Group #2 Project Final Report: Information Flows on Twitter

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1 Introduction

Twitter has become a very popular microblog website and had attracted millions of users up to 2009. It is generally considered as a social networking website but gradually also used as a media for people or companies to spread out news or marketing information. One reason for considering Twitter as a media that broadcasts information instead of a social network is that on Twitter the friendship between two users are asymmetric [1] and according to [1] only 22.1% of the relationships are reciprocal. This is very different from the online messenging services such as MSN or Google Chat. However, different from the traditional media like TV or newspapers, a user can easily propagate an information she saw from other users to her followers by *retweet*, which is an automatic way of duplicating others' posts on the reader's Twitter board. The retweet function is critical for making the information available to a large number of users. However, in the online environment, we know sometimes people *see* but not really *read* the content.

Therefore, the topic of our project is to study information flow on Twitter network, especially we want to understand the role played by the *reading rate* of a post and retweet rate after the user reads the message. We construct epidemic models according to the design of Twitter. Our epidemic model can better capture the nature of information cascade on the Twitter network. We will further explain our epidemic model in Section 3, here we only briefly describe the model setting.

On the Twitter network, the main relationship between users is called *following*. If u follows v, v's tweets will appear on u's Twitter page automatically. In this case, we call u being *exposed* to the information. While u sees a post by v, besides doing nothing she can choose to retweet or reply the post. If u retweets, the post will appear in the pages of u's followers. Therefore, we can consider retweet is one means of propagating information and mark a user *contagious* when she retweets the post. If u read the tweet but not retweet, we call u being *infected*. Please see Figure 1 for a summary of our epidemic model.

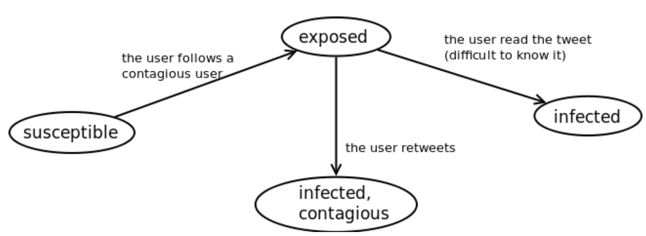


Figure 1: The Epidemic Model

We will use this model to help us understand how information flows on the Twitter network. In the rest of the report, we will describe our datasets in Section 2, our epidemic model in more detail in Section 3, and our simulation result on applying the model to our datasets in Section 4. In

[1]Using the graph theory terminology, the edge between two nodes is directed

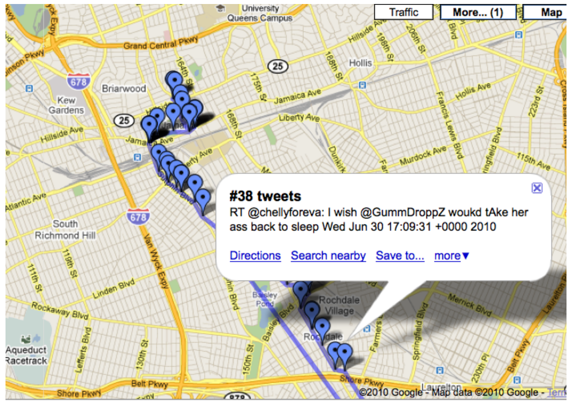


Figure 2: Visualization of One Twitter User in Our Log on a Single Day

Section 5, we will further discuss how retweet rate will be impacted by various factors. Then finally in Section 6, we will summarize our project and describe a few take way ideas.

2 Our Datasets

In this project, we are using two networks: one is collected by ourselves focused on mobile users in New York City and the other one is build from the dataset released by Kwak et.al [1]. One fundamental difference between these two networks are the users. For our dataset, we are focused on general mobile users who use twitter on-the-go; the users involve in the data are common people like you and me. For Kwak's dataset, they capture the dataset by crawling the twitter network from some popular figures and therefore most of the users in their network has a huge number of followers. As a result, the network structure of the two networks are very different and it is very interesting to see how the network structure impacts on the information diffusion. In this section, we will detail on how we collect the NYC dataset from twitter and how we construct a network from Kwak's dataset.

2.1 NYC Network: The Retweet Network for Mobile Users in NYC

In order to identify mobile users in New York City, we use Twitter's APIs to collect all the tweets generated by mobile devices and with GPS location within the NYC. Their geo-location APIs allows us to collect tweets that are posted within a pre-configured geographical range, and we further use the name of the twitter client to select the tweets generated by the twitter clients on mobile phones, such as "twitter for iPhone" and "twitter for android". We collect all these tweets from the 10 most populated cities in the United States, including New York City, Chicago, BayArea, Los Angeles, Houston, Dallas, San Antonio, Phoenix, Philadelphia and San Diego. However, among all the cities we collect data from, New Yorkers seems to use twitter the most and the most frequent. We can collect around 40-50MB of tweet from NYC each day. For the rest of the cities, it's around 10-20MB of tweet per day. Therefore, in the rest of the project, we will use the data from NYC to analyze how information flows on twitter's network. Figure 2 is a visualization on one of our users' tweets in one particular day; we plot each tweet according to the geo-location attached to it.

Since we are interested in knowing how the messages are propagated between people, we are also collecting the followee/follower relationship of the users in our trace. For each retweet, we would like to know how the tweet is propagated to the user. First of all, we collect whom the user's following, i.e., the user's friends in Twitter's terminology. Secondly, since retweets follows the format: "RT @Source: content", we parse the content of the retweet to retrieve the source of the tweet. After we learn the sources, we collect the sources' follower. In Figure 3, we plot out the data we collected and their relationship between each other. In our dataset, there are 440,135 tweets and

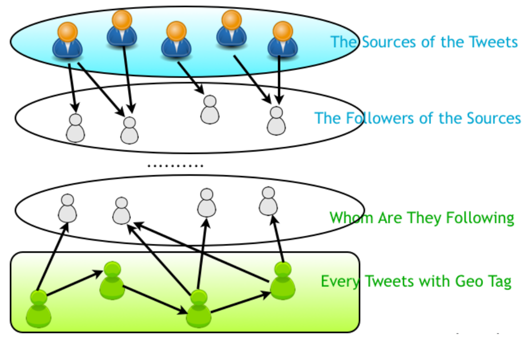


Figure 3: Data Collection for Building NYC Network

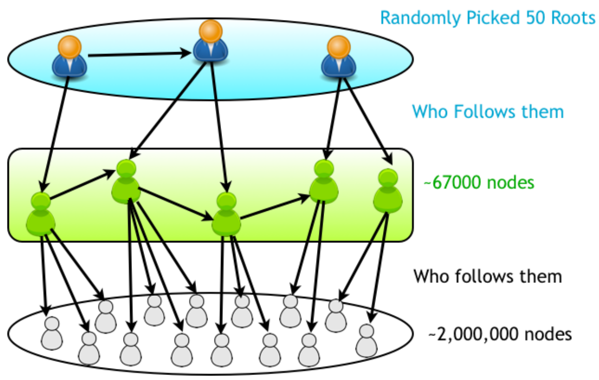


Figure 4: Network built from Kwak's Dataset

15,919 of them are retweets. The retweets are generated by 1407 unique users, whom we called seeds; while the sources of the retweets are 8517 unique users, whom we called sources. Among the 1407 seeds, 1244 of them allowing us to collect their friend list, and among the 8517 sources, 6167 of them allowing us to collect their follower list. After collecting the friends of the seeds and the followers of the sources, we have roughly 250,000 users (or nodes) and 4,000,000 edges in our network. In other words, this network is very well connected and most of the retweets can travel from the sources to the seeds within two steps.

2.2 Kwak Network: The Retweet Network for Users in Kwak's Dataset

Kwak's dataset provided the follower/followee relationship between followers and followees for 20 million users. However, in order to make a network comparable with the NYC network, we try to select a subset of Kwak's network and make the number of edges is at the same scale as the NYC Network.

Following is how we select the subset and the procedure is also plotted in Figure 4. First, we randomly pick 50 users. Secondly, we include in their followers and finally the followers of these followers. In the end, we have roughly 2,000,000 users and 8,000,000 of edges (i.e., the following relationships). To compare with the NYC network, which has 250,000 nodes and 4,000,000 edges, Kwak Network is more flat (i.e., each users have lots more followers), and less inter-connected.

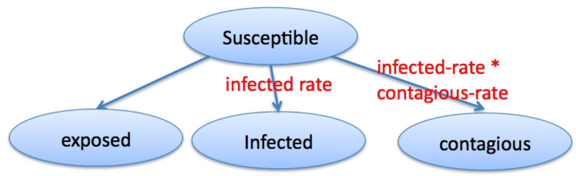


Figure 5: Diffusion Model Mode 0

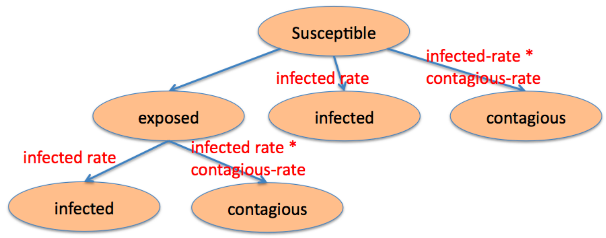


Figure 6: Diffusion Model Mode 1

3 Epidemic Models

In this section, we are going to model users' reaction to tweets. However, since we don't really know users' behavior, we come up with three different diffusion models based on our own experience. In our models, we have four states: susceptible, exposed, infected and contagious.

- Susceptible: a user is susceptible to a post when s/he is following a contagious user
- Exposed: a user is exposed to a tweet when the tweet shows up on his/her twitter page.
- Infected: a user is infected by a post when s/he read the tweet
- Contagious: a user is contagious when s/he retweet the tweet, i.e., his/her follower would become susceptible and exposed to the tweet as well.

3.1 Mode 0

Mode 0 is the simplest model. As soon as a friend of u generates a new tweet, u becomes susceptible and then automatically exposed to the tweet. Then, with a probability, named *infection rate*, the user would read the tweet. That is, the user would become *infected* with the probability of *infection rate*. After the user has read the tweet, there is also a probability, named *contagious rate* or *retweet rate*, that the user retweets the post, become *contagious* and makes his/her followers become susceptible. We summarize this mode in Figure 5.

Please note that in this model, the user has only one chance to decide whether it will be infected or contagious. Even when the tweet reappears on his/her twitter page through another route, the user won't change his/her decision.

3.2 Mode 1

Mode 1 is similar to the mode 0; however, if the same tweet appears on the user's page the second time, we assume that the user has another chance to decide whether she will read it or even retweet it. However, if the user has already read the tweet before and has decided not to retweet it. Then, in mode 1, the reappearance of the tweet would not change the user's decision. Mode 1 is summarized in Figure 6.

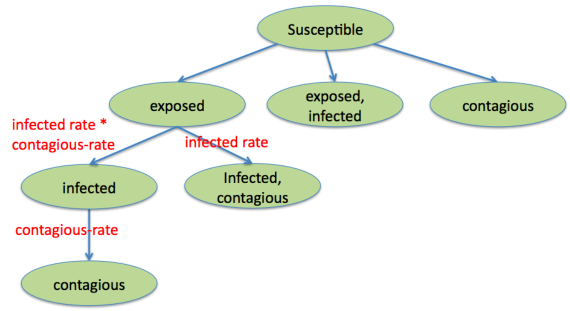


Figure 7: Diffusion Model Mode 2

3.3 Mode 2

Mode 2 is developed based on our observation that users' decision would also be influenced by other users' decision. Imagine a user originally decided not to retweet a post, which many of his friend later decided to retweet it. After seeing most of his friend's decision, the user might change its decision from only being *infected* to *contagious*. Thus, in mode 2, when a tweet reappear to the user's page, we give the infected user also another change to decide whether s/he would like to become *contagious* or not. Mode 2 is summarized in Figure 7.

4 Simulation Result

In order to simulate how the information propagates in the twitter network, we would need to decide the *infection rate* and *contagious rate* (or *retweet rate*). We are able to calculate retweet rate from our NYC dataset, which is around 0.03. However, it is very hard to determine the infection rate from the empirical data. In the following simulation, we fix infection rate at 0.3 and will briefly discuss the impact of different infection rates.

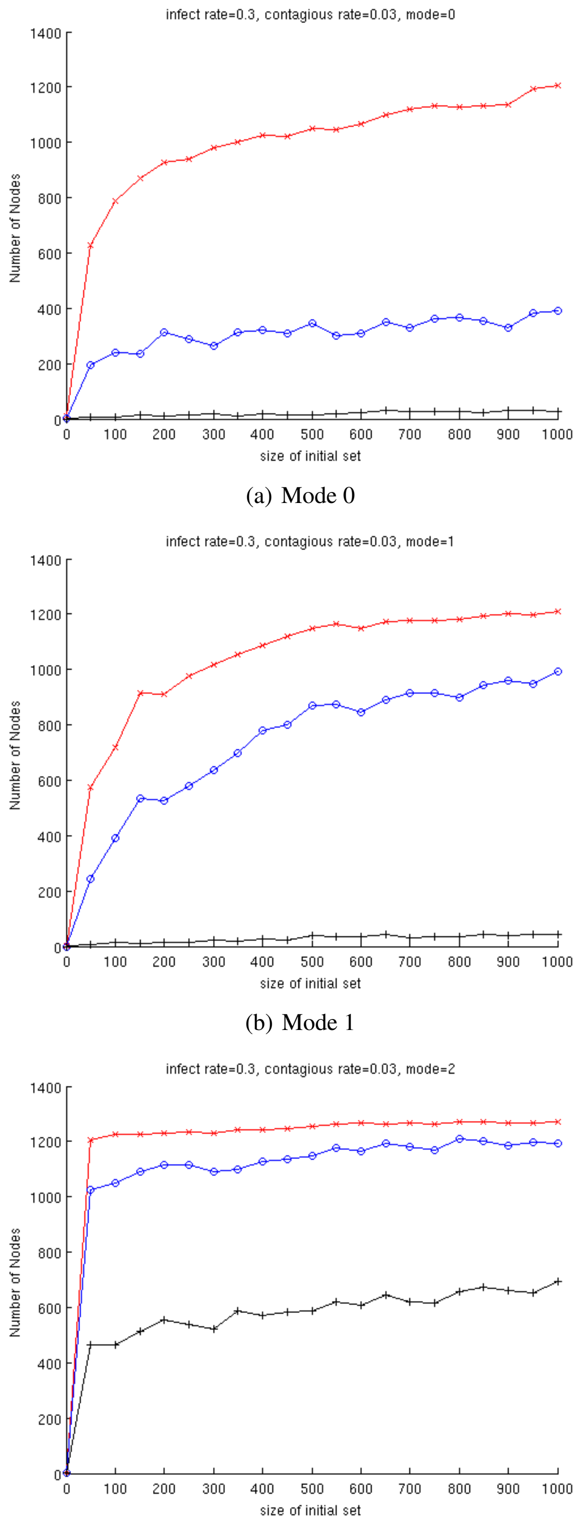
4.1 For NYC Network

We run the simulation by inject a message at a number of sources in the network, and calculate the number of seeds (out of the 1244 seeds) will become exposed/infected/contagious at the end of simulation. The simulation results for NYC Network is shown in Figure 8. The x-axis is the number of sources that we inject the information initially, and the y-axis is the number of seeds. The red line presents the number of exposed nodes, the blue line presents the number of infected nodes, and the black line presents the number of contagious nodes. If we compare mode 0 to the other two modes, we can see that the number of infected and contagious nodes are much less than mode 1 and mode 2. This is because, in mode 0, the user only has one chance to decide whether s/he would like to read/retweet the post, even when the tweet showed up several times in the page. Also, since our NYC Network is very well connected, we find that the difference between the number of exposed nodes and infected nodes is very small. This is because most of the nodes would receive the tweet more than once and therefore have greater chance to become infected/contagious.

We further investigate how different infection rates would impact on the number of infected nodes. We apply different infection rates on the NYC Network and the results are shown in Figure 9. From the result, we can see that infection rates indeed has huge impact on the number of infected node.

4.2 For Kwak's Network

We run the similar simulation on Kwak's Network, and present the result in Figure 10. Similar to the result in the NYC Network, mode 0 has the least number of nodes to be exposed/infected/contagious. However, different from the result in the NYC Network, even in mode 2, the difference between the



(a) Mode 0

(b) Mode 1

(c) Mode 2

Figure 8: Simulation Result For NYC Network

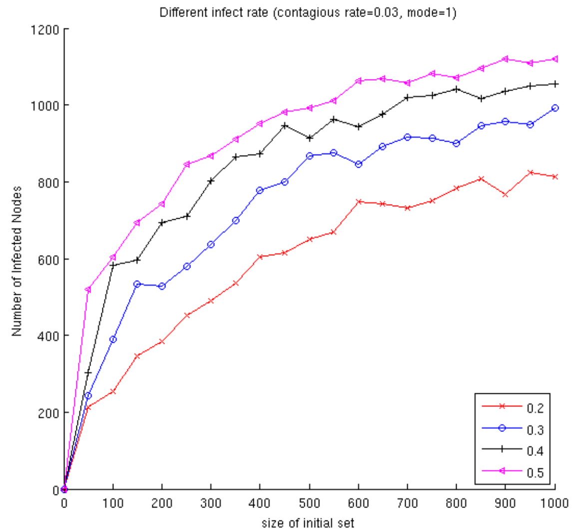


Figure 9: Impact of Infection Rate

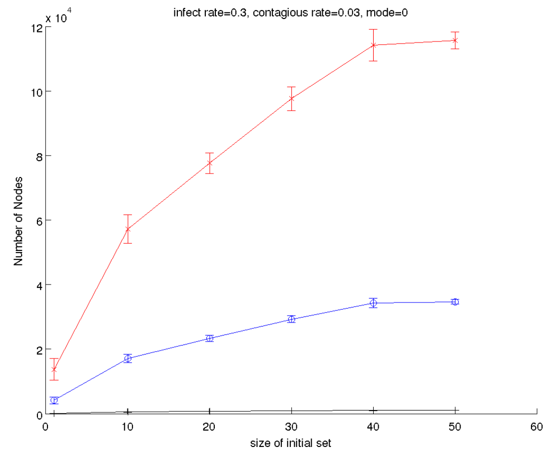
number of exposed and infected is huge in Kwak's network. This is because Kwak's network is more flat and less inter-connected than the NYC's network. Therefore, most of the nodes has only one chance to decide whether s/he would like to become infected/contagious or not.

4.3 Average Infection Time

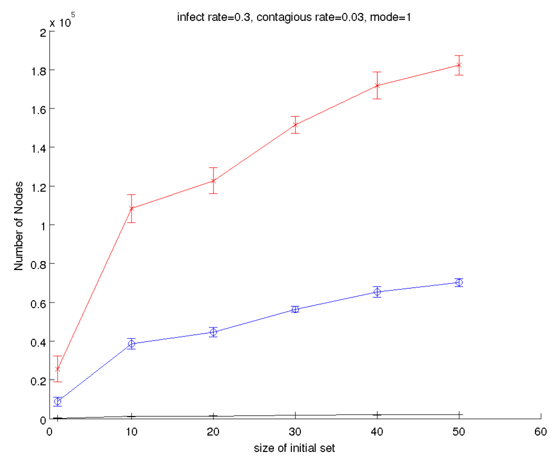
In [1], the authors reported that in their Twitter data, the average path length between two users is 4.12, the median and the mode are both 4. The average path length is very short especially when we consider the fact that the network is directed. However, in the setting of our diffusion model, existing a path between two nodes doesn't necessarily mean the information can flow from one end to the other. However, if we allow the information source to send out information more than once, then we can expect we can have most reachable nodes from the source be infected. We may then consider the *average infection time* of the receivers. The average infection time can be used as a notion of the *closeness* between two nodes in the network, which is similar to the idea of the *diffusion distance* in graph theory. We think this is more suitable than the traditional short-path distance under our model setting.

Again, we use simulation to compute the average infection time. At time 0, the information source send out the information. At time 1, we drew random numbers for the followers of the information source to decide whether followers are infected and become contagious. If a follower becomes infected at this step, we mark its infection time as 1. Then at time 2, we check the next layer of followers, mark the infection time accordingly and keep going until the follow stops. This is the same as the aforementioned diffusion simulation and we consider it one run of information cascade. If there is still any reachable but non-infected node, the information source can send out another run of information cascade and the time keeps accumulated.

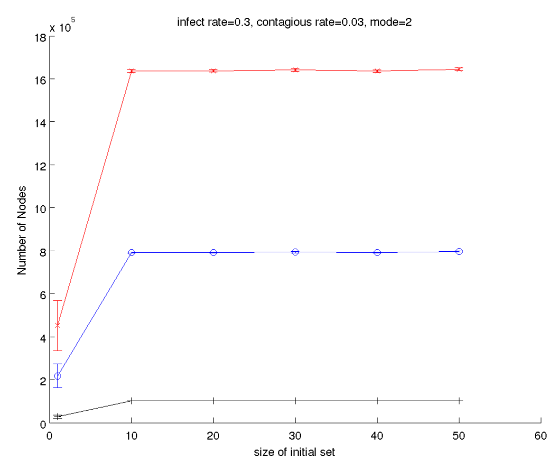
We simulated and computed the average infection time on our NYC Twitter dataset. We randomly select 100 nodes as our initial set. This idea is more appropriate when mode 1 or mode 2 is adopted. Here we use mode 1. Furthermore, we assume the maximum number of runs the initial set can send out information is 10. We again use 0.03 as our retweet rate and run the simulation using different values of infection rate. Similar to our previous simulation, the average infection time is computed only over the infected nodes of the seed. The results are summarized in the following table.



(a) Mode 0



(b) Mode 1



(c) Mode 2

Figure 10: Simulation Result For Kwak's Network

Infection Rate	Infected nodes	Avg Infection time
0.1	516	16.56
0.2	642	8.35
0.3	774	5.7
0.4	821	4.03
0.5	909	2.88

Table 1: The Impact of Infection Rates

5 Learning The Retweet Rate Prediction Function

There are two main parameters in our epidemic model: the infection rate, which is the probability for the user to read a post from whom the user follows, and the contagion rate (or retweet rate), which is the probability for the user to retweet a post after reading it. As we have shown in previous sections, the information cascade on the Twitter network is decided by the two parameters.

In stead of fitting the parameters of the network for each edge in the Twitter network, we want to learn functions to predict the rates for a given pair of Twitter following information. Using the Twitter API, we can obtain the posts by a given user. Furthermore, if a post is a retweet instead of an original post by this user, there will be a mark ”RT“ before it. Therefore, we can estimate the overall retweet rate. Even more, the retweet posts also record who is the source. Therefore, fix a pair of users (u, v), in which u follows v, we can compute the retweet rate between them.

On the other hand, it is difficult to know whether a user *read* a post from whom she follows, because the user can take no action on Twitter even she indeed read the post. Therefore, estimating the infection rate is not an easy task. As a result, here we focus on learning the retweet rate from the data and assume the infection rate is 1.

5.1 The Prediction Function and Cost Functions in The Learning Algorithm

To be specific, we select a set of (directed) edges E' in the NYC network, in which for each edge (u, v) in E' there exists at least one retweet [2]. We use the profile of u and v as the input (features) and compute the retweet rate of (u, v) as the output of a linear function f. Denote the features of the i-th edge in our dataset as $x^{(i)}$ and the retweet rate to be $r^{(i)}$. The features we used in the prediction function includes the following information of both u and v:

status_count The number of tweets the user has.

followers_count How many people follow this user.

friend_count How many people the user follows.

retweet_count How many retweets the use made before.

time_zone The time zone of the user.

We want to learn the coefficients α of $f(x) = \alpha^T x$ so that $f(x^{(i)})$ is close to $r^{(i)}$. For the *closeness* we can use the least square distance. Besides, since the rate is the parameter of a $Bernuli$ distribution, we can compute the KullbackLeibler divergence (KL-divergense) or the Bhattacharyya distance between the distributions as the distance. To sum up, we use the following three different cost functions for $f(x^{(i)})$ and $r^{(i)}$:

Least square distance :

$$\|f(x) - r\|^2$$

[2]Therefore, what the model really learned is the retweet rate given that the follower ever retweeted.

KullbackLeibler divergence :

$$D_{KL} = f(x)\log\frac{f(x)}{r} + (1-f(x))\log\frac{(1-f(x))}{1-r}$$

Bhattacharyya distance :

$$\sqrt{f(x)r} + \sqrt{(1-f(x))(1-r)}$$

For the case of using least-square distance, we solved it as a linear regression problem using the package in Matlab. For the other two cost functions, we do the optimization using gradient descent.

5.2 Evaluation

To evaluate the learned prediction function, we compute the log-likelihood of our data; that is,

$$\sum_{i=1}^{|E'|}\left[\#reweet(u^{(i)},v^{(i)}) \times \log f(x^{(i)}) + (\#post(v^{(i)}) - \#reweet(u^{(i)},v^{(i)})) \times \log(1-f(x^{(i)}))\right].$$

Besides the aforementioned three models using different cost functions, we also compute the log-likelihood using the total average retweet rate for comparison. The table below is the result:

	Least sequare	KL-divergence	Bhattacharyya	Avg
NYC	-68.7986	-70.2389	-70.0540	-93.2763

Besides the log-likelihood values, we also discovered an interesting fact in our dataset. In our learned model learned from the NYC dataset, we found the the number of posts of the information source has negative relationship with the infection rate. We guess this might be because that the users with a huge number of posts are some news media which post very often but not all tweet were read (infection rate is less than 1).

6 Summary

To sum up, during the past several weeks we did the data preparation and preprocessing. Besides, we also investigated the data to figure out what kind of learning model and features we can use to predict the model parameters. The model parameters and the coefficients of the prediction functions should be able to reflect some interesting properties of information cascade on Twitter network.

Remark

In our original proposal, we assume the infection rate to be the sum of retweet rate [3] and reply rate. However, after investigating our dataset, we found the obtained infection rate is too low to be realistic. Therefore, we decided to use the model mentioned in this report.

References

[1] Kwak H., Lee C., Park H., Moon S. (2010), *Proceedings of the 19th International World Wide Web (WWW) Conference*

[3] It is defined directly as the ratio of total number of retweet over total number of post as in our learning model instead of the definition we used in our final model