A latent shared-component generative model for real-time disease surveillance using Twitter data

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ABSTRACT
Exploiting the large amount of available data for addressing relevant social problems has been one of the key challenges in data mining. Such efforts have been recently named “data science for social good” and attracted the attention of several researchers and institutions. We give a contribution in this objective in this paper considering a difficult public health problem, the timely monitoring of dengue epidemics in small geographical areas. We develop a generative simple yet effective model to connect the fluctuations of disease cases and disease-related Twitter posts. We considered a hidden Markov process driving both, the fluctuations in dengue reported cases and the tweets issued in each region. We add a stable but random source of tweets to represent the posts when no disease cases are recorded. The model is learned through a Markov chain Monte Carlo algorithm that produces the posterior distribution of the relevant parameters. Using data from a significant number of large Brazilian towns, we demonstrate empirically that our model is able to predict well the next weeks of the disease counts using the tweets and disease cases jointly.

Categories and Subject Descriptors
H.2.8 [Database Applications]: Data mining

Keywords
Data mining, Disease surveillance, Dengue, Social media

1. INTRODUCTION
Exploiting the large amount of available data for addressing relevant social problems has been one of the key challenges in data mining. Such efforts have been recently named “data science for social good” and attracted the attention of several researchers and institutions. One example of such scenario is associated with the rise of text-based social media, which have created a whole new ecosystem composed of individuals sharing daily live information. The popularization of such platforms led people to report about almost everything, from their common activities, to their social interactions, preferences and health conditions [17]. Such a large amount of user generated content provides unprecedented valuable information that may be used for a variety of purposes. Among all the possibilities, event detection has received significant attention. In this context, data from social media channels are leveraged in order to predict real-world events, such as natural disasters [19] and disease outbreaks [19]. The common approach in this case is to consider users posting to a social media as sensors and their respective messages about an event as an indicator of its occurrence/intensity. In this sense, the intensity of an event is predicted as a function of the number of messages related to that event, which should be specified by a set of keywords.

In the particular case of disease surveillance, using data from social media provides a great advantage over traditional systems [18]. Usually, such systems are almost entirely manual and require a set of epidemiological procedures in order to monitor the intensity and location of the disease spread. The complete process may result in a long delay for decision making and prevents early monitoring. In a strikingly different way, messages posted to social platforms can be collected and analyzed almost instantly, enabling timely actions to control disease outbreaks or swift geographical spread of cases.

Dengue is an infectious disease that is currently a major concern for Brazilian public health officials (see section 1.1). There is still no effective cure or prevention (i.e., vaccine) for dengue fever and its painful symptoms and occasional associated death make it a common daily conversation topic. During the epidemic periods, it becomes a much more common issue in social interactions when people exchange their personal, close friends or relatives experiences with the disease, as well as discussions about the public health policies and counter measures. There is clear potential to use social network posts to probe and to monitor the fluctuations on the disease incidence rate, in addition to existing official disease surveillance systems, as demonstrated in previous works (see Section 2). However, the models proposed so far are not accurate enough, considering the diversity of factors that determine a dengue surge.

These are the main motivations behind our latent shared-component generative model to predict dengue outbreaks in Brazilian urban areas using data collected from Twitter. In this paper, we propose a concise yet flexible analytical model for the simultaneous rise and fall patterns of the diseases...
dengue cases and the dengue-related tweets. We envision a hierarchical and stochastic structure that is parsimonious in the number of parameters. In our model, the disease rate of dengue cases is a latent random process that drives the weekly reported number of dengue cases. As it is common in epidemic modeling, to reflect the smoothly varying and time-dependent aspect of the disease, we use a hidden Markov model for this underlying rate [3, 15, 4].

The novelty in our model is the joint effect of this underlying process in the dengue-related tweets time series. The weekly count of these tweets has two independent components. One of them is a Poisson process issuing a stable and random amount of tweets reflecting the relevance of the dengue in the usual conversation in Brazil. The evidence for the presence of this component has been verified in our dataset by observing a certain number of successive weeks with zero dengue cases but with a relatively small number of tweets mentioning the disease. The motivation for our second component in the tweets time series is the clear pattern in the observed data that more prominent temporal increase or decrease in the disease counts is accompanied by similar movements in the tweets time series.

In section 5, we explain how we connect these two components to model the tweets and, at the same time, the disease cases. We show the results of the application of this model to the analysis of dengue in the largest Brazilian towns. However, we consider that the general methodological framework and the main considerations are widely applicable, not only to other diseases, but also to other scenarios.

1.1 Dengue overview

With an estimated 50-100 million infections globally per year [5], dengue is currently regarded as the most important mosquito-borne viral disease. Dengue affects over 100 endemic countries in tropical and sub-tropical regions of the world, mostly in Asia, the Pacific Region and the Americas. Presenting four distinct viral serotypes, dengue fever may range from severe flu-like illness up to a potentially lethal complication known as severe (or hemorrhagic) dengue. The World Health Organization estimates that 3.9 billion people are at risk of infection with dengue viruses. However, the true impact of the disease is, sometimes, difficult to assess due to misdiagnosis and underreporting [2]. Global dengue incidence still grows in number/severity of cases and also in the amount of new affected areas. This is most due to modern climate changes, socioeconomics and viral evolution [16]. However, the potential drivers of dengue are often difficult to detect and factor out. Since there is no current approved vaccine to protect the population against the virus [16], epidemiological surveillance and effective vector control are still the mainstay of dengue prevention.

The Brazilian traditional surveillance system is almost entirely manual and relies on the ability to observe early cases of dengue for each location and time period. This process usually results in a huge delay for data acquisition. In 2013, the Brazilian Ministry of Health reported almost 1.5 million cases of dengue infection, resulting in 674 deaths [4]. The earlier an outbreak is detected, the greater is the opportunity for effective intervention. In this sense, social media provides a real time source of information to monitor and predict such outbreaks. The model proposed in this work leverages social media data in order to provide predictive estimations of dengue incidence allowing timely actions.

2. RELATED WORK

In recent years, a large number of researches focused on leveraging data from text-based social media towards monitoring and predicting real-world events [19, 7, 13]. Among all types of events considered, those related to disease surveillance usually receive significant attention, due to their potential impact on life conditions. Several studies show that the wealth of user generated content available through social media channels is a rich source of information to track the spread of a wide range of diseases, therefore enabling timely supporting actions.

In [21], tweets collected using a set of keywords related to the H1N1 virus were used to monitor the public concern about the disease in the United States. Flu was the major concern in [13, 9], where regression models were applied to estimate the disease incidence rate using data from Twitter and comparing to the reports provided by the official organizations. Regression models were also employed in a more recent work [20], combining data from Twitter and search engines to estimate the flu incidence in Portugal.

Despite flu being the most common disease monitored from social media, other studies employed this approach to the surveillance of other diseases. For instance, in [8] data from Twitter was used to estimate the incidence of cholera in Haiti, collecting the messages containing the terms “(#)cholera”. In a more comprehensive perspective [17, 18], considered a broader range of public health dimensions, expanding the analysis for different ailments, such as depression, obesity and others, showing that social media has a wide applicability for public health research.

Most of the aforementioned works focused on the disease surveillance at a global scale in the sense that one performs the analysis at state, region or even national level. Such coarse grain analysis lacks the specificity necessary for supporting epidemics counter measures at the local level. Contrasting to most previous works, [11] proposed an approach for monitoring dengue incidence rates based on dengue-related messages from Twitter at the city level. The strategy consists of performing a content analysis on collected data to assess the public perception about the disease. Based on this analysis, a regression model is built to estimate the number of dengue cases using the volume of messages expressing personal experience with the disease.

Our work also focuses on estimating the dengue epidemics, a neglected tropical disease, which is rarely explored in the context of social media channels. Differently from most works and similarly to [11], our approach considers a fine geographic-scale analysis. However, we propose a latent shared-component generative model that accommodates different aspects of the scenario regarding the behavior of users in social media channels.

3. LATENT SHARED-COMPONENT GENERATIVE MODEL

In this section we present in details our proposed method for estimating dengue incidence at the city granularity.

For each town, we have two time series, \( Y_t \) and \( X_t \), representing both the dengue incidence and the number of dengue-related tweets in week \( t \), respectively. Our main hypothesis is that these two time series are positively correlated and therefore the \( X_t \) time series (dengue tweets) can provide timely information on the dengue cases \( Y_t \). We assume that
the number \( Y_t \) of new dengue cases in week \( t \) follows a Poisson distribution with an evolving expected value. It has been shown in [6] that, under mild theoretical conditions, one can expect vital statistics, such as counts of deaths or disease cases in human populations, to follow the Poisson distribution. This has been extensively empirically verified in epidemiological and demographic studies to the point that the Poisson distribution is the standard distribution to analyze these type of data.

The expected value \( E(Y_t) \) is equal to Pop \( \times \Pi_t \times 10^{-5} \). That is, it is proportional to the population size and to the dynamically evolving rate \( \Pi_t \) (per 100 thousand people). This rate is a latent stochastic process following a hidden Markov process distribution in the form of a random walk:

\[
\log(\Pi_t) = \log(\Pi_{t-1}) + \epsilon_t
\]

where the shocks \( \epsilon_t \) are independent and identically distributed as a Gaussian with mean 0 and constant variance \( 1/\tau \). The reason for adopting a random walk is to allow non-stationary movements on the dengue rate and, at the same time, to be equally able to model stable or stationary processes. The need to allow non-stationary movements comes from the empirical observation that \( Y_t \) present quiet weeks followed by fast increase in the number of dengue cases, exhibiting an epidemic type of behavior. A random walk model has constant mean but increasing variance and naturally shows long and drastic upward or downward movements. Hence, it is a more appropriate prior distribution model for the time series \( Y_t \) than usual stationary processes, such as auto-regressive models, which are not able to accommodate these sudden changes on \( Y_t \).

The connection between \( Y_t \) and \( X_t \) is achieved through the hidden process \( \Pi_t \), a shared component that affects both counts, the dengue cases and the dengue-related tweets in week \( t \). Additionally to account for the tweets driven by the fluctuations of the underlying Markovian rate \( \Pi_t \), we allow a stable but random amount of dengue-related tweets in each week. This additional component acts as a random noise producing a stationary and random flow of events on top of the disease-related tweets. We found plenty of evidence for the presence of this random noise component when comparing the two time series \( Y_t \) and \( X_t \). In several weeks where no dengue cases are reported, we may find a few dengue-related tweets being posted. Moreover, the number of such tweets in no-dengue weeks does not seem to vary widely or to present obvious trends.

The remaining of the model assumes prior distributions for the parameters involved in the models for \( Y_t \), \( X_t \), and \( \Pi_t \). The graphical model describing our Bayesian GLM model is in Figure 1 and its analytical expression with all the conditional dependencies is the following:

\[
Y_t \mid \Pi_t \sim \text{Poi}\left(\frac{\text{Pop}}{10^5} \Pi_t\right)
\]

\[
X_t \mid \Pi_t \sim \text{Poi}\left(\lambda + \frac{\text{Pop}}{10^5} \alpha \Pi_t\right)
\]

\[
\log(\Pi_t) = \log(\Pi_{t-1}) + \mathcal{N}(0, \frac{1}{\tau})
\]

\[
\lambda \sim \text{Gamma}(0.0225, 0.0075)
\]

\[
\alpha \sim \text{Uniform}(0, 1)
\]

\[
\tau \sim \text{Gamma}(0.01, 0.01)
\]

The model for \( X_t \) is a Poisson with a basal rate \( \lambda \) to capture the random noise component on the tweets and a parameter \( \alpha \) to modulate the process \( \Pi_t \), effectively bringing it to the same range of values of the number of tweets. We selected the Gamma distribution because it is very flexible and it is the conjugate distribution of the Poisson distribution, facilitating the Bayesian posterior inference. The choice for the specific parameters of this Gamma distribution is motivated by the observation that, for most of the towns, we know that the number of tweets in no-dengue weeks is between 0 and 5, except for cities where the number of Twitter users is very large and random counts in no-dengue weeks can reach up to 50 messages. We selected the parameters in such a way that \( \lambda \) has a prior mean equal to 0.0225/0.0075 = 3 and a prior variance equal to 0.0225/0.0075^2 = 400, which implies in a standard deviation equals to 20 and a 1.7% chance of being larger than 50.

For the \( \alpha \) parameter, we anticipate that the number of dengue-related tweets will be much smaller than the number of dengue cases during the epidemic periods. However, we do not have enough knowledge to select a narrow range for \( \alpha \) and so we adopted a flat uniform distribution in the (0, 1) interval.

For the variance \( 1/\tau \), we selected an inverse-gamma distribution (or a Gamma distribution for the precision parameter \( \tau \)). Again, the reason is mathematical convenience of its conjugacy with the normal distribution and, at the same time, its great flexibility. The parameters 0.01 and 0.01 imply on a mean equal to 1 and a standard deviation of 10. Therefore, a large range of possible values for \( \tau \) is allowable and the prior is flat enough to accommodate itself to the observed data.

To carry out inference on the hidden structures of the model, we obtain the posterior or conditional distribution of \((\Pi_t, \lambda, \alpha, \tau)\) given the data \(\{Y_t, X_t\}\). Since analytical manipulation of this posterior distribution is not feasible, we obtain a large sample from it using a Markov chain Monte Carlo (MCMC) algorithm [10].

4. EXPERIMENTAL RESULTS

In this section we evaluate our latent shared-component generative model proposed in Section 3 on predicting the
dengue incidence rate in Brazilian cities using data collected from Twitter.

4.1 Data acquisition and preprocessing

The data used in our experiments were acquired through the Twitter streaming application programming interface (API) [23]. In order to obtain the dengue-related data we defined as keywords the terms “dengue” and “Aedes”. The collecting period comprises from January 2011 to December 2013. The Twitter API provides the user’s geographic location, when informed, in three different ways: (i) geographic coordinates, in case tweets are sent from mobile devices that release such information; (ii) an estimated location based on the issuer IP adress; and (iii) a text field that may contain a free set of terms provided by the user.

In Brazil the decision making process regarding public policies of dengue surveillance are in charge of each city hall. Therefore, we need to perform a fine-geographic scale analysis at the city granularity. In order to do so, a first step is to assign each message, when possible, to a valid location, or discard it when such assignment is not possible. We start by removing from the collected data all tweets not presenting “Brazil” (or “Brasil”) in the location field. We assume that those tweets come from places outside Brazil. We also carefully verified the location fields removing tweets presenting Brazil as another type of location but country. After that, we assume that all remaining messages were posted from Brazil and we exhaustively start to seek for consistent and non-ambiguous names of Brazilian cities along with their respective states. Those tweets whose location were not resolved after these steps were discarded. Table 1 provides some statistics about the location processing. Next we processed the messages by filtering out accents and URL’s. We also created bi-grams by joining adjacent words with a separator, and then removed the stop-words as well as bi-grams composed of two stop-words.

| Location details                             | #tweets (%total crawled) |
|----------------------------------------------|--------------------------|
| With geographic location                     | 2,096,975 (100%)         |
| “Brazil” in location field                   | 1,138,199 (54.28%)       |
| “Brazil” in country field                    | 899,660 (42.90%)         |
| Location resolved                            | 745,617 (35.56%)         |

4.2 Tweets classification and official reports

After pre-processing the tweets, we classified them in different groups according to the sentiment they express. We performed such classification in a supervised manner. In order to do so, we created a representative training dataset using a selective sampling approach [12] and manually labeled 2,142 tweets from 2010. Similarly to [11, 22], the tweets were classified into one out of five categories: Personal Experience, Information, Opinion, Campaign, Irony/Sarcasm. The classification was performed using the Lazy Associative Classification algorithm (LAC) [23]. This classifier employs association rules to assign textual patterns to predefined classes. Each rule represents a weighted vote based on the rule confidence. A message is then assigned to the class with the higher number of votes. Figure 2 shows the percentage of tweets belonging to each category over the 3 years of analysis. Notice that the percentage of each class remained stable through the years.

The official dengue reports for each city were provided by the Brazilian Health Ministry. The number of dengue cases is reported at a weekly granularity. Therefore, we also aggregated the number of tweets in the same way. After classifying and aggregating the messages, we start our analysis by observing the correlation between the tweets and official statistics. We found that, for most of the cities, the correlation between the number of tweets expressing personal experience and the actual dengue cases is higher than considering the other categories, specially for cities with a large population. Therefore, we decide to consider only the time series related to the tweets of that category. Figure 3 shows the time series of personal experience messages along with the official number of dengue cases for the city of Manaus, which presents the highest correlation amongst all cities considered (0.971).

4.3 Dengue incidence prediction

In this section we employ our proposed model to estimate the dengue incidence in Brazilian cities. We restricted our analysis to the 100 cities with the higher number of tweets. For each city, the procedure is the same, as described next. We fitted our Bayesian model via MCMC sampling using R in conjunction with the OpenBUGS software [14]. We generated 2 parallel MCMC chains, each one of length 10⁶ with a burn-in period of 500000 and thinning of 1000 to obtain 1000 samples of the joint posterior distribution. Recall that our data is composed of two time series, \( X_t \) and \( Y_t \), representing the number of tweets and official dengue reports, respectively. The data period comprises 156 weeks, from January 2011 to December 2013. In order to assess the prediction ability of the model, we considered a sliding window of size 12/4, which means that we fit our model using data from 12 weeks and estimate the number of dengue cases in the next 4 weeks only using the previously estimated parameters and values of \( X_t \) in these 4 weeks. Hence, we have 144 prediction windows. In order to compare our model, we perform a similar experiment using a linear univariate
countries such as Brazil, health, crime and education are the issues of major concern for the general population and they are intensively debated on social forums. The scarce resources allocated to these areas in these countries can receive useful and timely input from social network information. In this paper we attempt to help on this task by proposing a simple yet effective analytic model that puts together disease incidence and disease-related posts in a social network.

Our application scenario is a major infectious disease in Brazil and other tropical countries, dengue, and we were able to estimate its incidence based on dengue-related posts in Twitter. The model is parsimonious in its parameterization and requires little input from the user. Although simple, the model captures the main features associated with the disease process and how it manifests in social media. In particular, we modelled the tweets as the superposition of two independent processes, one representing a stable emission of a random number of posts and the other representing the additional contribution given by the disease rate swings. We show that our model is able to predict well the up to four weeks of the disease counts in advance using all the available information at the time.

We see our proposal as a first step on the direction of a more general and comprehensive model. In fact, future research directions abound, both for theoretical as well as experimental work. In addition to the tweets of personal experience, we will consider the integrated use of other categories such as tweets with dengue information, opinion, or campaigns. The model is flexible enough to include other predictive features such as weather data. Data on temperature and rainfall could be introduced to modulate the rate process. For example, a \(k\)-dimensional feature vector \(\mathbf{x}_t\) could be introduced in the model through a link function:

\[
\log(\Pi_t) = \log(\Pi_{t-1}) + \mathbf{x}_t \beta + N(0, \frac{1}{2})
\]

where the coefficients vector \(\beta\) captures the effect of the features in the disease rate.

A more ambitious and challenging extension is the simultaneous modeling of all geographical units. It is reasonable to think that neighboring areas tend to have a similar pat-
tern on disease process because they share many of the natural and social aspects that are relevant for the prevalence of the disease. This could be helpful specially in small population areas that do not have enough Twitter users to build a reliable time series of messages. The main idea is to allow small population areas to borrow strength from the evidence available on the neighboring areas.

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