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Abstract

Advanced satellite tracking technologies have collected a huge amount of wild birds’ migration data. These data are very useful for biologists to understand birds’ dynamic migration patterns, to study correlations between the habitats, and to predict global spread trends of avian influenza. We transform the biological problem into a machine learning problem by converting the migratory paths of wild birds to graphs. Our first step of H5N1 outbreak prediction is to discover weighted closed cliques from the graphs by our mining algorithm HELEN (short for High-wEight cLosed cliquE miNing), which are then used by our learning algorithm HELEN-p to predict potential H5N1 outbreaks at habitats. We show that the prediction is more accurate in comparison with the traditional method on the migration data obtained through a real satellite bird-tracking system. It is also confirmed by our empirical analysis that H5N1 spreads in a manner of high-weight closed cliques and frequent cliques.

Keywords
Computational Sustainability; Bird Flu Prediction; Wild-Bird Migration Data Mining; H5N1 Prediction in Qinghai Lake, China; Machine Learning and Graph Mining.

1 Introduction

Figure 1: A GPS tracking device attached to a bird.

The H5N1 virus outbreaks in poultry in 2003, 2004 and 2009 caused unprecedented geographical impact in Asia [2, 6, 8]. The H5N1 virus is a highly pathogenic avian influenza (HPAI) that has emerged in Southern China in the mid-1990s. A large number of wild birds died as a result of the highly pathogenic virus in Qinghai Lake, China in 2005; and the number of the protected bar-headed geese had decreased 5% – 10% worldwide due to the epizootic disease alone as estimated in 2009 [5].

The spread of H5N1 is believed to be closely related to
wild-bird migration across the globe [4]. However, as effective tracking systems and data analysis tools have been lacking for a long time in China, the study on the relationship between the spread of the H5N1 virus and the bird-migration network was not conducted in large scale. This situation is greatly improved now, and we have collected the movement data of about one million records from March 2007 to December 2009 by using a satellite tracking system and special GPS devices attached to birds (see Fig. 1). Specifically, migration birds were captured by ecologists and set up with GPS mobile sensor devices. And the tracking signals were then transmitted to the satellite continuously and the data were distributed by the USGS processing unit which were then received by the researchers.

Biologists found that bird migration routes in a small area can be best viewed as graph patterns like cliques [3] rather than simple location sequences in small scale. It is therefore important to understand the role that migratory birds play in the ecology and the transmission patterns of H5N1 by integrating data on habitats, seasonal movement chronology, routes, dates, and locations of H5N1 outbreak events. Recently, several studies at Qinghai Lake have shown that H5N1 viruses in Qinghai Lake spread with the bird migration patterns [5]. Most of these analysis were conducted at a relative coarse level of granularity (e.g. between countries) and the methods for discovering the correlations of bird migration routes have limited predictive power.

In this paper, we take a data mining and machine learning approach to exploit the collected data to build a bird-virus prediction model. We mine the bird-movement patterns, and learn the relationship between graphical clique patterns and virus propagation. In particular, we use vertex weights as an important factor to evaluate the seriousness of H5N1 virus. Weights are differently defined by using the degree of a habitat or vertex (the frequency that birds fly among habitats), the time that birds stay at a certain habitat, or the density of the birds in a particular habitat. These weighted graph features can make the virus prediction model more accurate because they can be used to estimate the correlations among the habitats better. As a result, our prediction algorithm HELEN-p can be used to accurately predict the future H5N1 outbreak from the migration graphs.

Our main contributions are summarized as below,

1. we transform the bird-migration data analysis problem into a high-weight closed clique mining problem; and
2. we propose a novel high-weight closed-clique mining algorithm (HELEN), which is then used by our prediction algorithm HELEN-p for accurate H5N1 outbreak prediction.

Compared with our previous work, we have extended previous work significantly. In our previous work, we analyzed bird virus outbreak reasons via mining the birds migration data such as sequence rule mining [8] and sub-graph mining [7]. In this paper, we focus on how to predict the future possible bird virus outbreak locations by machine learning methods. Specifically, our prediction method is based on the mined high-weight closed cliques, some newly developed habitat correlation criteria, and two machine learning algorithms (i.e., kNN and LapRLS [11]). More importantly, in LapRLS, we generalized the idea of label propagation in manifold based semi-supervised learning to H5N1 spreads in the bird migration network.

2 Algorithm

2.1 Mining High-Weight Closed Cliques

In our graph-based model, a bird habitat is denoted by a node (vertex) and a migration route is denoted by an edge. A clique C is a graph with fully connected edges. If a graph G contains a clique C, then G is said to be a support graph of C. For example, graph G1 in Fig. 2 is a support graph of clique C1 = “abc” (Fig. 2(e)).

Definition 1 The frequency-support of a clique C is defined as the ratio of the number of support graphs over the total number of graphs in a database D.

\[
support^f(C) = \frac{\sum_{G \in D} I(C \subseteq G)}{|D|},
\]

where \( \sum_{G \in D} I(C \subseteq G) \) is the number of support graphs of clique C, and |D| is the number of graphs in the database.

Given a support threshold \( \theta^f \), a clique C is a frequent clique if \( support^f(C) \geq \theta^f \). In addition, if there does not exist another clique C’ satisfying C \subseteq C’ and \( support^f(C’) = support^f(C) \), C is a frequent closed clique (FCC). Closed cliques are important since they greatly reduce the number of child cliques with the same level of support. FCC mining is to find all frequent closed cliques from a graph database. Given the graph database in Fig. 2 and \( \theta^f = 0.5 \), “abc” and “abde” are two frequent and closed cliques.

The weight of a vertex \( v \) is denoted by \( weight(v) \). Three weighting ideas are considered by this work:

1. \( W_{frequency} \) (or \( W_{freq} \)) which measures how frequently a bird flies among different habitats.
2. \( W_{time} = t_{arrive} - t_{leave} \) which measures how long a bird stays at a certain habitat, where \( t_{arrive} \) and \( t_{leave} \) are the arrival time and departure time of the bird.
3. \( W_{density} \) (or \( W_{dens} \)) which measures the density of the birds in the habitat, and is calculated by using the
area size of the habitat to divide the number of migration records received by the satellite tracking system from the habitat.

The weight of a graph $G$ is given by $weight(G) = \sum_{v \in G} weight(v)$.

**Definition 3** The "support" of a clique $C$ is defined as

$$support(C) = \frac{weight(C) \sum_{I \subseteq G} I \subseteq G \in D} {\sum_{G \in D} weight(G)}$$

where the numerator $weight(C) \sum_{I \subseteq G} I \subseteq G \in D$ denotes the total weight of the clique $C$ in the database $D$, and the denominator $\sum_{G \in D} weight(G)$ is simply a normalization term. Given a support threshold $\theta^w$, a clique $C$ is a high-weight-support clique if $support(C) \geq \theta^w$. In addition, if no other clique $C'$ exists that satisfies $C \subseteq C'$ and $support(C') \geq support(C)$, then $C$ is a high-weight-support closed clique (HWCC). We wish to find all frequent and closed cliques from the graph database $D$ with respect to the vertex weight. For example, given the graph database in Fig. 2, we have $support(abde) = (15 \times 2)/(49 + 29 + 47 + 43) = 0.18$, $support(abcd) = (47 \times 2)/(49 + 29 + 47 + 43) = 0.56$. If $\theta^w = 0.5$, the clique "abde" is a high-weight closed clique.

**Definition 3** The graph-weight-support of a clique $C$ is defined as follows,

$$support^w(C) = \frac{\sum_{G \in D} I(C \subseteq G) \cdot weight(G)} {\sum_{G \in D} weight(G)}$$

where the numerator $\sum_{G \in D} I(C \subseteq G) \cdot weight(G)$ denotes the total weight of support graphs of the clique $C$ in the database $D$, and the denominator $\sum_{G \in D} weight(G)$ is again for normalization. Given a support threshold $\theta^w$, a clique $C$ is a high-graph-weight-support clique if $support^w(C) \geq \theta^w$. In addition, if there does not exist a clique $C'$ satisfying $C \subseteq C'$ and $support^w(C') = support^w(C)$, $C$ is a high-graph-weight-support closed clique (HGWCC).

The "downward closure" property (anti-monotone property), which has been widely used to accelerate pattern mining algorithms, states that any child pattern (e.g. a subset of vertices) of a frequent pattern is also frequent. Hence, if no $k$-1-patterns are frequent, we do not need to explore $k$-patterns. However, we observe that the "downward closure" property does not hold in HWCC mining. For example, in Fig. 2, $support(abde) = 0.56$, $support(abd) = 0.32$. If we set the support threshold $\theta^w = 0.5$, then "abde" is a low-weight clique, while its parent-graph "abde" is a high-weight clique. So, this causes difficulties for mining algorithms. It can be proved that if any $k$-1-clique $C^{[k-1]}$ is not a high-graph-weight-support clique, then $k$-clique $C^k$ is not either. This "downward closure" property is useful in the process of enumerating cliques. If we know that a $k$-1-clique, $C^{[k-1]}$ is not a high-graph-weight-support clique, there is no need to enumerate any $k$-clique. It can be also proved that if $\theta^g = \theta^w$, then HWCC $\subseteq$ HGWCC.

The main idea of HELEN algorithm is to search over a clique lattice as shown in Fig. 3. Its pseudo codes covering three major computational steps are presented as follows:

**Input:** Graph database $D$ and vertex weight, threshold $\theta^g$ and $\theta^w$;

**Output:** HWCC.

Step 1: Calculate the graph weight using $D$ and vertex weight; Step 2: Search the lattice and obtain HGWCC using $D$, vertex weight and $\theta^w$; and Step 3: Check the HGWCC and obtain HWCC using $D$, vertex weight and $\theta^w$.

The mined HWCCs from the illustration data are shown in the last column of the Table in Fig. 3.

### 2.2 Calculating Habitat Correlation

Our prediction method also involves two types of habitat correlations, location-based correlation and clique-based correlation.

**Definition 4** For any two habitats $i$ and $j$, the location-based correlation is defined by the distance $d_{ij}$ of the two habitats. It is calculated by using

$$\frac{1}{d_{ij}} \max_{i,j} \frac{1}{d_{ij}},$$

where the denominator, $\max_{i,j} 1/d_{ij}$, is a normalization term to make the correlation in the range of $[0, 1]$. 
Two types of distance are considered in our correlation estimation.

1. The Euclidean distance, $d_{ij}^{cc} = \sqrt{(\phi_i - \phi_j)^2 + (\lambda_i - \lambda_j)^2}$, where $(\phi_i, \lambda_i)$ and $(\phi_j, \lambda_j)$ are the latitude and longitude of habitats $i$ and $j$, respectively.

2. The great-circle distance [9], $d_{ij}^{gc} = r \Delta \theta_{ij}$, where $r$ is the radius, $\Delta \lambda = \lambda_i - \lambda_j$, and $\Delta \theta_{ij} = \arctan \left( \frac{\cos \phi_i \sin \Delta \lambda \sin \phi_j - \sin \phi_i \cos \phi_j \cos \Delta \lambda}{\sin \phi_i \sin \phi_j \cos \phi_j \cos \Delta \lambda} \right)$.

**Definition 5** For any two habitats $i$ and $j$, the clique-based correlation is defined by using the weighted supports of closed cliques that $i$ and $j$ belong to.

$$c_{ij}^w = \frac{\sum_{C \in C} I((i, j) \subseteq C) \text{support}^w(C)}{\max_{i' \neq j'} \sum_{C \in C} I((i', j') \in C) \text{support}^w(C)}, \quad (5)$$

where $C$ is a set of high-weight closed cliques (HWCC), and $\sum_{C \in C} I((i, j) \subseteq C) \text{support}^w(C)$ denotes the summation of the weighted support of the closed cliques the habitats $i$ and $j$ belong to.

For example, in Figure 3, $C = \{"abde", "ad", "ade"\}$ and $\sum_{C \in C} I((a, e) \subseteq C) \text{support}^w(C) = \text{support}^w("abde") + \text{support}^w("ade")$. The correlations among "a", "b", "c", "d" and "e" are: $e_{ab} = 0.31$, $e_{ac} = 0$, $e_{ad} = 1$, $e_{ae} = 0.72$, $e_{bc} = 0$, $e_{bd} = 0.31$, $e_{be} = 0.31$, $e_{cd} = 0$, $e_{ce} = 0$ and $e_{de} = 0.72$.

2.3 The Prediction Algorithm

We take the following pseudo codes in the prediction of H5N1 virus outbreaks:

**Input:** Graph database $D$, vertex weight, threshold $\theta^w$ and $\theta^p$, positive instance $p$, number of predicted habitats $k$;  

**Output:** A ranked list of $k$ predicted habitats.

(1) Call the HELEN algorithm to obtain HWCC; (2) Calculate the correlations of any two habitats according to Eq.(4) or Eq.(5) using the mined HWCC; and (3) Run kNN or LapRLS algorithm to find the top $k$ likely outbreak habitats.

The two machine learning methods kNN and LapRLS are explained as follows. We hypothesize that H5N1 outbreak is highly correlated with the migration network, which is reflected in the mined high-weight closed cliques. We verify this hypothesis in the experimental section. Given a habitat with an H5N1 outbreak (Habitat$_p$) and the habitat correlation ($c_{ip}^w$, $c_{ip}^p$ or $c_{ip}^r$), we can rank the remaining habitats and obtain the top $k$ habitats with the largest correlation based on the $k$ nearest neighbor method (kNN). For example, if “a” in Fig. 3 is taken as a positive habitat, we have the ranking list of “d”, “c”, “b” and “e” according to the correlations. We denote the corresponding HELEN-p variant as HELEN-p(kNN).

Under a kernel learning approach, we take the originating habitat of the H5N1 outbreak as a single positive instance. We predict other outbreak habitats by using the
yond p(LapRLS) has the potential of bridging two habitats beyond habitats with the high-

Then, we apply the LapLS objective function with a single positive instance,

\[
\min_f f^T \mathcal{L} f + \frac{\alpha}{n} \| f - y \|_F^2,
\]

where \( f \in \mathbb{R}^{n \times 1} \) is the prediction vector, \( y \) is the label vector with \( y_i = \begin{cases} 1 & \text{if } i = p, \\ 0 & \text{if } i \neq p. \end{cases} \) Above, \( \| \cdot \|_F \) denotes the Frobenius norm and \( \alpha \) is the tradeoff parameter. So, the final obtained score vector \( f \) can be used to rank the remaining habitats and find the top \( k \) habitats with the highest probability of an H5N1 outbreak. We denote the corresponding HELEN-p variant as HELEN-p(LapRLS).

Compared with the HELEN-p(kNN) method, HELEN-p(LapRLS) has the potential of bridging two habitats beyond \( k \) nearest neighbors, since it can propagate the label via local connections [1], which is also supported by our experimental results in Section 3.2.

3 Experiments

3.1 Data Collection

Our on-site studies were conducted at the Qinghai Lake National Nature Reserve, Qinghai Province, China, between March 2007 and December 2009. 59 birds were selected randomly from different flocks to tie a battery powered GPS device to each of them. More details of the data are presented in Table 1. We had collected nearly one million migration records by December 25, 2009. We selected those 29 bar-headed geese in our subsequent analysis for the same type of birds. Finally, we have 103 habitats (i.e., nodes in graphs) and 29 graphs (one for each bird).

The reverse transcription-polymerase chain reaction (RT-PCR) \(^1\) technique was used to confirm whether a bird is or not infected with the virus. All of the samples were immediately placed into small tubes containing transferring solution and then stored in a container of liquid nitrogen within two hours. We tested 1,055 samples by using RT-PCR, and 12 bar-headed geese, three ruddy shelducks and 14 brown-headed gulls were confirmed to be positive for an H5N1 subtype. These data are shown in the last column of Table 1, which indicates that the prevalence of H5N1 in Qinghai Lake was high. In order to obtain the relationship between migratory birds and H5N1 outbreaks, information about H5N1 outbreaks were extracted from the Ministry of Agriculture of the People’s Republic of China Database and OIE Database for the period of February 2004 - May 2009.

3.2 Summary of Experimental Results

3.2.1 H5N1 Outbreak Analysis Using Mined Cliques

In this section, we focus on result analysis of clique mining. We applied the HELEN algorithm to those 29 graphs and 103 vertices to extract cliques. One high-weight clique \( C_{15} \) is shown in Fig. 4. If we only consider its frequency support (\( \text{support}^f = 3/29 \)), \( C_{15} \) would be pruned. However, the clique has a weight of 0.13, 0.16 and 0.052, respectively, according to \( W_{\text{frequency}}, W_{\text{time}} \) and \( W_{\text{density}} \) weighting strategies, and contributes to more than 5.2% of the total time of the birds’ spring migration time. The table in Fig. 4 shows that the migration network has a strong relationship with H5N1 outbreaks. For example, while birds prefer to stay at habitat 4 (H4), three cases of H5N1 outbreak are reported. In addition, this clique shows that the habitat H4 has a strong correlation with its neighboring habitats (H1, H2, H3, and H5) under the high weight of \( W_{\text{density}} \). Interestingly, habitats (H2, H3, and H5) are also reported to have H5N1 outbreak. The weight of those habitats does reflect the possibility of virus transmission.

From the above analysis, we can see that high-weight closed-clique mining can help biological professionals make better decisions, e.g., highlight some high-weighted cliques. More importantly, we discovered that 24% of mined cliques have low frequency but high weighted support, which shows the importance of weight clique mining, since otherwise, these low frequency cliques would be pruned by the traditional frequent closed clique mining algorithms. More mining results can be found at Link\(^1\).

3.2.2 H5N1 Outbreak Prediction Using Mined Cliques

In this section, we describe our prediction experiments. We reserve all of the 245 cliques that are mined from those 29 graphs and 103 habitats (\( \theta^s = 0, \theta^w = 0 \)), where each clique has four different weights, \( W_{\text{frequency}}, W_{\text{time}}, W_{\text{density}} \) and \( \text{support}^f \), respectively. Among those 103 habitats, 16 habitats have been reported one or more cases


\(^2\)Link: www.qinghailake.csdb.cn/qhakesdm/page/paper/link1.htm

\(^3\)Link: www.qinghailake.csdb.cn/qhakesdm/page/paper/link2.htm

\(^4\)Link: www.qinghailake.csdb.cn/qhakesdm/page/paper/link3.htm

\(^5\)Link: www.qinghailake.csdb.cn/qhakesdm/page/paper/link4.htm

\(^6\)Link: www.qinghailake.csdb.cn/qhakesdm/page/paper/link5.htm
Table 1: Description of the data used in the experiments.

<table>
<thead>
<tr>
<th>Bird type</th>
<th>Bird number</th>
<th>Active time</th>
<th>Stay (days)</th>
<th>Migration record number</th>
<th>H5N1 rate (RT-PCR)</th>
</tr>
</thead>
<tbody>
<tr>
<td>bar-headed goose</td>
<td>29</td>
<td>2007-03-21 - 2009-10-21</td>
<td>745</td>
<td>48</td>
<td>783,240</td>
</tr>
<tr>
<td>ruddy shelduck</td>
<td>20</td>
<td>2007-03-21 - 2009-02-01</td>
<td>347</td>
<td>28</td>
<td>179,302</td>
</tr>
<tr>
<td>brown-headed gull</td>
<td>10</td>
<td>2007-06-21 - 2008-06-07</td>
<td>159</td>
<td>41</td>
<td>37,242</td>
</tr>
</tbody>
</table>

Table 2: The H5N1 outbreak prediction performance of HELEN-p(kNN) using habitat correlation estimated from geometric locations and migration data of bird satellite tracking system. Note, Pre@k= a positive habitat, threshold $\theta^w = 0$ and $\alpha = 1$.

<table>
<thead>
<tr>
<th>Geometric locations</th>
<th>Using bird satellite tracking system</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>HELEN-p(kNN)</td>
</tr>
<tr>
<td>$c_{ij}^w$</td>
<td>$c_{ij}^w$</td>
</tr>
<tr>
<td>Pre@1</td>
<td>0.13 ± 0.04</td>
</tr>
<tr>
<td>Pre@5</td>
<td>0.10 ± 0.15</td>
</tr>
<tr>
<td>Pre@10</td>
<td>0.15 ± 0.09</td>
</tr>
<tr>
<td>Pre@15</td>
<td>0.14 ± 0.08</td>
</tr>
</tbody>
</table>

Figure 4: A mined high-weight closed clique, $C_{15}$, with low frequency support ($support^f = 3/29$). Detailed information of the habitats and weight about the clique $C_{15}$ are shown in the table.

Figure 5: The H5N1 outbreak prediction performance of HELEN-p(LapRLS) with different values of $\theta^w$.

To gain more insights on HWCC and the effect of the support threshold $\theta^w$, we first study the prediction performance with $\theta^w = 0$, and then increase its value gradually with $\theta^w \in \{0.05, 0.1, 0.15\}$.

The prediction results with $\theta^w = 0$ are shown in Table 2, from which we can have the following observations: (1) the approach of using clique-based correlation is much better than that using the habitats’ geometric information, which clearly shows the usefulness of the bird satellite tracking system or migration network in habitat correlation estima-
tion; and (2) although the clique-based correlation may fail to build connections of two habitats that never appear in any of the same cliques as shown by the results of HELEN-p(kNN), HELEN-p(LapRLS) can complement this weakness via label propagation (or H5N1 spread). More empirical studies of HELEN-p(kNN) and HELEN-p(LapRLS) can be found at Link1, from which we can see that HELEN-p(LapRLS) improves the prediction performance and beats kNN in all cases.

The prediction performance of HELEN-p(LapRLS) with different values of $\theta^w$ are shown in Fig. 5. We can see that, (1) using a relatively larger threshold further improves the prediction performance in most cases, and this effect can be explained by the fact that a reduction of noise in the clique weights results in a better correlation estimation in Eq.(5); and (2) using a too large threshold may reduce the prediction performance, which makes sense since the correlation between two habitats may not appear when using too few selected closed cliques. We can conclude that using a relatively higher threshold is better in prediction, which supports our assumption that H5N1 spreads via high-weight closed cliques.

4 Conclusions and Future Work

In this paper, we have developed a novel H5N1 outbreak prediction algorithm (HELEN-p). In particular, we make use of the mined cliques and machine learning methods for H5N1 outbreak prediction. The experimental results show that the mined cliques, habitat correlation calculations and machine learning methods can greatly assist biologists in H5N1 outbreak analysis and prediction. More importantly, our assumption that H5N1 spreads via high-weight closed cliques and frequent cliques is also supported by the experimental results (see Link4 and Link5 for more results). For future work, we are interested in exploiting some sophisticated algorithms to integrate different weighting strategies, where some preliminary results using linear combinations are shown at Link4 and Link5.

Acknowledgement

This work is supported by the Natural Science Foundation of China (NSFC) under Grant No. 61003138 and 91224006, the Strategic Priority Research Program of the Chinese Academy of Sciences under Grant No. XDA06010202 and XDA05150401, and the Hong Kong RGC Project under Grant No. 621010.

References


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