Using BERT and Semantic Patterns to Analyze Disease Outbreak Context over Social Network Data

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Abstract: Predicting disease outbreaks has been a focus for various institutions and researchers for many years. However, any models that seemed to get close to resolve this issue have failed to predict potential outbreaks with accuracy over time. For leveraging the social media data effectively, it is crucial to filter out noisy information from the large volume of data flux so that we could better estimate potential disease outbreaks with growing social data. Not satisfied with essential keyword-based filtration, many researchers turn to machine learning for a solution. In this paper, we apply deep learning techniques to address the Tweets classification problem concerning disease outbreak predictions. To achieve this, we curated a labeled corpus of Tweets that reflect different types of disease-related reports, showcasing diverse community sentiment and varied potential usages in emergency responses. Further, we used BERT, a word embedding and deep learning method to apply transfer learning against our curated dataset. Applying BERT showed that it performs better in comparable results to Long short-term memory (LSTM) and outperforming the baseline model on average in terms of accuracy and F-score.

1 INTRODUCTION

Social media over the past years has increased the potential of how information is collected and analyzed over time, as the data grows (Collier and Doan, 2012). Researchers to date have been leveraging such a platform to aggregate and find patterns in community behavior, information retrieval, sentiment analysis, outbreak detection, and damage assessment (Keshtkar and Inkpen, 2009). A foundation that guarantees the success of all these tasks is an (or some) effective filtering technique(s) that could filter out noisy information carried by the data stream and cream off those messages containing rich information about such analytical patterns (Lampos and Cristianini, 2010).

This study intends to examine such data, especially tweets, for modeling a disease-related outbreak detection system. Our model allows users to monitor and estimate potential disease-outbreaks within a selected area (NYC). The model pipeline illustrated in Figure 1 describes our process of identifying tweets as personal, news, or disease-related and further utilizes a combination of natural language processing techniques, machine learning algorithms, and deep learning models to determine features, patterns, topics, word embedding, and other linguistics patterns. We then conducted various analyses, such as; Identifying language models, Document-based Clustering, Spam Classification, Tf-idf, Word2Vector, Topic Modeling (LDA), and finally creating BERT Classification Model for Sickness Related Tweets.

At the first glance, we investigated that many tweets on just simple keyword-based streaming collected many noise-related tweets like news articles, retweets, known-sickness-related health mentions, and so on so forth. So to obtain relevant tweets out of our noisy streams, we applied spam filtration, classified tweets for importance and then applied different preprocessing techniques and analysis to identify suitable features and patterns, to further train and hypertune our sickness related tweets classification model. (Saeed et al., 2019)

Post model creation, we obtain a unique corpus of tweets, which are health and sickness-related, showing interesting patterns. Based on our collected and processed corpus, we investigated that our final Tweets based disease distribution obtained a very close correlation (0.983) with the best model published by CDC for the 2012-13 flu season (Shah, 2017).

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Our model identified various pattern in unique term usage within sickness-related tweets, for example, most frequent keywords found within our corpus hinted towards the measles outbreak in the year 2012 and locality-wide sickness in general (Collier and Doan, 2012). Most frequent keywords included terms such as; hope, better, got, flu, feel, sick, allergy, chicken, vaccine. In other findings, we investigated most trigrams patterns, such as: 'I, got, measles,' 'chickenpox measles,' 'got, chicken, pox,' 'think, got, measles.' and so forth.

Another interesting pattern that we investigated using the Word2vector model and t-SNE visualization was that the term 'sick' represented itself as the center of the network and was closely surrounded by frequent terms such as health, elderly, mentally, dirt, chicken, and hospital, among others. Seeing this as a suitable feature we also enabled this as a visual feature within our system's dashboard to allow user to visualize any related word in the tweet, and visualize all the surrounded patterns. (Wang et al., 2017)

Using sentiment analysis; we used the positive, negative and neutral sentiment to identify further if the tweet present within our corpus of sick and health tweets convey negative and neutral sentiment so it may act as a cross measure to confirm the tweet as a suitable document for disease intent.

Lastly, in time series analysis, called temporal analysis; we identified total 104,293 sickness and health-related tweets from New York area itself, where the weekly number of tweets indicated that disease symptoms were strongly correlated with weekly CDC ILI outpatient counts from October 2012 - May 2013 ($r = 0.93$; $p < 0.001$) (Aramaki et al., 2011). Other findings and analysis were also observed within our conducted EDA Reports as well.

This paper is organized in following sections: **Section 2** describes different datasets collected for the study. **Section 3** describes the methods utilized for data preprocessing. **Section 4** explains our methodology and how models are curated. **Section 5** explain obtained results of classification, clustering, and other analysis.

2 DATA ACQUISITION

For our study we curated a unique collection of datasets from various sources for measuring accuracy against ground truth values as well as a streaming collection of 1.2 Million unique tweets from New York City (NYC) Region.

2.1 CDC Dataset

To curate our ground truth dataset, we utilized the data published by Epidemiology and Prevention Branch in the Influenza Division at the Centers for Disease Control (CDC), where they collect, compile and analyze information on influenza related activity year-round in the United States and produce FluView, a weekly influenza surveillance report, and FluView Interactive, which allows for more in-depth exploration of influenza and flu related surveillance data across states (Cooper et al., 2015).

Information gathered within these published data dumps on CDC site marks information within five categories from eight different data sources, such as:

- when and where influenza and sickness related activity is occurring.
- Track influenza-related and flu related illness cases.
- Determine what type of viruses are circulating within states.
- Measure the impact influenza and other viruses have on hospitalizations and deaths.

Based on these data sources the following data was extracted, transformed and loaded (ETL) within our environment for validating results:

2.1.1 ILI Net Data

ILINet consists of more than thirty five hundrred enrolled outpatient healthcare providers in all 50 states, Puerto Rico, the District of Columbia and the U.S. Virgin Islands reporting more than 47 million patient visits each year (Wang et al., 2017). Each week, approximately two thousand and two hundred outpatient healthcare providers around the country report data to CDC on the total number of patients seen for any reason and the number of those patients with influenza-like illness (ILI) by age group (0-4 years, 5-24 years, 25-49 years, 50-64 years, and >65 years) (Collier and Doan, 2012).

Baseline levels for flu activity are calculated using this data both nationally and for each region. Percentages at or above the baseline level are considered elevated and thus a potential outbreak. This baseline is used as our threshold.

2.1.2 WHO Data / NREVSS Data

Data collection from both the U.S. World Health Organization (WHO) Collaborating Laboratories and National Respiratory and Enteric Virus Surveillance System (NREVSS) laboratories began during the

1997-98 season (Ji et al., 2013). The volume of tested specimens has greatly increased during this time due to increased participation and increased testing. During the 1997-98 season 43 state public health laboratories participated in surveillance, and by the 2004-05 season all state public health laboratories were participating in surveillance (Lamb et al., 2015). The addition of NREVSS data during the 2000 season onwards roughly doubled the amount of virologic data reported each week.

The number of specimens tested and percentage positive rate vary by region and season based on different testing practices including triaging of specimens by the reporting labs, therefore it is not appropriate to compare the magnitude of positivity rates or the number of positive specimens between regions or seasons. (Long-Hay et al., 2019)

To avoid such bias in our ground truth dataset, this data source was also used in addition to the ILI Net data as a filter to generate a better and more accurate Annual Curve Series of our ground truth values.

2.2 Twitter Historic Data Stream

This tweet dataset was acquired via Full-Archive Search (FAS) Closed Enterprise Twitter API used by Prof. Xiang Ji and Prof. James Geller at New Jersey Institute of Technology, and Dr. Soon Chun at City University of New York - College of Staten Island, as part of their research. (Ji et al., 2013)

Within their paper on page 2, authors describe their dataset and mention that they keep a track of 4 twitter API key-word based streams which gathered unique tweets (no retweets) from New York area for 2 bacterial based diseases, listeria and Tuberculosis respectively, and, two viral diseases chickenpox and measles. For an easier accessibility to their dataset, on an approved request, their dataset was shared and is now stored within our MySQL DB instance. We utilize these collected tweet datasets as a data input for analyzing and understanding a unique pipeline for detecting NLP patterns and clues for further predicting potential outbreaks.

The acquired dataset has following components:

- listeria related tweets: 49023 tweet count (2011-10-18 to 2012-4-6) and (2012-5-10 to 2012-11-30)
- measles related tweets: 88205 tweet count (2011-10-18 to 2012-4-6) and (2012-5-10 to 2012-11-30)
- swine-flu related tweets: 284,531 tweet count (2011-10-18 to 2012-4-6) and (2012-5-10 to 2012-11-30)
- tuberculosis related tweets: 167,380 tweet count (2011-10-18 to 2012-4-6) and (2012-5-10 to 2012-11-30)

2.2.1 ATAM Twitter Historic Data

This tweet dataset was curated by M. Paul and M. Dredze, during their study (Paul et al., 2017). This dataset collection includes the set of tweets used as input for training Ailment Topic Aspect Model (ATAM) for tweets which further allowed them to identify and tag named entities associated with ailments and sickness and their symptoms (Paul et al., 2017). We utilized their training dataset along with our previous FAS collected corpus to further generate a smoother time series dataset for generating a ILI based Tweet frequency curve for sickness related tweets.

The tweets used in their study was streamed using a keywords text file which contains a total of two hundred and fifty six health-related keywords describing the names of diseases, symptoms, and treatments and medications (Paul et al., 2017). These keyword lists are used to create input for ATAM (which requires phrases to be labeled as symptoms or treatments), and also to initially filter our dataset when constructing our health classifiers.

Based on above keyword streams their dataset was further organized in two columns for distribution where first column represented unique tweet IDs and the second column indicated the ailment ID for the ailment sampled for that tweet.

The dataset being rather large for API query rate limit only Tweet ID was provided which through tweet hydration process (Paul et al., 2017) was further successfully retrieved, processed and loaded within our twitter dataset leading to a total final count of two million four hundred and seventy-five thousand, two hundred and seventy-two tweets.

2.3 Twitter Spam Annotation

As in all social networks, spam messages drastically increase distribution noise and provide no saliency when generating the ILI distribution (Aramaki et al., 2011). In this study, we consider as spam all tweets that do not refer to disease.

To achieve this we used a pre-labeled health tweets annotations dataset, of 5000 tweets which was tagged using Amazon's Mechanical Turk, as produced by Michael J. Paul and Mark Dredze, during their research at Johns Hopkins University (Paul et al., 2017). The annotations as described on page 2 of their paper, label tweets as they relate to health.

For our use case we utilized above dataset to place tweets in one of the five categories, and that each indi-

Table 1: Spam Annotation Tags and Label Index.

tags	label
health	0
notenglish	1
notsure	2
sick	3
unrelated	4

vidual tweet must reside in a given category. We only took into account self-reported tweets in our pipeline; in this process, we eliminate anomalies in our generated curve due to mass media coverage of rare diseases (Lampos and Cristianini, 2010). We additionally distinguish individuals who have a disease from those who are worried about another's ailments, with the former affecting the resultant distribution.

The annotations proposed in the study, label tweets for if as they relate to person talking about their sickness, health-information or not. The labels which were used to tag tweets as important vs spam are shown in Table 1.

For current study, we trained an SVM Model using linear kernel over n-grams for 1-3 tokens to predict the tags on our 2 million tweet corpora, we obtained total of 135,547 tweets which were sickness and health related and the rest were marked as spam with an accuracy of 0.983. After obtaining sickness and health related tweets, we conducted feature engineering processes to build our outbreak prediction pipeline. The process of how this predication model was curated and it's results are explained more precisely in section 4 of this paper.

3 PREPROCESSING AND FEATURE SELECTION

3.1 UTF-8 Unicode-encoding

All tweets over loading within SQL Database with UTF-8 encoding, many tweets retained it's original form, but when retrieved within our analysis pipeline even though the tweets were intact, by observing at some randomly selected entries, we observed strange patterns of characters "\xef \xbf \xbd", occurring consistently over corpus, in exploratory analysis report we discovered most of them represented encoded emoji text, which is an essential aspect in addition to identifying proper sentiment in modern text (Keshtkar and Inkpen, 2009). So instead of discarding such information during format translation, we normalized and decomposed tweet text for obtaining the original tweet form. This process is commonly known as NF (Normalization Form) + KD (Compatibility Decomposition) (Keshtkar and Inkpen, 2009). We applied this process over our tweets corpus with ASCII setting and as a result we obtained proper tweets with intact emoji text, preserved URLs, hashtags and mentions with minimal special characters within our corpus.

3.2 Tokenization

Once we have cleaner pure tweets with no retweets, we then applied tokenization methods: for this we used a python based NLTK package's Twitter-aware tokenizer. This tokenizer is designed to be flexible and easy to adapt to new domains and tasks. The basic logic follows that the tuple regex defines a list of regular expression strings that are then put, in order, into a compiled regular expression object where we then apply tokenization where preserve_case option is set to be False enabling us to reduce the number of duplicate tokens caused due to capitalization issue.

Once our tweet was tokenized with twitter aware tokenizer, we noticed some inconsistencies still left within our processed tweets like '@', 'http', 'https'. This was mainly due to the presence of weblinks and mentions. To deal with such, we utilized a third party, preprocessing package called "twitter-preprocessor". This preprocessor cleaned and parsed tweets of, URLs, Hashtags, Mentions and Reserved words (RT, FAV).

3.3 Stemming and Lemmatization

Before proceeding to analysis, it is suggested to have more common terms within the corpora, to achieve better vectors (Brownstein et al., 2010). We processed our corpora further by stemming the words/tokens itself. To do this we used snowball stemmer as it's known to be better model for stemming documents with more than one language. Once, with the stemmer we trimmed our words for all the ending action words like "-ing", "-ed" or "-s". Through this process, we obtained the word's pure dictionary form. But usually, when we stem words, we tend to lose the actual meaning of the word itself, as the trim may happen either too much or too less. So, to resolve this we applied a WordNet Lemma trained on Google News Corpus, which then converted our stemmed words to its closest dictionary form.

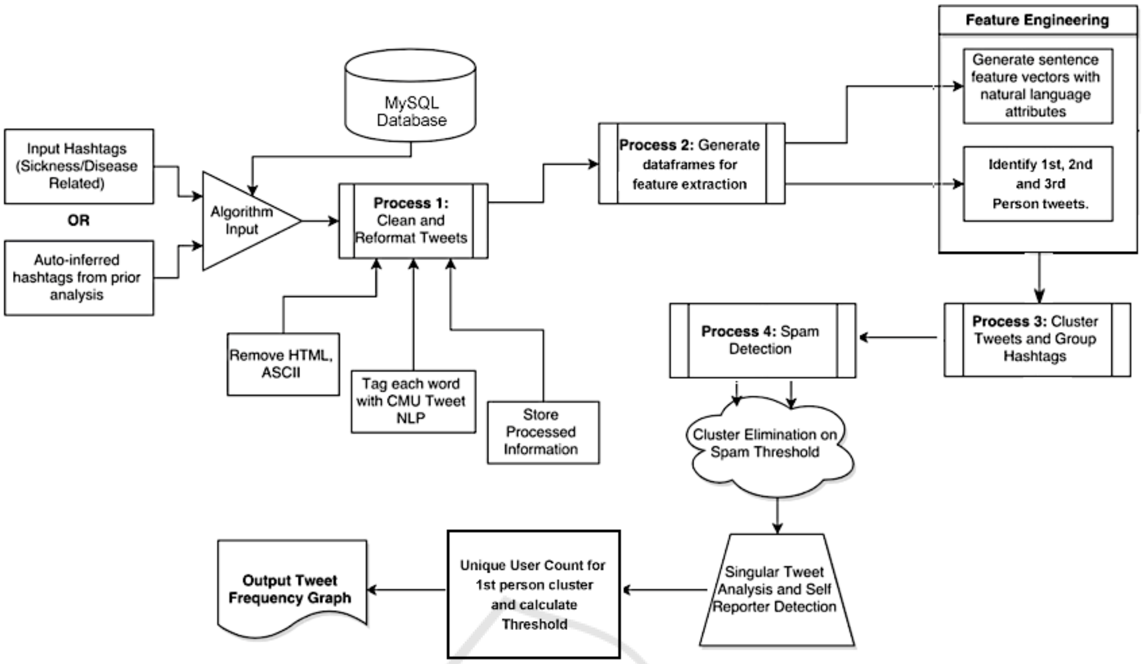

Input Hashtags (Sickness/Disease Related)
OR
Auto-inferred hashtags from prior analysis
MySQL Database
Algorithm Input
Process 1: Clean and Reformat Tweets
Remove HTML, ASCII
Tag each word with CMU Tweet NLP
Store Processed Information
Process 2: Generate dataframes for feature extraction
Feature Engineering
Generate sentence feature vectors with natural language attributes
Identify 1st, 2nd and 3rd Person tweets.
Process 3: Cluster Tweets and Group Hashtags
Process 4: Spam Detection
Cluster Elimination on Spam Threshold
Singular Tweet Analysis and Self Reporter Detection
Unique User Count for 1st person cluster and calculate Threshold
Output Tweet Frequency Graph

Figure 1: System flowchart for tweets pre-processing.

3.4 N-Grams

Once we obtained our sickness and health related tweets post preprocessing, we first produced a frequency distribution graph to find the most common words and collections of words within our tweet corpus. The results obtained from this are shown in Figure 2a and Figure 2b.

3.5 TF-IDF and Bag of Words

Once, done tokenizing, we performed a term-frequency and inverse document frequency score on our tweet corpus to identify top terms occurring together within our dataset. The following are some terms which occurred most frequently together: hope, better, got, flu, feel, sick, allergy, chicken, vaccine. In Bag of words findings, we investigated most tri-grams patterns repeating, such as: ‘I, got, measles,’ ‘chickenpox measles,’ ‘got, chicken, pox,’ ‘think, got, measles.’ and so forth.

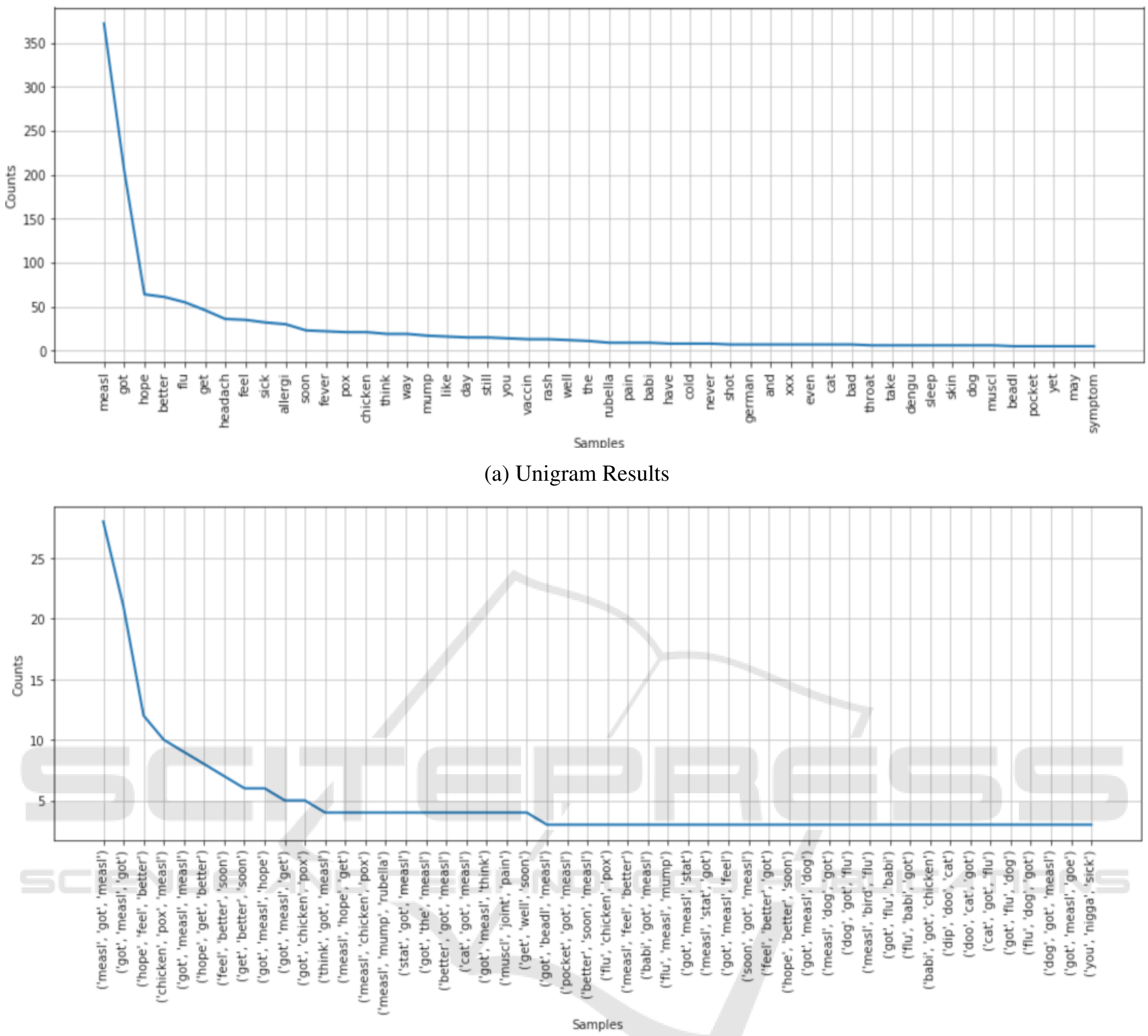
3.6 Sentiment Polarity

VADER (Valence Aware Dictionary and sEntiment Reasoner) is a lexicon and rule-based sentiment analysis tool that is specifically attuned to sentiments expressed in social media. This sentiment lexicon takes care of emoji’s and as well as sentiment expressed via slang keywords.

Some examples of term combinations detected as score boosters within sentiment analysis done by this package, including proper handling of sentences is:

- typical negations (e.g., “not good”) and use of contractions as negations (e.g., “wasn’t very good”)
- conventional use of punctuation to signal increased sentiment intensity (e.g., “Good!!!”) and word-shape to signal emphasis (e.g., using ALL CAPS for words/phrases)
- Use of degree modifiers to alter sentiment intensity (e.g., intensity boosters such as “very” and intensity dampeners such as “kind of”)
- understanding many sentiment-laden slang words as modifiers such as ‘wassup’ or ‘friggin’ or ‘kinda’ and many sentiment-laden emoticons such as “:(” and “:/”
- translating utf-8 encoded emojis and sentiment-laden initialisms and acronyms.

Out of all scores provided by this package we used compound score to analyze tweet sentiment. The compound score is computed by summing the valence scores of each word in the lexicon, adjusted according to the rules, and then normalized to be between -1 (most extreme negative) and +1 (most extreme positive). This is the most useful metric in our case as it gives a single unidimensional measure of sentiment for a given sentence (Collier and Doan, 2012).



(a) Unigram Results

(b) Trigram Results

Figure 2: Term frequency charts (a, b), represents x axis as terms and y axis as each term's frequency count.

Calling it a 'normalized, weighted composite score' (NWCS for short) is accurate. We set standardized thresholds for classifying sentences as either positive, neutral, or negative. Typical threshold values for grading sentiment labels are:

- positive sentiment: NWCS >= 0.05
- neutral sentiment: -0.05 <NWCS <0.05
- negative sentiment: NWCS <= -0.05

The positive, neutral, and negative scores are ratios for proportions of text that fall in each category (so these should all add up to be 1 or close to it with float operation). We use the positive negative and neutral sentiment to further identify if the tweet present within our corpus of sick and health tweets convey negative and neutral sentiment so it may act as a cross measure to confirm the corpus as suitable document for disease intent.

3.7 Part-Of-Speech (POS) Tags

In NLTK, POS functionality is present in a form of a drop in tagger, that reads text in around all languages for us mainly English and assigns parts of speech to each word (and other token), such as noun, verb, adjective, etc., as shown in Figure 4. We focus mainly on pronouns and nouns to identify if the tweet is initiated by a 1st person, second person or 3rd person

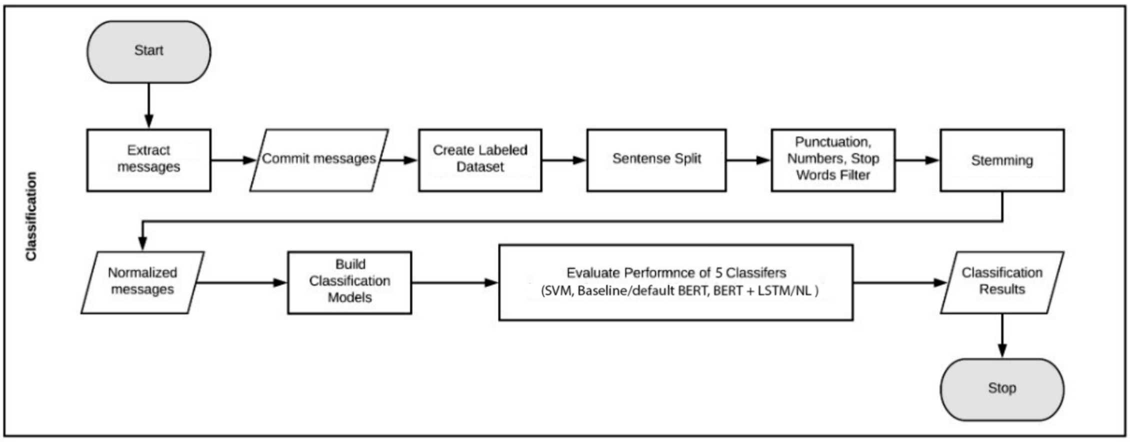
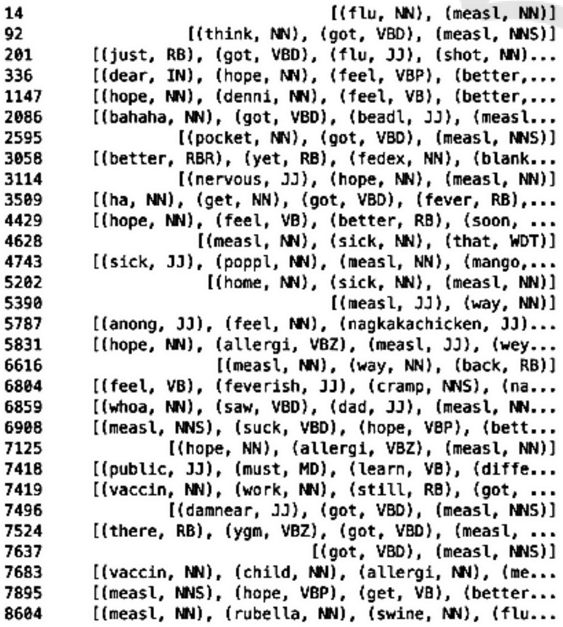

Classification
Start
Extract messages
Commit messages
Create Labeled Dataset
Sentense Split
Punctuation, Numbers, Stop Words Filter
Stemming
Normalized messages
Build Classification Models
Evaluate Performnce of 5 Classifers (SVM, Baseline/default BERT, BERT + LSTM/NL)
Classification Results
Stop

Figure 3: Classification Pipeline.

speech and use noun tags to identify, if the nouns present within our corpus match with any Symptoms and disease type so we may have an estimate to what type of disease is highlighted predominantly within our corpus (Collier and Doan, 2012).

3.8 Significant Tweet Isolation

Based on the processed tweet corpora and Euclidean-cosine similarity measure we produce similar documents clusters, in which we systematically identify our spam vs not spam tweets, then train, and apply a linguistic attribute-based classifiers to randomly selected subsets of each cluster, rejecting an entire cluster if its chosen subset contains a sufficiently large number of non-sickness tweets.



```
14                                  [(flu, NN), (measl, NN)]
92                   [(think, NN), (got, VBD), (measl, NNS)]
201        [(just, RB), (got, VBD), (flu, JJ), (shot, NN)...
336        [(dear, IN), (hope, NN), (feel, VBP), (better,...
1147       [(hope, NN), (denni, NN), (feel, VB), (better,...
2086       [(bahaha, NN), (got, VBD), (beadl, JJ), (measl...
2595                [(pocket, NN), (got, VBD), (measl, NNS)]
3058       [(better, RBR), (yet, RB), (fedex, NN), (blank...
3114                [(nervous, JJ), (hope, NN), (measl, NN)]
3509       [(ha, NN), (get, NN), (got, VBD), (fever, RB),...
4429       [(hope, NN), (feel, VB), (better, RB), (soon, ...
4628                  [(measl, NN), (sick, NN), (that, WDT)]
4743       [(sick, JJ), (poppl, NN), (measl, NN), (mango,...
5202                   [(home, NN), (sick, NN), (measl, NN)]
5390                                [(measl, JJ), (way, NN)]
5787       [(anong, JJ), (feel, NN), (nagkakachicken, JJ)...
5831       [(hope, NN), (allergi, VBZ), (measl, JJ), (wey...
6616                    [(measl, NN), (way, NN), (back, RB)]
6804       [(feel, VB), (feverish, JJ), (cramp, NNS), (na...
6859       [(whoa, NN), (saw, VBD), (dad, JJ), (measl, NN...
6908       [(measl, NNS), (suck, VBD), (hope, VBP), (bett...
7125               [(hope, NN), (allergi, VBZ), (measl, NN)]
7418       [(public, JJ), (must, MD), (learn, VB), (diffe...
7419       [(vaccin, NN), (work, NN), (still, RB), (got, ...
7496               [(damnear, JJ), (got, VBD), (measl, NNS)]
7524       [(there, RB), (ygm, VBZ), (got, VBD), (measl, ...
7637                              [(got, VBD), (measl, NNS)]
7683       [(vaccin, NN), (child, NN), (allergi, NN), (me...
7895       [(measl, NNS), (hope, VBP), (get, VB), (better...
8604       [(measl, NN), (rubella, NN), (swine, NN), (flu...
```

Figure 4: Terms associated with their respective tags.

3.9 Topic Modeling

As shown in Fig 5, with the use of LDA we identify the popular topics among each batch of remaining tweets clusters allowing us to identify most talked symptoms which further shows us information about most common disease within the outbreak.

3.10 Outbreak Threshold

The outbreak baseline is provided by CDC each year per region. As our stream checks for many influenza like illnesses we utilized similar calculation methods as cdc to calculate baseline threshold. As NYC falls under Region 2 in CDC ILI Net Dataset, therefore as per CDC the base line is 3.1% (New Jersey, New York City, Puerto Rico, and the U.S. Virgin Islands). The national percentage of patient visits to healthcare providers for ILI reported each week is calculated by combining state-specific data weighted by state population. This percentage is then compared each week with the national baseline of 2.2%. As baseline is compared in percentage, for us to convert our Tweets-ILI Corpus distribution into baseline format we do this by calculating the mean percentage of tweets for a non-influenza time period and comparing it against total number of tweets scraped for that season. A non-flu or non-sickness week is defined as periods of two or more consecutive weeks in which each week accounted for less than 2% of the season's total number of specimens that tested positive for sickness in public health laboratories (Blei et al., 2003).

Table 2: Evaluation metrics.

Model	Accuracy	Matthew's coeff	Macro precision	Macro recall	Macro F1
SVM-LinearSVC (5 k-fold)	0.63	-	0.62 (avg)	0.33 (avg)	0.36 (avg)
baseline BERT	0.71	0.56	0.58	0.6843	0.6071
default BERT	0.67	0.59	0.6043	0.7114	0.64
BERT+NL	0.67	0.59	0.6057	0.68	0.6314
BERT+LSTM	0.69	0.60	0.6129	0.6986	0.6400

4 RESULTS AND DISCUSSION

Figure 1 details our model pipeline to its fullest extent marking each relevant process. The pipeline accepts as input either a list of hashtags or auto-inferred terms from prior analysis (determined via linguistic term association). Our system then leverages the API to stream twitter data and runs an in-depth uninformative tweet elimination to allow identification of anomalies and unique disease outbreaks, thus providing predictive significance.

4.1 Tweet Clustering

Using the TF-IDF features ascertained in previous step and a mixed Euclidean-cosine similarity measure, we cluster tweets according to minimal cluster RSS value via the centroid-based k-means approach. Once our preprocessing and feature extraction was done, we wanted to identify topic clusters for all tweets identified as health and sickness related and see what topics were most common among our tweet-corpus.

To achieve this we applied Latent Dirichlet Allocation (LDA) over our clustered corpus to further identify 1st Person Tweets and Health related tweets to find topics and related words. This topic modelling step gave us insights into understanding the specific disease talk and also highlighted symptom information further assisting us in nailing down a potential outbreak disease name when compared against current disease ontology (Mikolov et al., 2014). For example, for the measles corpus topics as shown in Figure 5 were identified as significant.

4.2 SVM and BERT Classification

We used classification techniques to identify tweets as either sickness or health related using Health Tweet Annotation dataset. The flowchart diagram as shown in Figure 3 overviews our comprehensive process of cleaning up corpus and identifying a classifier with maximum accuracy.

Post aggregating and preprocessing our the dataset with the aforementioned health-tweet annotation and spam filtration, we used our resultant corpus as training data to create a health tweet classifier for disease related tweets. To compare our model, we use SVM classifier with LinearSVC kernel and BERT along with it's other customized variations.

On further result comparison as shown in table 2, we investigated that the fine-tuned approach in the paper of Devlin et al (Wang et al., 2017). and BERT-based bidirectional LSTM achieved best performance, boosting up 3.34% in terms of accuracy. And F-1 as compared to results obtained via our Linear Kernel SVM model and other customized BERT Variations.

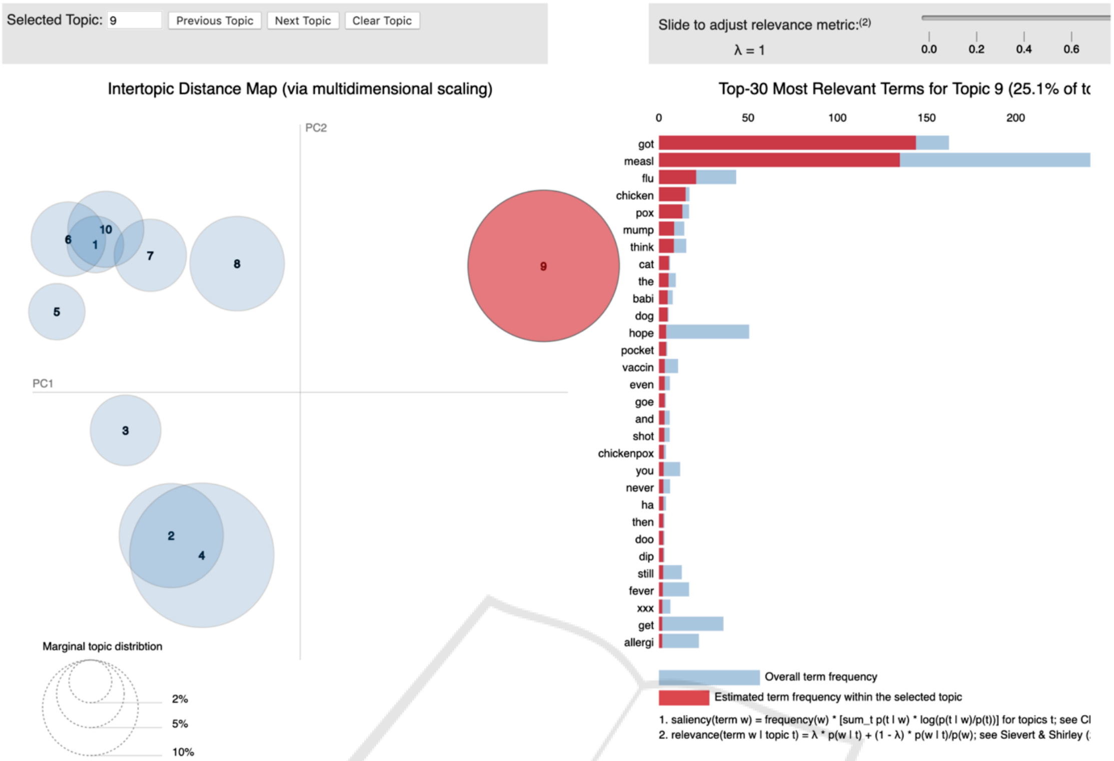
The reason we choose BERT over other classifiers, it has achieved state-of-art performance in many NLP tasks. For baseline, we set up a bidirectional LSTM with GloVe Twitter embeddings. These models are built based on the pytorch-pretrained-BERT repository possessed by huggingface [1]. All the BERT models are built upon BERT base uncased model, which has 12 transformer layers, 12 self-attention heads, and with a hidden size 768. The baseline model is a single-layer bidirectional LSTM neural network with hidden size 256. The model receives pre-trained GloVe Twitter 27B embeddings (200d) as input. The stacked final hidden state of the sequence is linked to a fully connected layer to perform softmax.

4.3 Time Series Analysis

We subsequently plot the frequency distribution of relevant tweets over time in order to compare our model's predicted health and sickness tweets upon the CDC-ILI curve.

Our system when given 2012-2013 tweet dataset which was known for a major measles outbreak dur-

[1] https://github.com/huggingface/pytorch-pretrained-BERT



1. saliency(term w) = frequency(w) * [sum_t p(t l w) * log(p(t l w)/p(t))] for topics t; see Cl
2. relevance(term w l topic t) = λ * p(w l t) + (1 - λ) * p(w l t)/p(w); see Sievert & Shirley (

Figure 5: Prominent measles related topics in our corpus.

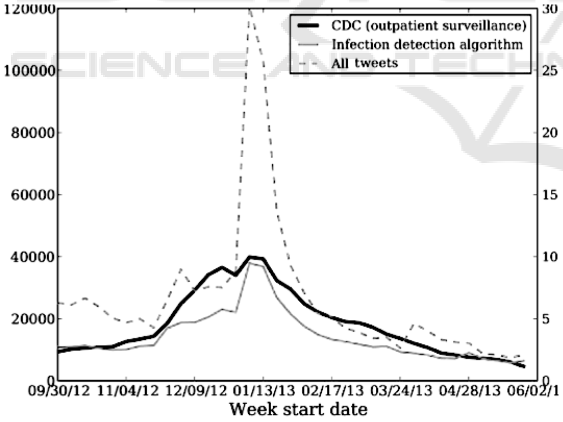


Figure 6: Tweets vs CDC ILI 2012.

ing those times; it identified 104,200 sickness and health tweets from New York Area itself and the weekly number of tweets indicating disease symptoms showed a strong correlation with weekly CDC ILI outpatient counts from October 2012 - May 2013 (r = 0.93; p <0.001). The difference between these correlations were also significant at the p<0.001 level.

The mean absolute error of the keyword-based estimates is 0.0102 after normalizing the weekly rates sum to 1. The mean absolute error of our symptoms in tweet estimates is 0.0046, a 45% reduction in error over the keyword filter. The national estimates produced by our classification model alongside the CDC rates is shown in Figure 6.

5 CONCLUSION

In this paper, we apply deep learning techniques, such as BERT, LSTM and word embedding, to address the Tweets classification for disease outbreak predictions. We used a labeled corpus of Tweets that reflect different types of disease-related reports. We used different features, i.e, ngrams, Part-of-speech, TFIDF, to measure our analysis. As results, we investigated some semantics patterns that users used in their tweet are very relevant to disease outbreak, i.e, ‘I, got, measles,’ ‘chickenpox measles,’ ‘got, chicken, pox,’ ‘think, got, measles’. For future work, we plan to apply other dataset related to other disease to compare with current work.

REFERENCES

Aramaki, E., Maskawa, S., and Morita, M. (2011). Twitter Catches The Flu: Detecting Influenza Epidemics using Twitter. In *Proceedings of the 2011 Conference on Empirical Methods in Natural Language Processing*, pages 1568–1576, Edinburgh, Scotland, UK. Association for Computational Linguistics.

Blei, D. M., Ng, A. Y., and Jordan, M. I. (2003). Latent Dirichlet Allocation. *Journal of Machine Learning Research*, 3(Jan):993–1022.

Brownstein, J. S., Freifeld, C. C., Chan, E. H., Keller, M., Sonricker, A. L., Mekaru, S. R., and Buckeridge, D. L. (2010). Information Technology and Global Surveillance of Cases of 2009 H1n1 Influenza. *New England Journal of Medicine*, 362(18):1731–1735.

Collier, N. and Doan, S. (2012). Syndromic Classification of Twitter Messages. In Kostkova, P., Szomszor, M., and Fowler, D., editors, *Electronic Healthcare*, volume 91, pages 186–195. Springer Berlin Heidelberg, Berlin, Heidelberg.

Cooper, G. F., Villamarin, R., Tsui, F.-C. R., Millett, N., Espino, J. U., and Wagner, M. M. (2015). A Method for Detecting and Characterizing Outbreaks of Infectious Disease from Clinical Reports. *J Biomed Inform*, 53:15–26.

Ji, X., Chun, S. A., and Geller, J. (2013). Monitoring public health concerns using twitter sentiment classifications. In *2013 IEEE International Conference on Healthcare Informatics*, pages 335–344.

Ji, X., Chun, S. A., and Geller, J. (2013). Monitoring Public Health Concerns Using Twitter Sentiment Classifications. In *2013 IEEE International Conference on Healthcare Informatics*, pages 335–344, Philadelphia, PA, USA. IEEE.

Keshtkar, F. and Inkpen, D. (2009). Using sentiment orientation features for mood classification in blogs. In *2009 International Conference on Natural Language Processing and Knowledge Engineering*, pages 1–6.

Lamb, A., Paul, M. J., and Dredze, M. (2015). Separating Fact from Fear: Tracking Flu Infections on Twitter. page 7.

Lampos, V. and Cristianini, N. (2010). Tracking the flu pandemic by monitoring the social web. In *2010 2nd International Workshop on Cognitive Information Processing*, pages 411–416, Elba Island, Italy. IEEE.

Long-Hay, P., Yamamoto, E., Bun, S., Savuth, T., Buntha, S., Sokdaro, S., Kariya, T., Saw, Y. M., Sengdoeurn, Y., and Hamajima, N. (2019). Outbreak detection of influenza-like illness in Prey Veng Province, Cambodia: a community-based surveillance. *Nagoya J Med Sci*, 81(2):269–280.

Mikolov, T., Yih, W.-t., and Zweig, G. (2014). Linguistic Regularities in Continuous Space Word Representations. page 6.

Paul, M. J., Dredze, M., and University, J. H. (2017). You Are What You Tweet: Analyzing Twitter for Public Health. page 8.

Saeed, Z., Abbasi, R. A., Maqbool, O., Sadaf, A., Razzak, I., Daud, A., Aljohani, N. R., and Xu, G. (2019). What's Happening Around the World? A Survey and Framework on Event Detection Techniques on Twitter. *J Grid Computing*, 17(2):279–312.

Shah, M. (2017). Disease Propagation in Social Networks: A Novel Study of Infection Genesis and Spread on Twitter. page 17.

Wang, C.-K., Singh, O., Tang, Z.-L., and Dai, H.-J. (2017). Using a Recurrent Neural Network Model for Classification of Tweets Conveyed Influenza-related Information. In *Proceedings of the International Workshop on Digital Disease Detection using Social Media 2017 (DDDSM-2017)*, pages 33–38, Taipei, Taiwan. Association for Computational Linguistics.