On the Ground Validation of Online Diagnosis with Twitter and Medical Records

Todd Bodnar[*]
Pennsylvania State University
Department of Biology
University Park, PA 16802
tjb5215@psu.edu

Vicki Barclay

Conrad S Tucker

Marcel Salathé
Pennsylvania State Unive
Department of Biology
University Park, PA 168
salathe@psu.edu

ABSTRACT
This is an abstract

Categories and Subject Descriptors
I.2.1 [**Artificial Intelligence**]: Applications and Expert Systems—*Medicine and Science*

General Terms
Experimentation, Validation

Keywords
Twitter, Validation, Digital Epidemiology, Remote Diagnosis

1. INTRODUCTION
Digital epidemiology → novel disease detection mechanisms.

Validation of this idea is important, but not done.

Pull med info of individuals professionally diagnosed with ILI and their twitter accts. Compare old methods. Suggest some new things.

In section 3 we describe the collection of diagnosis and Twitter information. In section 4 we consider extracting textual information from Tweets as a method for diagnosing influenza. In section 5 we consider anomalies in a user's Tweeting behavior as a signal for diagnosing influenza. In section 6 we extend these methods to other users on a persons social network to diagnose that person. In section 7 we aggregate the results of the previous classifiers to develop a more accurate classifier.

2. RELATED WORK
People with issues [1, 2, 6] also plos paper!

---

[*]Corresponding author

Most work to this point considers finding messages in tweets (i.e. "I'm sick") or in keyword frequencies.

Keyword [3, 4]

Tweet classification [3, 6, 8]

3. DATA COLLECTION
3.1 Medical Records
3.2 Twitter Records
We received a total of 119 user accounts for Twitter from the survey; 15 of which were discarded because the associated accounts were either non-existent, banned, or private. For each of the remaining 104 accounts, we pulled their profile information, their friends and followers information, their most recent 3000 tweets, and their friends profiles and tweets. Some users did not tweet during the month that they were sick; we kept those accounts as part of the control group. We were limited to the most recent 3000 tweets by Twitter's time line query, but this only effected two accounts – both of which posted multiple times per hour and were thrown out because we could only look back a few days.

We collected data by calling the Twitter API on the user account that we queried the longest time ago. Tweets, profile and follower information queries have separate rate limits and were collected in parallel. The 104 seed accounts collected above were given higher priority over their friends and followers. In total, we collected 37,599 tweets from the seed accounts and XX tweets from YY accounts that they either followed or were followed by.

4. TEXT BASED SIGNALS
In this section, we consider diagnosis based on classifying an individual tweet's content as either about ILI or not. We begin by dividing the tweets into two sets: tweets that were posted the same month that a user was sick, and tweets that were posted other times. We find a total of 1609 tweets from 35 users in the first category.

First we go the route of AUTHOR and AUTHOR by defining a set of keywords that are positive signals of influenza. We chose {flu, influenza, sick, cough, cold, medicine, fever} as our set of keywords. Of these seven keywords, we find a significant effect in 6 of the keywords during months when the user had ILI. (See table 1). Additionally, we try algorithmically selecting keywords by first finding the 12,393

Word	Total	Odds Ratio	Significance
flu	25	40.13898	2.707071e-49
influenza	1	0	0.8325418
sick	128	5.224356	5.366579e-16
cough	18	4.479715	0.009395649
cold	82	1.453834	0.4154262
medicin	9	11.19795	1.654012e-05
fever	13	26.19746	1.030862e-18

Table 1: Keyword effects.

most common keywords in the data set. We then rank them based off of information gain and choose the top 10, 100 or 1000 keywords from the list. In both of these cases, we preprocess the data by tokenizing the text on the characters ".,;':"()?!" - as well as spaces, tabs and line breaks - remove stop words[1], perform Porter stemming [7, 9] and convert the text to lower case. We then use the occurance or absence of these keywords as features for classification. We use naive bayes, random forest, J48, logistic regression and support vector machines to classify a user as being sick in a given month or not (see figure 1).
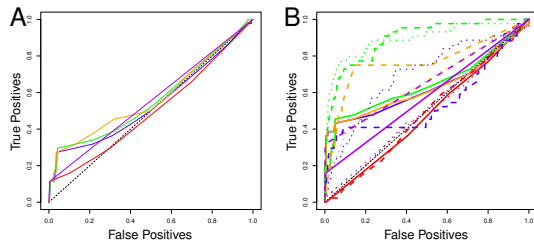

Figure 1: The ROC of classifiers that use hand chosen keywords (a) and algorithmically chosen keywords (b) to determine if an individual is ill. The top 10 (solid line), 100 (dashed line) and 1000 (dotted line) were selected as the features. (COMMENT: untill I add it to figures. Green is Naive bayes, red is j48, blue is logistic, orange is random forest and purple is SVM.)

Additionally, we hand rate all 1609 tweets, that were posted by individuals during the time of their illness, for information regarding the user's health. Additionally we sample a randomly selected set of 1609 tweets from times when the users did not have ILI as a control. We find 58 tweets from 17 (17/35 = 48.57%) individuals in our study that are about the user being sick. We also find zero tweets about ILI during times when they did *not* have ILI. While the use of a "human" classifier clearly does not scale, it allows for an approxamatly 100.0% accurate classification. Since regular machine learning algorithms preform much worse than 100.0% accuracy, the human classifier gives us an upper limit to the accuracy of a health monitoring system based off of tweet classification . (See table 2)

5. FREQUENCY BASED SIGNALS
We perform one-dimensional anomaly detection on each user's monthly tweeting rate as follows. First, we calculate the

---
[1]Stop words taken from Weka's stoplist version 3.7.10.

Sick	Not Sick	
17	18	Sick
0	66	Not Sick

Table 2: Confusion matrix of a Tweet-Classification based diagnosis system. Rows are of true values, columns are of predicted values.

Sick	Not Sick	
14	25	Sick
27	192	Not Sick

Table 3: Confusion matrix of the classifier based on anomalous tweeting rates. Rows are of true values, columns are of predicted values.

number of tweets in each month in the study period and discard any months where the user tweets less than ten times. This avoids issues caused by the user starting or stopping to use Twitter. We then calculate the z-score of the tweeting rate of the month that the user is ill by

$$z = \frac{|x - \bar{x}|}{\hat{s}} \quad (1)$$

Where $\bar{x}$ and $\hat{s}$ are the estimated mean and standard deviation of the user's tweeting rate. [5] We repeat this process for months when the user is not sick. We then decide that the user is sick if $z > 1.411$ where 1.411 was chosen through leave one out cross validation. We find a significant difference between the z-scores for months when a user was had ILI and months when the user did not ($p = 0.01303$, two-sample Kolmogorov-Smirnov test). Most of the time individuals are not sick (219 / 258 = 84.88%), resulting in a highly biased sample. Thus we optimize based on the F_1 score. The optimal z-score cutoff results in $F_1 = 35.0\%$. (See table 3.)

6. NETWORK BASED SIGNALS
Preliminary idea. Cascade effects causing echoes on social network. Also consider friends becoming ill around same time. Check @ tag

7. META CLASSIFIER
Combine features based off of previous signals, get something that's – hopefully – more accurate.

To this point, we have considered five approaches to detecting illness – keyword detection, keyword mining, human classification, frequency-based anomaly detection and network based classifiers – independently. Now we consider combining the results of the previous classifiers and develop a meta-classifier. (See figure 2) Concretely, we begin by selecting the classifier from each approach that has the largest area under the ROC curve. Then we use....

8. CONCLUSIONS
Comment on ∼ 250 mill active T users → 75 mill active US users, possibility of detecting ∼ 10% anual ILI rate, ∼ half
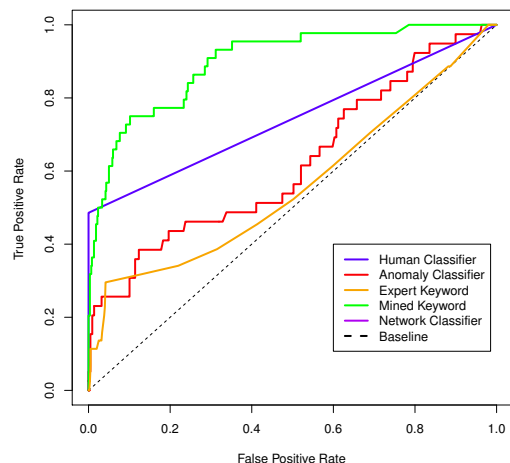
Figure 2: The accuracy of the previous classifiers (a) and the accuracy of various classifiers that use the previous classifier's results as features (b).

are detectable on twitter Twitter, so 12.5 mill cases as upper estimate.

9. REFERENCES

[1] T. Bodnar and M. Salathé. Validating Models for Disease Detection Using Twitter. *WWW 2013 Companion*, June 2013.

[2] D. Butler. When Google got flu wrong. *Nature*, 494(7436):155–156, Feb. 2013.

[3] A. Culotta. Towards detecting influenza epidemics by analyzing Twitter messages . In *the First Workshop*, pages 115–122, New York, New York, USA, 2010. ACM Press.

[4] S. Goel, J. M. Hofman, S. Lahaie, D. M. Pennock, and D. J. Watts. Predicting consumer behavior with Web search. *Proceedings of the National Academy of Sciences of the United States of America*, 107(41):17486–17490, Oct. 2010.

[5] F. E. Grubbs. Procedures for Detecting Outlying Observations in Samples. *Technometrics*, 11(1):1–21, 1969.

[6] A. Lamb, M. J. Paul, and M. Dredze. Separating Fact from Fear: Tracking Flu Infections on Twitter. *cs.jhu.edu*, 2013.

[7] M. F. Porter. An algorithm for suffix stripping. *Program: electronic library and information systems*, 14(3):130–137, 1980.

[8] M. Salathé and S. Khandelwal. Assessing vaccination sentiments with online social media: implications for infectious disease dynamics and control. *PLoS computational biology*, 7(10):e1002199, Oct. 2011.

[9] P. Willett. The Porter stemming algorithm: then and now. *Program: electronic library and information systems*, 2006.