. *Scientific Data*, 2019a. ISSN 20524463. doi:10.1038/s41597-019-0055-0.

Y. Zhang, Q. Chen, Z. Yang, H. Lin, and Z. Lu. BioWordVec, improving biomedical word embeddings with subword information and MeSH. *Scientific data*, 6(1):52, 2019b. ISSN 20524463. doi:10.1038/s41597-019-0055-0. URL http://dx.doi.org/10.1038/s41597-019-0055-0.

Z. Zhang, J. Han, J. Deng, X. Xu, F. Ringeval, and B. Schuller. Leveraging Unlabeled Data for Emotion Recognition with Enhanced Collaborative Semi-Supervised Learning. *IEEE Access*, 2018. ISSN 21693536. doi:10.1109/ACCESS.2018.2821192.

B. L. Zhong, W. Luo, H. M. Li, Q. Q. Zhang, X. G. Liu, W. T. Li, and Y. Li. Knowledge, attitudes, and practices towards COVID-19 among chinese residents during the rapid rise period of the COVID-19 outbreak: A quick online cross-sectional survey. *International Journal of Biological Sciences*, 2020. ISSN 14492288. doi:10.7150/ijbs.45221.

W. Zhou, V. I. Torvik, and N. R. Smalheiser. ADAM: Another database of abbreviations in MEDLINE. *Bioinformatics*, 2006. ISSN 13674803. doi:10.1093/bioinformatics/btl480.

M. Zolnoori, K. W. Fung, T. B. Patrick, P. Fontelo, H. Kharrazi, A. Faiola, N. D. Shah, Y. S. Shirley Wu, C. E. Eldredge, J. Luo, M. Conway, J. Zhu, S. K. Park, K. Xu, and H. Moayyed. The PsyTAR dataset: From patients generated narratives to a corpus of adverse drug events and effectiveness of psychiatric medications. *Data in Brief*, 2019. ISSN 23523409. doi:10.1016/j.dib.2019.103838.

C. Zucco, S. Bella, C. Paglia, P. Tabarini, and M. Cannataro. Predicting abandonment in telehomecare programs using sentiment analysis: A system proposal. In *2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pages 1734–1739, 2018. doi:10.1109/BIBM.2018.8621481.

E. Zuo, H. Zhao, B. Chen, and Q. Chen. Context-Specific Heterogeneous Graph Convolutional Network for Implicit Sentiment Analysis. *IEEE Access*, 8:37967–37975, 2020. ISSN 21693536. doi:10.1109/ACCESS.2020.2975244.