Predict Information Diffusion using a Latent Representation Space

Abstract

Information propagation is a hard task where the goal is to predict users behavior. We introduce an extension of a model which make use of a kernel to modelize diffusion in a latent space. This extension introduce a threshold to differentiate if users are contaminated or not.

1. Introduction

The emergence of Social Networks and Social Media sites has motivated a large amount of recent research. Different generic tasks, such as Social Network Analysis, Social Network annotation, Community Detection or Link Prediction, are currently studied. Another active research topic is the study of temporal propagation of information through this type of media. It aims at studying how interactions between users, like sharing a link on facebook or retweeting something on Twitter, effects the spread of items such as pictures, videos or gossip on the internet. While the study of this word-of-mouth phenomenon pre-dates the development of computer science, the amount of data made available by the growth of online social networks offers an unprecedented field of study and enabled new developments. Propagation models aim at predicting and understanding the dynamic of observed propagation.

In this paper, we propose a new diffusion model based on the heat diffusion. It aims to project users in a latent space where propagation occurs like the heat diffusion. This projection is based on the order in which users have been infected in cascades of the train dataset. In order to be able to find which users have been infected and not only who is the most likely to be infected, we define a threshold to split users in two groups: infected or not. This model is an extension of the CDK model (Content Diffusion Kernel) presented in (Bourigault et al., 2014) where no threshold was defined.

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2. Notations

Traditionally, diffusion on networks is represented with the notion of cascade. A cascade is a sequence of users infected by some information (for instance, it could be the list of users who "liked" a specific YouTube video). A cascade describes to whom and when an item spreads through the network, but not how diffusion happens: while it is easy to know when a user got infected by some content, it is usually not possible to know who infected him.

Given a social network composed of a set of $N$ users $U = \{u_1, ..., u_N\}$, cascades correspond to sets of users infected by the propagated information. Depending on the kind of network and the task in concern, the propagated information can for instance correspond to a given topic, a particular url, a specific tag, etc...

In the following, we consider $C$ as a set of cascades over a given network, and two sets of distinct cascades: $C_t \subseteq C$ the set of testing cascades and $C_t \subseteq C$ the set of training cascades. A cascade $c \in C$ is defined as:

- A source $s^c \in U$ which is the user at the source of the cascade - i.e, the first user that published the item concerned by the diffusion.
- A set of contaminated users $S^c \subseteq U$ such that $u_i \in S^c$ means that $u_i$ has participated to the cascade $c$ $S^c$ is the set of users who have not participated in $c$.
- A contamination timestamp function defined over $S^c$ such that $t^c(u_i)$ corresponds to the timestamp at which $u_i \in S^c$ has first participated in the cascade. We consider that the contamination timestamp of the source is equal to 0.

3. Model

The proposed model aims at predicting information diffusion. The central idea of this model is to map the observed information diffusion process into a heat diffusion process in a continuous (euclidean) space. To perform this, we learn diffusion kernels that capture the dynamics of diffusion from a set of training cascades. Let us denote $Z = \mathbb{R}^n$ an euclidean space of dimension $n$ - also called latent space. Learning such
a diffusion kernel comes down in our case to learning
a mapping of each node of the network to a particular
location in \( \mathcal{Z} \) such that, for a given metric, the latent
space explains the contamination timestamps observed
in the training cascades.

### Learning using a diffusion kernel

We define a diffusion kernel \( K(t, y, x) \) such that \( K : \mathbb{R}^+ \times \mathcal{X} \times \mathcal{X} \to \mathbb{R} \) which models the heat diffusion in a latent space. It

\( h_r \) corresponds here to the contamination propensity of a
d node \( x \) at time \( t \) given a particular information source
y. For learning the kernel function, there is however no
full supervision available - this would correspond to a
continuous time function giving the heat evolution at
any point. The observations only provide the contam-
ination time of the different nodes in a cascade. This
partial supervision will be used to constrain the kernel
to contaminate the different nodes in their actual
temporal order of infection.

In practice, we will use the following constraints:

- Given two nodes \( u_i \) and \( u_j \) such that \( u_i \) and \( u_j \)
are contaminated during cascade \( c \), i.e. \( u_i \in S^c \)
and \( u_j \in S^c \), and respecting \( t^c(u_i) > t^c(u_j) \),
\( K_Z \) must be defined such that \( \forall t, K_Z(t, s, u_i) > \)
\( K_Z(t, s, u_j) \)

- We define a heat threshold \( h_r \) which determine
the heat users have to reach to be contaminated. Thus:
- Given a node \( u_i \) such that \( u_i \) is contaminated
during a cascade \( c \), \( K_Z \) must be defined such that
\( \exists t, K_Z(t, s, u_i) > h_r \)
- Given a node \( u_i \) such that \( u_i \) is not contami-
nated during a cascade \( c \), \( K_Z \) must be defined
such that \( \forall t, K_Z(t, s, u_i) < h_r \)

These constraints basically aim at finding embeddings
such that users who are contaminated first are closer
to the source of the contamination than users contami-
nated later (or not contaminated at all). \( h_r \) is a unique
heat threshold which split users in two groups in or-
der to determine which users will be contaminated and
not only an order of contamination. Based on the heat
equation, we can thus easily rewrite these three con-
straints as:

\[
\begin{align*}
\forall u_i \in S^c, & \quad ||z_{sc} - z_{u_i}||^2 < \tau \\
\forall u_i \in S^c, & \quad \tau < ||z_{sc} - z_{u_i}||^2 \\
\forall (u_i, u_j) \in S^c \times S^c, & \quad t^c(u_i) < t^c(u_j) \Rightarrow ||z_{sc} - z_{u_i}||^2 < ||z_{sc} - z_{u_j}||^2 \\
\end{align*}
\]

where \( \tau \) is a distance threshold. It corresponds to the
distance from the source of the diffusion beyond which
users are not contaminated: their heat never reach \( h_r \).

By the use of classical hinge loss functions, these con-
straints can be handled by defining a ranking objective
\( \Delta_{rank} \) such as:

\[
\Delta_{rank}(K_Z(. , s^c , .), c, \tau) = \\
\sum_{u_i \in S^c} \max(0, 1 - (\tau - ||z_{sc} - z_{u_i}||^2)) \\
+ \sum_{u_i \in S^c} \max(0, 1 - (||z_{sc} - z_{u_i}||^2 - \tau)) \\
+ \sum_{u_i, u_j \in S^c \times S^c, t^c(u_i) < t^c(u_j)} \max(0, 1 - (||z_{sc} - z_{u_i}||^2 - ||z_{sc} - z_{u_j}||^2)) \\
\]

(2)

### Learning Algorithm

The final training objective is:

\[
L_{rank}(Z, \tau) = \sum_{c \in C_t} \Delta_{rank}(K_Z(. , s^c , .), c, \tau) \\
\]

(3)

We name this model "Content Diffusion Kernel with
Threshold" (CDKT). Different methods can be used to
optimize the objective function. We propose to use a
classical stochastic gradient descent method, which it-
erates until having reached a stop criterion (typically a
number of iterations without significant improvement
of the global loss). After having randomly initialized\(^1\)
all embeddings for nodes in \( U \), the algorithm samples
at each iteration a cascade \( c \) from the training set \( C_t \)
and two nodes \( u_i \) and \( u_j \) with \( u_j \) a node that is either
non-infected, or contaminated after \( u_i \) in the diffusion
process described by cascade \( c \). If constraints defined
in equation 1 are not respected with a sufficient mar-
gin\(^2\) for this cascade \( c \) and the nodes \( u_i \) and \( u_j \), em-
bodiments \( z_{u_i}, z_{u_j}, z_{sc} \) and \( \tau \) are modified towards their
respective steepest gradient direction with a learning
rate \( \alpha \) which is a decreasing function of the number of
iterations. The learning process is illustrated in algo-

\[1\] Different initialization strategies can be adopted. In
our experiments, we used an uniform initialization between
-1 and 1.

\[2\] As defined by the hinge loss function, see equation 2.

### 4. Experiments

#### Datasets

We tested our model on several datasets from various online sources: ICWSM (Burton et al., 2009), Memetracker (Leskovec et al., 2009) and Digg.

The first two datasets are sets of blog posts crawled
from the web. We define a cascade as a set of posts
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linked by hyperlinks. Digg est a plateform where users can share news stories with each other. A cascade is thus the set of users who share the same story. We filtered the users of each dataset to keep about 5000 users with the most posts.

Quality of the ranking In order to test the quality of this model, we compared it to several baselines using the same protocol we used in (Bourigault et al., 2014). The goal is to compute the average precision of the model obtained on all cascades. We show the results of 3 baselines IC (Saito et al., 2008), Netrate (Gomez-Rodriguez et al., 2011) and Heat Diffusion (Ma et al., 2008) and the 2 latent models CDK and CDKT. IC obtains better results than other baselines.

CDK obtains slightly better results than CDKT. They outperform baselines on both ICWSM and Digg while IC obtains better results on Memetracker.

Learning and Inference complexity Let \( T \) be the number of iterations. The learning complexity is \( O(T \times n) \), where \( n \) is the size of the latent space. Once \( Z \) has been learned, the inference process is simple. For a cascade \( c \), we just compute the distance between the user \( s^c \) and every other user in \( U \). The inference complexity for every cascade is then \( O(N \times n) \), where \( N \) is the number of users. Considering that \( n \ll N \), this turns out to be much smaller than the complexity of most alternative discrete methods. For instance, the inference step of the very famous Independant Cascade model (IC), which is a probabilistic model where diffusion propabilities are defined on edges of the network’s graph, requires to consider at each time step of the diffusion \( t \) every possible infection situation at previous time \( t - 1 \), which quickly becomes untractable. In practice, inference of graphical models is done by employing a Monte-Carlo approximation that consists in performing a high amount of simulations of the diffusion process starting from the source of the cascade and following the diffusion probabilities on links of the graph. The inference complexity of this approximation of IC is \( O(r \times \text{ Succs} \times |S^c|) \), where \( |S^c| \) is the average number of infected nodes in the performed simulations, \( \text{Succs} \) is their average outdegree and \( r \) is the number of simulations used for the MCMC approximation. The weaker the probabilities defined on links are, the greater \( r \) must be set to obtain a correct approximation of the distribution of final infection probabilities.

| Model       | Memetracker | ICWSM | Digg   |
|-------------|-------------|-------|--------|
| CDK-500     | 0.363       | 0.773 | 0.280  |
| CDKT-500    | 0.324       | 0.746 | 0.233  |
| IC          | 0.372       | 0.712 | 0.197  |
| Netrate     | 0.287       | 0.187 | 0.162  |
| Heat Diff.  | 0.374       | 0.483 | 0.082  |

Table 1. MAP on 3 real datasets: Memetracker, ICWSM and Digg. Results of CDK and CDKT are given for a latent space of 500 dimensions.

Comparison between CDK and CDKT We compare here the two kernel models in the task of predicting which users will be contaminated at the end of the diffusion. The main problem to achieve this task with the CDK model is that all cascades are not on the same scale and it is very difficult to find a unique threshold which properly split data in two clusters: contaminated or not. For this reason we don’t have any threshold for the CDK model and thus couldn’t compare clusters made.

We use the following protocol: after predicting a score
Table 2. P@50 on 3 real datasets: Memetracker, ICWSM and Digg. Results of CDK and CDKT are given for two values of \( n \), the dimension of the latent space \( Z \) (50 and 500 dimensions).

|                | Memetracker | ICWSM | Digg |
|----------------|-------------|-------|------|
| CDK-50         | 0.0001      | 1.0   | 0.450|
| CDKT-50        | 0.297       | 1.0   | 0.543|
| CDK-500        | 0.625       | 0.794 | 0.067|
| CDKT-500       | 0.417       | 1.0   | 0.862|

Table 2 shows the precision at rank 50 (P@50) on all datasets for the two models using two latent spaces with different dimension. It corresponds to their ability to find 50 contaminated users. We see that both CDK and CDKT obtain better results on ICWSM. They also obtain a better MAP. This is because the ICWSM dataset is easier than the 2 others. While CDKT is obtain better resultats than CDK on most of the datasets and dimension spaces.

As the P@50 doesn’t show all information, figure 1 shows the precision/recall curve for the Digg datasets in 500 dimensions spaces. As for the P@50, the curve shows that CDKT is better than CDK.

5. Conclusion

The CDK model use the phenomenon of heat diffusion to modelize the propagation of content in a latent space. This model is based on a ranking of users and because of the different scale of each representation, there is no easy way to find which user will be contaminated. We proposed in this article an extension of this model CDKT which learns a threshold to split users in two groups: contaminated or not. On several real datasets, we showed that this model is better to find contaminated users. Our next step with this model will be to understand in which contexts (low/high diffusion, network type, etc) it outperforms CDK.

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