Early Stage Influenza Detection from Twitter

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ABSTRACT
Influenza is an acute respiratory illness that occurs virtually every year and results in substantial disease, death and expense. Detection of Influenza in its earliest stage would facilitate timely action that could reduce the spread of the illness. Existing systems such as CDC and EISS which try to collect diagnosis data, are almost entirely manual, resulting in about two-week delays for clinical data acquisition. Twitter, a popular microblogging service, provides us with a perfect source for early-stage flu detection due to its real-time nature. For example, when a flu breaks out, people that get the flu may post related tweets which enables the detection of the flu breakout promptly. In this paper, we investigate the real-time flu detection problem on Twitter data by proposing Flu Markov Network (Flu-MN): a spatio-temporal unsupervised Bayesian algorithm based on a 4 phase Markov Network, trying to identify the flu breakout at the earliest stage. We test our model on real Twitter datasets from the United States along with baselines in multiple applications, such as real-time flu breakout detection, future epidemic phase prediction, or Influenza-like illness (ILI) physician visits. Experimental results show the robustness and effectiveness of our approach. We build up a real time flu reporting system based on the proposed approach, and we are hopeful that it would help government or health organizations in identifying flu outbreaks and facilitating timely actions to decrease unnecessary mortality.

Categories and Subject Descriptors
H.0 [Information Systems]: General

General Terms
Algorithm, Performance, Experimentation

Keywords
twitter, event detection, influenza detection

∗Dr. Trovato insisted his name be first.
†The secretary disavows any knowledge of this author’s actions.

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1. INTRODUCTION
Influenza is an acute respiratory illness that occurs every year. Approximately 10-15% of people get influenza each year and such disease results in up to 50 million illnesses and 500,000 deaths in the world every year. Detection of Influenza in its earliest stage would facilitate timely action that could reduce the spread of the illness and decrease the number of deaths. Indeed, early stage influenza detection has gained increasing importance recently due to the threat of newly emerging infections such as SARS, H5N1 and H5N9. Influenza surveillance systems have been established via the European Influenza Surveillance Scheme (EISS) in Europe and the Center for Disease Control (CDC) in the US to collect data from clinical diagnoses. Unfortunately, these systems are almost entirely manual, resulting in about two-week delays for clinical data acquisition. Public health authorities need to forecast the breakout of Influenza at the earliest time to ensure effective preventive intervention, giving rise to the increasing need for efficient sources of data for forecasting.

In an attempt to create new sources of flu reporting systems, early researchers used different types of influenza signals for surveillance, such as telephone calls [15] or drug sales [27]. The exten-
The qualitative diction suffers the following two limitations: (1) breakout detection. In addition, existing works on Twitter flu prediction usually use real world CDC data, but seldom explored the algorithm for flu breakout. To be specific, in Twitter, most existing works pay more attention to how well tweet data can fit real-world CDC data, but seldom explored the algorithm for flu breakout detection. In addition, existing works on Twitter flu prediction suffer the following two limitations: (1) spatial information is seldom considered. Spatial dependency is important in early-stage flu detection, especially in the case where current location does not show clear clue for flu breakout but most of its neighbors do. This has been demonstrated in many works in Epidemiology [5, 7, 14, 29]. (2) daily effect corresponds to fluctuation of the number of tweets posted based on what day it is within a week, or whether it is holiday etc. Such effect is seldom considered in existing works. As we can see in Figure 3 users publish tweets about flu almost twice as much on Monday as they do on Sunday. Neglecting such effects would result in mistakes in flu reporting.

To address these problems, in this paper, we introduce an unsupervised approach called Flu Markov Network (Flu-MN) for early stage flu detection by framing spatial and temporal information in a unified Markov Network. Our approach assumes Twitter users as "sensors" and collective tweets containing flu keywords as early indicators and robust predictors of influenza. Spatial and temporal information are modeled in a four-phase Markov switching model, i.e. non-epidemic phase (NE), rising epidemic phase (RE), stationary epidemic phase (SE) and declining epidemic phase (DE), where the dynamics of NE and SE are characterized by small changes in the number of flu-indicator tweets, modeled as a Gaussian process based on daily effect, while the dynamics of RE and SE are modeled as an autoregressive process to account for the auto-dependent changes expected in the number of flu-indicator tweets.

Unlike existing approaches for spatio-temporal data analysis such as linear regressive process [12,32] or Markov Random Field [24], which require labeling data for weight training (which would be hard for our case), our approach is totally unsupervised. We further used a Markov Chain Monte Carlo (MCMC) methods for parameter inference. We conduct experiments in multiple real-time applications (e.g. flu outbreak prediction, ILI physician visits prediction). Our research results verify (1) the effectiveness of using real-time Twitter data for the task of flu detection (2) the good performances of our proposed model. In sum, the main contributions of this paper are as follows:

1. We introduce an unsupervised Bayesian framework based on a spatio-temporal Markov Network algorithm for early stage flu detection on Twitter. Our algorithm can capture flu outbreaks more promptly and accurately compared with baselines.

2. Based on our proposed algorithm, we create a real-time flu surveillance system. From the system, we verify that Twitter serves a better flu prediction resource than other types of signals, say query-click on search engine (See Section 4.4).

The rest of this paper is organized as follows: In the next section, we present our approach for the identification of flu-indicator tweets. Our Flu-MN model is illustrated in Section 2. We describe the creation of our dataset in Section 3. Experimental results are illustrated in Section 4. Section 5 is devoted to an explanation of related work. We conclude this paper in Section 6.

2. MODEL

For early stage flu detection, we use a probabilistic graphical Bayesian approach based on Markov Network. We first describe the details of our model and then the inference procedure.

Suppose we collect flu-related tweet data from N locations. In this paper, each location denotes a State in the US. For each location $i \in [1, N]$, we segment the data into a time series. $Z_{i,t}$ denotes

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The DHHS competition relied solely on keyword counting. [http://www.google.org/flutrends/]

The Flu-MN Model is illustrated in Figure 3. Average flu related tweets rate within the week based on twitter data from Jun. 08 to Jun. 09. [http://www.nowtrendingchallenge.com/]

Figure 3: Average flu related tweets rate within the week based on twitter data from Jun. 08 to Jun. 09.

Figure 4: Pipeline for Flu detection on Twitter.
the phase location $i$ takes on at time $t$. $Z_{i,t}$ is the observant variable, which denotes the number of flu related tweets at time $t$, location $i$. $\Delta Y_{i,t} = (Y_{i,t} - Y_{i,t-1}) / Y_{i,t-1}$. For location $i$, $\text{Neigh}(i)$ denotes the subset containing its neighbors. We simplify the model by only considering bordering States in $\text{Neigh}(i)$.

### 2.1 Daily Effect

The first thing we should consider is what we call daily effect, which describes the people’s inclination to post flu related tweets on each day within the week. As we observe from Figure 3 more users publish flu-related tweets on weekdays than on weekends. To capture the dynamics of daily effect, we use a Gaussian distribution. Let $k = \text{day}(t)$ denote the day within the week (e.g. Monday, Tuesday). For time $t$, the observations $\Delta Y_{i,t}$ are modeled as a drawn from a Gaussian distribution with mean $L_k$ and variance $\delta_k^2$:

$$\Delta Y_{i,t} \sim N(L_k, \delta_k^2)$$

Based on Bayesian perspective, we give a Gaussian prior for $L_k$ and an Inverse-$\chi^2$ prior for $\delta_k^2$ based on previous data. $W_k$ denotes the mean of $\Delta Y_{i,t}$ with $\text{day}(t) = k$ within that time period and $G_k^2$ denotes the variance based on previous data from Jun.08 to Jun.09.

$$L_k \sim N(W_k, \phi_k^2)$$

$$\delta_k^2 \sim \text{Inv-}\chi^2(\mu_k, G_k^2)$$

### 2.2 Flu-MN

The key of the flu detection task is to detect the transition time from non-epidemic phase to epidemic phase. As we examine the actual data at Figure 2 we can clearly identify non-epidemic phase (NE), rising-epidemic phase (RE) and declining-epidemic phase (DE) in flu dynamics in each year. For some years (i.e. 2009), we can also find a stationary-epidemic phase (SE) where the number ofILI physician visits approximately keeps at a fixed high value. Hence, we segment each time into four phases NE, RE, SE and DE. Such description of four-phase population characteristics can be found in many areas such as economy [9], bacteriology [10], ecology [12] or anthropology [6].

#### Spatial and Temporal dependency.

We model the spatial and temporal information in a unified Markov Network, where the phase for location $i$ at each time is not only dependent upon its previous phase, but its neighbors. Since the influence from non-bordering states can be transmitted through bordering ones, such simplification makes sense and experimental results also demonstrate this point. We use a Generalized Linear Model to integrate the temporal and spatial information in a unified framework. For location $i$ at time $t$, the probability that $Z_{i,t}$ takes on value $Z$ is illustrated as follows:

$$Pr(Z_{i,t} | Z_{i,t-1}, Z_{j,t-1}, 1 \leq j \leq \text{Neigh}(i)) = \frac{\exp(\Theta_{z_{i,t-1},z_{i,t}} + \Theta_{z_{i,t},z_{i,t+1}} + \sum_{j \in \text{Neigh}(i)} \Psi_{z_{j,t},z_{i,t}})}{\sum_z \exp(\Theta_{z_{i,t-1},z_{i,t}} + \Theta_{z_{i,t},z_{i,t+1}} + \sum_{j \in \text{Neigh}(i)} \Psi_{z_{j,t},z_{i,t}})}$$

where $\Theta$ and $\Psi$ respectively correspond to parameters that control temporal and spatial influence. Take $\Theta$ for example, it is a $4 \times 4$ matrices. $\Theta_{i,j}$ represents how likely phase $Z_{i,t}$ is to take value $j$ at time $t$ given that phase $Z_{i,t-1}$ takes on value of $i$ at $t-1$. We give a non-informative Gaussian prior for each element in $\Theta$ and $\Psi$:

$$\Theta_{i,j} \sim N(0, \sigma_{i,j}^2) \quad \Psi_{i,j} \sim N(0, \Phi_{i,j}^2)$$

#### Epidemic Dynamics

Next, we describe the characteristics for the dynamics of different phases. For NE and SE, the dynamics would only be affected by daily effect, where $\Delta Y_{i,t}$ is characterized as Gaussian process:

$$Pr(\Delta Y_{i,t} | z) \sim N(L_{\text{day}(t)}, \delta_{\text{day}(t)}^2)$$

For RE and DE phases, the changes for epidemic dynamic would be great and inter-related. We model the conditional distribution of $\Delta Y_{i,t}$ as an autoregressive process combined with daily effect.

$$Pr(\Delta Y_{i,t} | z) \sim N(\rho t_{\text{day}(t)}, \Sigma_2^2 + \delta_{\text{day}(t)}^2)$$

$\Sigma_2^2$ denotes the variance for $\Delta Y_{i,t}$ and we give a inverse $\chi^2$ prior for them. $\rho$ is the autoregressive parameter rising and declining process, and we give a uniform prior for them.

$$\Sigma_2^2 \sim 1_{\nu} - \chi^2(\nu, \psi_0^2) \quad \rho_{i,t} \sim \text{Uniform}(0, 2) \quad \rho_{i,t} \sim \text{Uniform}(-2, 0)$$
2.3 Inference

Along standard lines for Bayesian graphical models, the joint density of the variables are described as follows: $p(\cdot)$ denotes a probability density and $p(\cdot|\cdot)$ denotes the conditional density of parameter $\theta$. We adopt Gibbs Sampling based on Markov Chain Monte Carlo where each latent parameter is sampled from posterior distribution given other parameters.

**Sampling $Z_{i,t}$**

$$Z_{i,t} | - \sim [Z_{i,t}|Z_{i,t-1}, Z_{i,t+1}, Z_{j,t}, Z_{j,t}, Z_{j,t-1}, Z_{j,t+1}, Z_{j,t}, j \in Neigh(i)] \cdot [\Delta Y_{i,t}|Z_{i,t}]$$

$$\propto \exp(\theta_{z_{i,t}, x_{i,t}} + \Theta_{z_{i,t}, x_{i,t}} + \sum_{j \in Neigh(i)} \psi_{z_{j,t}, x_{i,t}})$$

where

$$\Delta Y_{i,t} = [\Delta Y_{i,t} | Z_{i,t}]$$

**Sampling $L_k$ and $\delta^2_k$:** $L_k$ and $\delta^2_k$ are updated at NE and SE phases:

$$[L_k| \cdot ] = [L_k] \cdot \prod_{\text{day}(t)=k} [\Delta Y_{i,t} | \delta^2_k, L_k] \propto N(\frac{M_k}{\delta^2_k} + \frac{W_k}{\delta^2_k} \mu_k^2, \frac{1}{\delta^2_k} + \frac{1}{\delta^2_k})$$

**Sampling $\Theta_{z,t, z'|t}$ and $\Psi$:**

$$[\Theta_{z,t, z'|t} | - \sim [\Theta_{z,t, z'|t} | Z, \Psi] \propto \exp(-\frac{\Theta_{z,t, z'|t}}{2\sigma^2_{z,t}})$$

$$\propto \prod_{\text{day}(t)=k} [\Delta Y_{i,t} | Z_{i,t} = z, \Theta, \Psi] \sum_{\text{day}(t)=k} [\Delta Y_{i,t} | Z_{i,t} = z, \Theta, \Psi]$$

3.1 Collecting Data

Based on the Twitter API, we developed a crawler to fetch data at regular time intervals. We fetched tweets containing indicator words shown in Table I and collect 3.6 million flu-related tweets from 0.9 million twitter users starting from Jun. 2008 to Jun. 2010. Location details can be obtained from the profile page or mobile client. We select tweets whose locations are in USA and discard those ones with meaningless locations such as “Marvel”, “in my bed” or “in the universe”. Olosable locations of users are then inferred by using Google Geocoding. By first converting the address into geographic coordinates of latitude and longitude and then rematching the coordinates to the name of State. From the data we crawled, 19% of the total number of tweets are with exact locations. The State-wise distribution of tweets are shown in Figure 7.

| Indicator words | flu, influenza, H5N1, H5N9, swine flu, bird flu |

3.2 Identifying flu-indicator tweets

Not all tweets containing indicator keywords indicate that the user is ill. Twitter dataset needs to be processed before be used for our task. The necessity of tweets filtering in real-time task has been demonstrated in many existing works [4, 23, 38].

Tweets can include mentions of target events. A user might post tweets such as “not feeling well, maybe got a flu” when he indeed has got a flu. But not all tweets that include mentions of influenza or flu are true flu indicators indicating that the Twitter user has been affected. For example, a user may say “Starting to get worried about swine flu” to express his concerned awareness, or “Swine flu vaccine is not good for pupils” to report the news. In addition, even if a tweet is referring to a flu breakout, it might not be appropriate to treat it as an event report. For instance, a user may post tweets such as “the bird flu last year is scaring”, describing an out-of-date event, but not a real-time one. These kinds of inaccurate or biased information would have negative effect in our task.
To filter out these bias tweets, we first prepared manually labeled training data, which was comprised of 5000 tweets containing key words such as “flu” or “influenza”. We manually annotate them as positive examples (flu indicators) and negative ones (not indicative of the flu). We intentionally included the following cases in negative examples:

- Starting to get worried about swine flu. [Awareness].
- Swine flu vaccine is not only for pupils. [Related News].
- The bird flu last year is scary. [Out of date].
- My son got flu, really worried. [Referring Another person].
- Do you think swine flu will come to America? [Question].
- Doctors urged people at risk of contracting swine flu to get vaccinated. [Warning].

We built a classifier based on support vector machine. We use SVMlight [21] with a polynomial kernel. We employ the following simple text-based features:

**Feature A**: Collocational features, representing words before and after the query word within a window size of three.

**Feature B**: unigrams, denoting the presence or absence of the terms from the dataset.

**Feature C**: tweet length in tokens.

**Feature D**: position of the keyword within the tweet

Performance for different combinations of features (shown at Section 2.1) are illustrated at Table 2. We observe that the performance of A+B and A+B+D are much better than A+B+C and A+B+C+D. This illustrated that the consideration of tweet length (feature C) would largely affect the performance of classifier. We can also find that the position of keyword (feature D) does not contribute much to the classification performance. So in our following experiments, tweets are selected according to a classifier based on feature A+B.

| Features   | Accuracy | Precision | Recall |
|------------|----------|-----------|--------|
| A          | 84.41%   | 83.31%    | 91.40% |
| B          | 85.40%   | 86.94%    | 88.00% |
| A+B        | 87.30%   | 88.65%    | 89.54% |
| A+B+D      | 87.26%   | 88.35%    | 89.85% |
| A+B+C      | 74.49%   | 73.61%    | 87.21% |
| All        | 73.04%   | 71.75%    | 88.16% |

Table 2: Performance for different combinations of features for tweets filtering

### 3.3 Further Tweets Selection

For later analysis, tweets dataset needs to be further processed to filter redundant tweets [1][2]. Issues are explained as follows:

- **Retweets**: A retweet is a tweeted post originally made by one user and then followed or forwarded by someone else. For flu tracking, it does not indicate a new user being affected. Retweets would be filtered out in our system.

- **Duplicate Tweets**: An individual may publish more than one tweets talking about his symptoms when he got a flu. He may first tweet “seems like caught a flu”, then “feel bad, got a flu” and at last “finally recovered from the flu”. To get rid of duplicating tweets, we remove tweets from the same user within the same syndrome time (two weeks).

### 4. EXPERIMENTS

In this subsection, we briefly demonstrate the relatedness between Twitter data and CDC data, which would support the claim that Twitter data can be used for the flu detection task. We quantitatively evaluate the correlated performance between CDC data and twitter data by reporting *correlation* and *RMSE error* in Table 3.

We observe that performing SVM filtering and tweets selection would definitely make twitter data more correlated with real world CDC data. Figure 8 presents the distribution map published by CDC in week 45 (Nov15-Nov21), 2009 (left column) and week 6 (Feb7-Feb13), 2010 (right column) and the correspondent visualization of tweets containing keywords according to geo-location. In left column of Figure 8, we can clearly identify the states with big clusters of flu related tweets including California, Arizona, Florida, Georgia and most states in New England, which are highly correlated with CDC reports. These results illustrate the high correlation between Twitter data and clinical data(CDC), which enables twitter data to be used for early-stage flu detection in the real world.

![Figure 8: Visual illustration of CDC data and flu-related tweets distribution. The upper CDC data pictures are from [1]](image)

|                | non-processing | processing |
|----------------|----------------|------------|
| United States  | 0.965          | 0.974      |
| New England    | 0.963          | 0.972      |
| Mid-Atlantic   | 0.970          | 0.978      |
| East-North Central | 0.958    | 0.958      |
| West-North Central | 0.982    | 0.984      |
| Mountain       | 0.973          | 0.981      |
| Pacific        | 0.964          | 0.982      |
| West South Central | 0.962  | 0.977      |
| East South Central | 0.974   | 0.982      |
| South Atlantic | 0.966          | 0.980      |

Table 3: Correlation between twitter data and CDC data. non-processing corresponds to approach without SVM filtering and further tweets selection.

### 3.4 Comparing Tweet Trend with CDC

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place at time $t$ given that phase $j$ appeared at the previous time $t-1$. We observe that a NE phase has very low probability to transit to DE, and likewise for the transiting probability from SE to NE and DE to RE, which agree with general rules. To better illustrate this point, in Table 4 we further present the value of $Pr(z_{i,t}|z_{i,t-1})$ and $Pr(z_{i,t}|z_{j,t})$ by integrating out other parameters in Eqn.4. As we can observe, the model estimates that each location is very likely to stay at the phase it took on during the previous time and neighboring locations tend to share similar phases.

Figure 9: Visualization of (a) $\Theta$: Temporal Dependency (b) $\Psi$: Spatial Dependency

Table 4: Value for (a) $Pr(z_{i,t}|z_{i,t-1})$ and (b) $Pr(z_{i,t}|z_{j,t})$

Table 5: Posterior of the parameters in our model.

4.2 Flu Detection from Real-time Data

The main goal of our task is to help government or health organizations to raise an alarm at those moments when there is a high probability that the flu breaks out. In real time situations, for each time, available data only comes from the previous days, and there is no known information about what will happen in the following days or weeks. By adding the data day by day, we calculate the posterior probability for transiting to (or staying at) epidemic states (including RE, SE and DE) based on previous observed data. The prediction for phase $Z_{i,t}$ would be attained by maximizing the likelihood given $Y_{i,t}$ as follows:

$$Z_{i,t} = \arg\max_{z} P(Z_{i,t} = z|Y_{i,t}, Y_{i,t-1}, \ldots)$$

$$= \arg\max_{z} \sum_{Z_{i,t-1}} P(Z_{i,t} = z|Z_{i,t-1}, Z_{i,t-2}, \ldots, Y_{i,t}, Y_{i,t-1}, \ldots)$$

(16)

The sum over parameter $Z_{i,t-1}$ and $Z_{j,t}$ makes it infeasible to calculate. We again use Gibbs Sampling by first sampling $Z_{i,t-1}$ and $Z_{j,t}$ first and then attain the value of $Z_{i,t}$ given $Z_{i,t-1}, Z_{i,t-2}, \ldots$

$$Z_{i,t} = \arg\max_{z} P(Z_{i,t} = z|Z_{i,t-1}, Z_{i,t-2}, \ldots, Y_{j,t}, Y_{i,t-1}, \ldots)$$

(17)

Figure 10 shows the performance of our real-time analysis based on twitter data from Jun.2009 to Jun.2010. We randomly select 15 States in United States. For each State in Figure 10 the left hand side figure corresponds to number of flu-related tweets over time. Blue symbols denote the phase transition point detected by our approach from non-epidemic phase (NE) to epidemic phase (RE,NE or DE). The right hand side figure corresponds to posterior probability of being at epidemic phase. The dotted line denotes $Pr(\text{epidemic}) = 0.5$ when the alarm would be sent out. Note that these probabilities can be very useful for government and organizations. In particular, value exceeding 0.5 indicates that at that time, the State witnesses a higher probability being at epidemic phase than non-epidemic one. The black dotted line represents $Pr(\text{epidemic}) = 0.5$, where there should be a flu alarm signal.

Another interesting thing we observe from Figure 10 is that jumps from one phase to another are quite robust in our model. There is no more than one epidemic transition from NE to RE (i.e. non-epidemic phase to epidemic phase) per season even though the model allows for any number of changes. This further demonstrates the robustness of our model.

For comparison, we employ the following baselines in this paper:

**Average:** An approach that uses the average frequency of tweets containing keywords based on previous yearn as the threshold. Days with larger frequency of tweets would be treated as epidemic.

**Flu-MN(r):** A revised version of Flu-MN where daily effect is not considered. The dynamics for NE and SE are modeled as a white Gaussian noise process, the expectation of which is 0.

**Time HMM:** A simplified version of flu-MN where temporal dependency is modeled as four-phase Markov chain but spatial dependency is neglected.

**Two-Phase:** A simple version of our approach but using a simpler two-phase (epidemic phase and non-epidemic phase) Markovian network. Both spatial and temporal dependency is considered. In Table 6 we present the performance from different baselines along with Flu-MN based on 50 States twitter data in Unites States States from Jun 2009 to Jun 2010. The peak time denotes the moment when

$\text{Since most of phase transiting times detected by Flu-MN would also detected by Flu-MN(r) (but Flu-MN(r) involve more fluctuation and wrongly detected phase transiting times due to the neglect}$

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Figure 10: Examples of our model on the whole year Twitter data from different States.

| State      | Peak Time | Flu-MN | Average | HMM | Two Phase |
|------------|-----------|--------|---------|-----|-----------|
| Oregon     | Oct.01    | Aug.14 | Sep.02  | Aug.25 | Aug.22   |
| Idaho      | Sep.23    | Aug.08 | Aug.25  | Aug.17 | Aug.12   |
| Utah       | Oct.06    | Jul.26 | Aug.18  | Aug.01 | Aug.04   |
| Arizona    | Sep.26    | Aug.08 | Aug.28  | Aug.12 | Aug.14   |
| Montana    | Oct.12    | Aug.18 | Sep.16  | Aug.24 | Aug.28   |
| Colorado   | Sep.30    | Aug.03 | Aug.31  | Aug.14 | Aug.12   |
| Kansas     | Oct.01    | Jul.30 | Aug.22  | Aug.08 | Jul.30   |
| Texas      | Sep.24    | Aug.14 | Sep.4   | Aug.16 | Aug.18   |
| Florida    | Sep.12    | Jul.28 | Aug.16  | Jul.28 | Aug.02   |
| Iowa       | Oct.09    | Aug.30 | Sep.12  | Sep.11 | Sep.08   |
| Nevada     | Sep.14    | Aug.15 | Sep.04  | Aug.25 | Aug.22   |
| Michigan   | Oct.08    | Aug.14 | Aug.29  | Aug.27 | Aug.22   |
| Ohio       | Oct.04    | Aug.06 | Aug.20  | Aug.06 | Aug.08   |
| Indiana    | Oct.07    | Aug.12 | Oct.01  | Aug.17 | Aug.17   |
| Georgia    | Sep.17    | Jul.28 | Aug.15  | Aug.02 | Aug.06   |
| Maine      | Oct.16    | Aug.22 | Sep.14  | Aug.28 | Aug.30   |
| Vermont    | Oct.18    | Aug.21 | Sep.12  | Aug.26 | Aug.30   |
| Delaware   | Oct.14    | Aug.16 | Sep.18  | Aug.29 | Aug.30   |
| Maryland   | Oct.08    | Aug.12 | Sep.06  | Aug.18 | Aug.22   |
| Alabama    | Sep.18    | Jul.25 | Aug.14  | Aug.04 | Aug.07   |
| Louisiana  | Sep.20    | Jul.28 | Aug.10  | Sep.29 | Sep.27   |
| Virginia   | Oct.14    | Aug.14 | Sep.12  | Aug.18 | Aug.24   |
| Missouri   | Sep.16    | Jul.18 | Aug.26  | Jul.28 | Jul.31   |
| Hawaii     | Jun.16    | Apr.18 | May.16  | Apr.18 | Apr.25   |
| Alaska     | Sep.20    | Aug.16 | Sep.04  | Aug.16 | Aug.26   |

Table 6: Comparison with different for real-time phase prediction detection from Jun, 2009 to Jun. 2010.

of daily effect), we do not report results for Flu-MN(r) here.
| Days | Peak | Flu-MN | Average | Time HMM | Two-Phase |
|------|------|--------|---------|----------|-----------|
|      |      | -48.6  | -25.8  | -36.0   | -34.4     |

Table 7: DIC value in regard to different baselines.

|       | Flu-MN | Flu-MN(r) | Time HMM | Two-Phase |
|-------|--------|-----------|----------|-----------|
| DIC   | 2441   | 2388      | 2742     | 2767      |

Table 8: DIC value in regard to different baselines.

The tweet frequency containing keywords reaches the peak. From Table[6] we can clearly identify that for most states, Flu-MN would detect the breakout of influenza earlier than Time HMM. This validates our assumption that by considering neighboring influence, we can achieve a better flu prediction performance. It is also worth noting that, for some States (i.e. Hawaii, Alaska, Florida), which have very few (or no) bordering States, Flu-MN would degenerate into Time HMM. That is why for these States, Flu-MN and HMM achieve very similar results. Flu-MN detects the phase transition time more promptly than two-state, illustrating the effectiveness of using a more sophisticated four-phase framework to model flu dynamics than a simpler two-state one. Table[5] illustrates the average days that each model predicts the flu breakout before the number of flu-related tweets reaches its peak.

Further, in order to quantitatively compare competing models, we report devition information criterion (DIC) at Table[8]. DIC is defined as a classical estimate of fit, plus twice the effective number of parameters $p_D$, the details of which can be found in Spiegelhalter et al.’s work[41]. Flu-MN outperforms (by providing a better fit, which can be seen by a lower DIC) the other three models.

### 4.3 Future Prediction

Given observers from previous days, people are interested in asking questions like how likely flu will break out tomorrow, or how likely flu will come to an end next week, or how many flu-related tweets there would be next week. We can use a similar approach we take at Section 5.2 for $Y_{i,t+1}$ prediction. Suppose that we have already attained the values of $Z_{i,t}, Z_{i,t-1}, \ldots$ from a Gibbs Sampling. Then, $Y_{i,t+1}$ and $Z_{i,t+1}$ can be predicted as follows:

$$Z_{i,t+1} = \text{argmax}_{Z} P(Z_{i,t+1} = z | Y_{i-1,t}, \ldots)$$

$$Y_{i,t+1} = \text{argmax}_{Y} \sum_{Z_{i,t+1} = z} P(Y|z) P(Z_{i,t+1} = z | Z_{i-1,t}, \ldots)$$

For comparison, in addition to Time HMM and Two-Phase for future $Y_{i,t+1}$ prediction, we employ the following baseline:

**Auto-regression:** An approach for $Y_{i,t}$ prediction based on $Y_{i,t-1}, Y_{i,t-2}, \ldots$ based on regressive model.

$$Y_{i,t} = \sum_{j=1}^{n} b_{j} Y_{i,t-j} + c + e_{i,t}$$

where $e_{i,t}$ is a sequence of independent random variables and $c$ is a constant term to account for the offset. Parameters are trained on tweet data from Jul.2008 to Jul.2009.

Figure[11] presents $Y_{i,t+1}$ prediction performance compared with CDC data from Jul.2009 to Jul.2010. Due to space limit, we only report performances for 8 States. As we can see, Flu-MN (the red curve) can best fit the actual twitter data (the black curve). Time HMM and Two Phase attain similar performances. Auto-regression achieves the worst results. This can be explained as follows: flu trends vary quite a lot from each other in different years. So parameters trained from data in 2008-2009 may not be well tailored for 2009-2010. For a better illustration, quantitative evaluations are reported at Table[9].

### 4.4 Twitter or Google Flu Trend?

Another interesting task involved is the prediction of the ILI related physician visits, which, actually, is a main task addressed in Google Flu trend [17]. Here, we adopt the linear model using log-odds which is used in Ginsberg et al.’s work[17] to link the number of ILI physician visits with the number of flu-related tweets. Let $N_{i,t}^{ILI}$ be the number of ILI visits from CDC only provides weekly data according to regions, we focus on weekly regional ILI prediction.
5. RELATED WORK

Real-world event detection on Twitter.

Twitter serves as a good source for quick event detection due to its real time nature. As described in the introduction, Sakaki et al. [38] were the first to build an earthquake and typhoon detection system from Twitter data, making the assumption that each Twitter user could be regarded as a sensor. They produced a probabilistic model that can find the center of the earthquake and its trajectory and is able to send alerts faster than meteorological agencies.

Online Flu Surveillance.

Early work on web-based influenza surveillance usually makes use of click-through data from search engines [16,11,17,19,22,24], such as using medical website with influenza [19], counting visitors to health websites [22], or users’ clicks on a search keyword advertisement [16]. Google’s flu trend is also a online-click based flu system that uses a linear model to link the number of ILI-related search query to the number of ILI-related physician visit.

Twitter has been proved to be useful for flu surveillance [20,36,37]. Achrekar et al. [2] studied the correlation between CDC data and flu-related tweets in twitter. Aramaki et al. [4] and Lamb et al. [23] explored multiple features in supervised learning by classifying different kinds of tweets containing keywords, trying to select out tweets indicating flu around.

Flu Detection in Epidemiology.

Influenza detection and prediction problem can be traced back to Serfling’s work [40] in 1963 in epidemiology, which tried to find a threshold for influenza breakout. Since then, various approaches have been proposed for flu detection and prediction in multiple situations [1,8,18,25,30,31]. LeStrat and Carrat [25] segmented the time series of influenza indicators into epidemic and nonepидemic phases by incorporating Markovian Assumption and used an EM algorithm for parameter estimation. Subsequently, Rath et al. [35] and Madigan [26] presented further investigation of the model from the Bayesian perspective. As for current efforts, Muglin [31] treat the disease fonts as a realization of multivariate autoregressive process and Sebastiani et al. [39] integrate different sources of data into a multivariate model for influenza surveillance. These approaches are mostly based on CDC or EISS datasets.

6. CONCLUSION

In this paper, we introduced a unsupervised Bayesian model based on Markov Network for early stage flu detection on Twitter. We test our model on real time datasets for multiple applications and experiments results demonstrate the effectiveness of our model. We are hopeful that our approach would help to facilitate timely action by government and health organizations who want to decrease the number and cost of unnecessary illnesses and deaths.

7. REFERENCES

[1] Online social network flu tracker, a novel sensory approach to predict flu trends. author=ACHREKAR Harshavardhan Achrekar, journal=PHD Thesis.

[2] H. Achrekar, A. Gandhe, R. Lazarus, S.-H. Yu, and B. Liu. Predicting flu trends using twitter data. In Computer Communications Workshops (INFOCOM WKSHPS), 2011 IEEE Conference on, IEEE, 2011.

[3] H. Achrekar, A. Gandhe, R. Lazarus, S.-H. Yu, and B. Liu. Twitter improves seasonal influenza prediction. In HEALTHINF, 2012.
