Development of Modeling to Find the Hub Nodes on Growing Scale-free Network based on Stochastic Community Bridge Node Finder

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확장하는 Scale-free 네트워크에서의 허브노드 도출을 위한 Stochastic Community Bridge Node Finder 개발

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초록 : 네트워크를 분석하는 방법인 stochastic 기반의 community bridge node finder는 네트워크 구조의 일부 정보만을 이용하여 중심지 및 확산 경로의 유추가 가능하다. 그러나, heterogeneity 네트워크에 적용하기 어려운 단점을 보유하고 있어, 본 연구에서는 이를 개선하고자 하였다. heterogeneity 네트워크에 적용할 수 있는 community bridge node finder 방법을 개발하기 위해 네트워크의 modularity를 계측하는 방법을 적용하였으며, 개선된 방법을 통해 community bridge node를 정량적으로 평가할 수 있어 heterogeneity 네트워크의 분석이 가능하였다. 농촌계획분야 정보의 경우, 대부분 자료의 불확실성이 존재하며 무결성이 떨어지는 특성을 가지고 있는 바 본 연구에서 적용한 전염병 확산 예측 뿐만 아니라 개선된 방법을 활용할 경우 주산지 정비 거점 분석 등 다양한 형태로 이용될 수 있을 것으로 기대된다.

ABSTRACT : The community bridge node finder, based on the stochastic method of network analysis, can compute hubs spot, which would enable the use of network structures with limited information. However, applying this node finder to heterogeneity networks, which are efficient to analyze the main farm complex in fields and the spread of infectious disease, is difficult. These problems, The most connected point that is called hub is often a major role in the heterogeneity network. In this study, we therefore improved the community bridge node finder to enable it to be applied to heterogeneity networks. We attempted to calculate the bridge node quantitatively by using the modularity of cohesion analysis method and the community bridge node finder. Application of the improved method to the HPAI(Highly Pathogenic Avian Influenza) spread in Korea 2008 produced a quarantine coefficient that was 4 – 37% higher than the quarantine coefficient obtained with the centrality method for the first 14 days after the HPAI outbreak. We concluded that the improved method has the ability to successfully calculate the bridge node in heterogeneity networks based on network structures with scant information, such as those describing the spread of infectious disease in domestic animals. And Our method should be capable to find main farm complex in fields.

Key words : Farm Complex, Hub, Infection Interdiction Point, Social Network Analysis, Bridge Node

I. Introduction

Network analysis can be used advantageously for finding

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important place as the farm complex in fields and the spread point of infectious disease. Previous research has determined that the main point that is major spread point or the key point to make farm complex using specialist opinion investigation(Anderson et al., 1991; Keeling and Rohani, 2008). Thereby improving the economic efficiency,

it needed a better way. Such as The economic loss because of damage to poultry farms in Korea attributable to HPAI has increased by 10% every year, with the economic loss in 2013 estimated at $3 trillion. Thus, information regarding the route or scope of the infectious disease was required to limit its spread to reduce its negative impact on the economy.

It is possible to increase the efficiency of the farm complex, in the case farm complex is hub that is optimization point from agricultural product producer, local assemblers, and involved in farms. Especially, The network structure and extension precess of farm complex related with agricultural product producer, local assemblers, and involved in farms due to the fact that farm complex is a small example of the current business. HPAI spread that between the farms is carried out by the movement of farmer, veterinary, and deliverer. HPAI spread block, it is possible to find the point at which farmer, veterinary, and deliverer pass through mainly. In other words, to find the HPAI block point things like find the farm complex is a same problem to find a hub in a growing network as increases to sclae free, which is composed of heterogeneity node and edge. Since the data of find state of are examples is not sufficient, it tries to validate the methodology presented in this study to HPAI spreading that there is a variety of data.

A network can be used advantageously to prevent the spread of infectious disease. Using network-based methods has the advantage that discrete elements can be used to predict the change expected for the whole phenomenon, because this method can estimate the scope of the spread of the infectious disease and trace the place of first outbreak using subsequent places of outbreak(Haydon et al., 2003; Riley et al., 2003; Fraser et al., 2004). A study to calculate the hub of the network was often used because it is a guaranteed low-budget approach. The hub, which is calculated by using the centrality method of degree, betweenness, and closeness, is the important place that determines the route along which the infection spreads(Keeling and Eames, 2005).

The ability of the centrality method to prevent infection spread was studied. The centrality method has been found to prevent the spread of infectious disease because it can be used to calculate places with a high possibility of outbreak, whereupon these places can be placed under quarantine(Lee et al., 2014). The prevention of the spread of infection based on the centrality method is efficient when the network structure of the outbreak of the infectious disease is widely known(Barabasi et al., 2000; Lloyd and May, 2001).Other workers studied a breakout of HPAI, an infectious disease affecting domestic animals, on a farm in a densely small-scale place where it existed for a short period of about one month. The lack of data resulting from these circumstances complicated the survey intended to obtain data related to infectious disease in domestic animals(Hayama et al., 2012). Another study, based on the centrality method, found that this method was able to efficiently reduce the spread of infectious disease in domestic animals, even though the spread network contained insufficient information(Shivakumar et al., 2012). A method based on the use of community analysis together with some network information was developed to prevent the spread of infection(Eames, 2008; House et al., 2009; Smieszek et al., 2009).

The use of a model based on the application of a stochastic community for quarantining the infectious disease has also been studied. This model uses a method to calculate the bridge node of the critical path of the epidemic spread based on information of a portion of the network, where the network was constructed using one factor relating to the spread of infectious disease(Shu et al., 2012; Xu et al., 2010). The efficiency of the method based on a stochastic community has been proven by quarantine simulation and involved blocking the spread of a single spreading factor(Salathe and Jones, 2010; Gong et al., 2013). The application limit of model based on stochastic community about variable spreading factors. The structure of homogeneity networks configured using a single node or edge and heterogeneity networks configured using various nodes or edges was important to calculate the path along which an infectious disease spreads. In the case of domestic animals, various spreading paths are possible; thus, in this situation a heterogeneity network is more efficient to calculate the major spreading path(Hosseini et al., 2013; Danon, 2011). The existing model based on a stochastic community that was appropriate to calculate the major path of spread, was based on a homogeneity network constructed using a single node and edge; thus, it is difficult to use this method to calculate the major path for a heterogeneity network.

The purpose of this study is to develop and verify a model based on a stochastic community for calculating points of quarantine to limit the spread of infectious disease in domestic animals. The model incorporates various spreading factors.

1) Suggestion of improved model.

2) Estimation of improvement and effectiveness based on a comparison between the existing and new model.

3) Application of the model to the outbreak of HPAI in Korea to estimate places of quarantine.

II. Materials and Methods

1. Community Bridge Finder Based on Modularity

Our proposed model, named the community bridge node finder based on modularity(CBFM), uses quantitative analysis to perform a relative calculation of the bridge node. The model, which is based on existing models capable of finding the stochastic bridge node, uses modularity to compute the quarantine points in a heterogeneity network. Existing models designed to find the stochastic bridge node are the community bridge finder(CBF) and bridge hub detector(BHD). These models calculate bridge nodes within a community based on a non-comprehensive random-walk method for network structures with limited information. A bridge node connects one community with another in a network; thus, these bridge nodes, which serve to pass an infectious disease from an infected community to a disease-free community, form a major propagation path. Elimination of the bridge node results in the disintegration of the network into community fractions, thereby reducing the cohesion of the network. However, rather than using a random walk to calculate network or community cohesion, our approach is to use a modularity model to perform a walking trip. Accordingly, in this study the community bridge node finder based on modularity(CBFM) is used to calculate bridge nodes. It is shown that replacement of the random walk of existing methods by the walk trip successfully reduces the cohesion of a network by eliminating the bridge node.

$$CBFM_i = (Q_0 - Q_i)/Q_0 \tag{1}$$

where is the cohesion related to the modularity without node i, and is the cohesion of the network includeing all nodes.

2. Composition of heterogeneity network

The heterogeneity network structure was used for predicting disease spread and estimating the transmission routine. Network theory determines that an individual vector can be used to calculate any aspect of an epidemic spread that has changed. This requires a set of nodes and links(edges) to construct the network structure that would enable the spread of the disease infection to be calculated. Construction of an ideal network structure that signifies the limit of the epidemic spread requires an inferred network structure. Person-to-person epidemic spread, i.e., a directed connection, can be described by a homogeneity network with the same kind of nodes and links(edges).

In contrast, description of the spread of animal disease requires the use of a heterogeneity network structure for increased accuracy. This is because networks describing the spread of animal infectious disease include various nodes and weighted links(edges) inferring an indirect connection. The weighted links(edges) and the vector related to the epidemic spread were calculated by using binary logistic regression. Risk factors included as fixed effects were: (1) The number of contacts among poultry-related farms and businesses, (2) The occurrence of disease infection on the farm, (3) The kind of connection, (4) The scale of the damage on the farm, and (5) The time of onset.

$$Logit(P_i) = \alpha + \sum \beta x_i + \gamma_i \tag{2}$$

where the neighboring farm, is the probability that the disease status of each neighboring farm formed a binary outcome (0, not infected; 1, infected), adenotes the model intercept, bis a coefficient, xrepresents the fixed effects with in the univariate analysis, gis the local cluster-level random effect, and the subscript i notes the cluster to which the neighboring farm belonged.

3. Modeling procedure

In this study we use our proposed CBFM method to calculate areas requiring quarantine. Then, we compare

these results with the results obtained with the BHD and centrality methods to confirm the applicability and effectiveness of CBFM. We implement the quarantine areas obtained using CBFM and BHD in a network that was constructed by an existing study using BHD and CBF, after which the results of all the methods are compared. Next, a heterogeneity network based on the spread of HPAI was constructed to enable us to use data of the HPAI outbreak in Korea in 2008 to confirm the applicability of CBFM. The data relating to the HPAI outbreak were collected by an epidemiological survey of the national veterinary research and quarantine service in Korea, and the data consisted of the location of farms, contact details of poultry-related business clients, condition, and onset age. We used the data to calculate the quarantine area using CBFM and compared these results with those obtained using the method of centrality.

III. Results and Discussion

1. Simulation of finding hub using developing method

We calculated the community bridge node by using the CBFM method. This enabled us to compare the points determined to be community bridge nodes with those calculated using BHD. The network structure was composed of 9 nodes and 12 links, which we used to construct weighted and non-weighted networks to identify changes in the community bridge node according to the weighted links(Figure1). The community bridge nodes in these networks were calculated by using BHD and CBFM. The result was that the value obtained with CBFM, which determines the proportional relation of the potential of a quarantine spot, was 0.895 to 0.625. The community bridge nodes calculated by BHD and CBFM was in the same range, i.e., the value of CBFM was 0.833. In contrast, the community bridge node in the weighted network calculated by BHD and the community bridge node in the weighted network calculated by CBFM were not similar. This result can be attributed to the fact that the community bridge node calculated by BHD is not relevant to the use of weighted links in the network; however, the community bridge node that was calculated by CBFM is influenced by weighted links in the network.

We calculated the efficiency and applicability of a quarantine strategy based on CBFM to networks of which the structure was generated randomly according to modularity and weighted links.The ratio of quarantine based
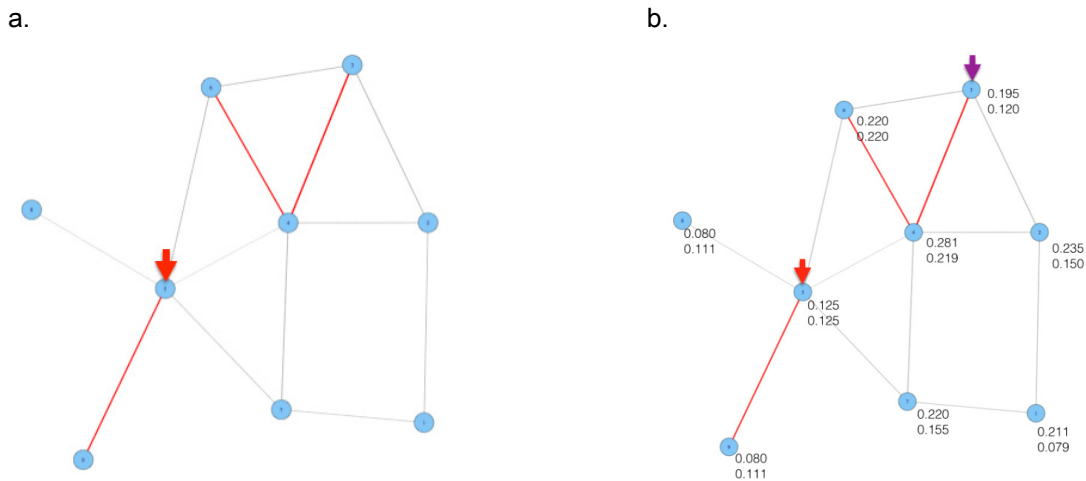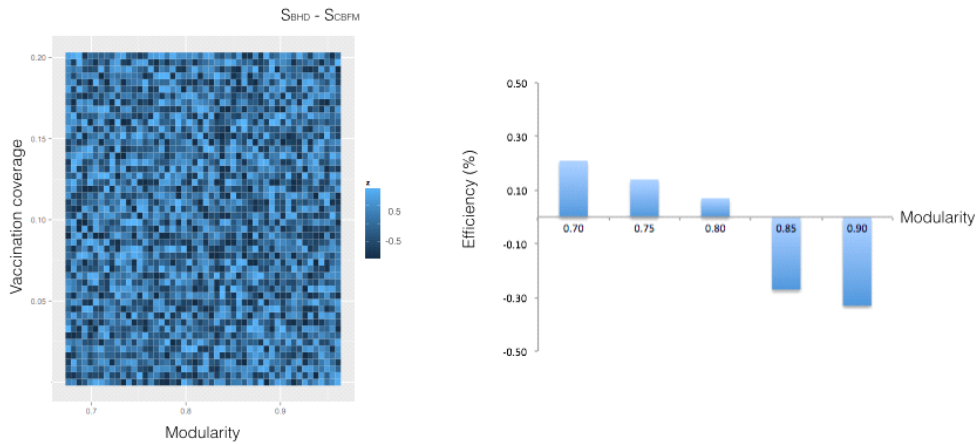

Figure 1. Comparison of the quarantine areas calculated by BHD or CBFM according to the size of the links (edges) in the network. The infectious disease started spreading from node number 1. Links (edges) exceeding 0.7 are expressed in red color. a. Areas of quarantine calculated by BHD. The sign of the red arrow indicates areas unaffected by weighted links (edges). b. Areas of quarantine calculated by CBFM. Numbers indicate the value of CBFM: the upper and lower numbers were calculated for non-weighted and weighted networks, respectively. The signs of the red and purple arrows indicate quarantine areas calculated by CBFM for non-weighted and weighted networks, respectively.

on CBFM is higher than that using BHD for weighted networks, whereas the ratio of quarantine based on CBFM is same as that using BHD for non-weighted networks(Figure2). Quarantine simulation was used to calculate the difference of quarantine efficiency between CBFM and BHD. We generated various networks randomly according to the weighted links to obtain the simulated modularity (0.950 to 0.675) and used a standard SIR model to simulate the spread of infectious disease across the network. The number of nodes range from 1500 to
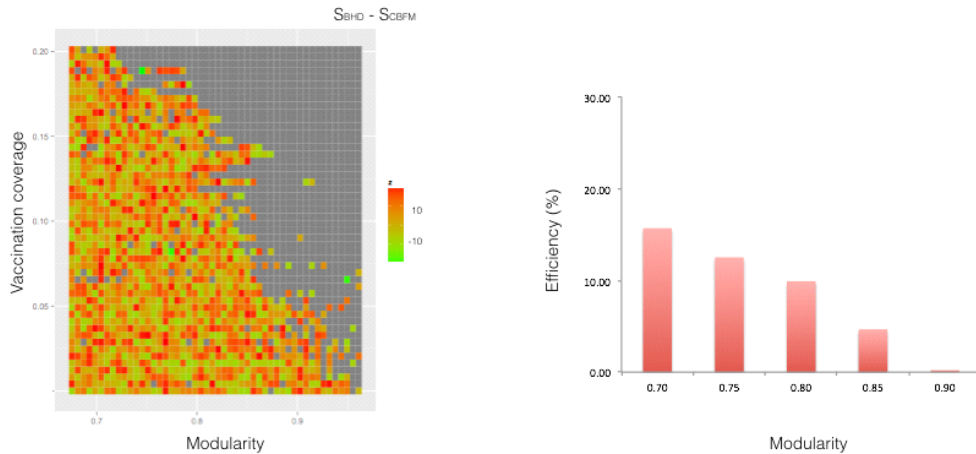
a.

b.

Figure 2. Comparison between CBFM and BHD of the ratio of infectious disease prevention according to the structure of the network and scope of quarantine. The color in the field is the difference S comprising the ratio between the number of non-infected and the number of infected nodes. a. Comparison of effectiveness between CBFM and BHD in a non-weighted network. The difference ratio of quarantine between CBFM and BHD was about 1% that was not affected by modularity and the scope of quarantine. b. Comparison of effectiveness between CBFM and BHD in a weighted network. The difference ratio of quarantine between CBFM and BHD was about 2% that was affected by modularity and the scope of quarantine. The quarantine strategy based on CBFM was more effective for smaller modularity or a smaller scope of quarantine in networks for which the modularity exceeded 0.8.

1 - 104: shipment clients
105 - 138: medicine clients
139 - 171: feed clients
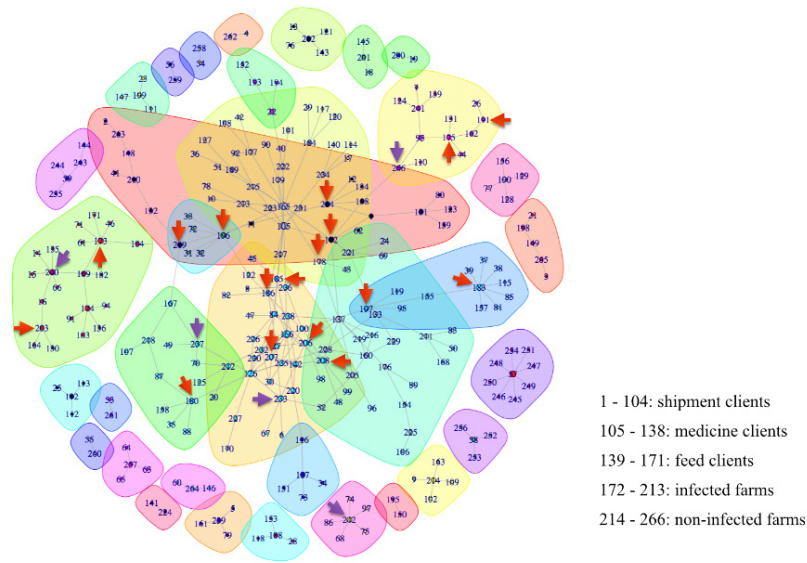172 - 213: infected farms
214 - 266: non-infected farms

Figure 3. HPAI spread network based on heterogeneity structure. The network was constructed by using the HPAI spread-related factor and the relation among factors in Korea in 2008. The community, which was calculated using the method of Newman modularity, is expressed according to background color, with nodes in the same color community having similar characteristics. "Shipment" refers to distribution companies, "medicine" refers to drug companies related to livestock, "feed" refers to companies providing poultry feed, and "farm" was divided into two categories based on disease occurrence. The spot indicated by the red arrow has a higher value of centrality.

2000, the value of the link is 1, and the weight of the link is between 0.3 and 1. S is the number of infected nodes, the fading color in Figure2(a) means that the quarantine strategy based on CBFM is more efficient than that of BHD, in Figure2(b), the color approaching red means that the quarantine strategy based on CBFM is more efficient than BHD, and the color grey means that the difference in quarantine efficiency is below 0.1%. The quarantine efficiency between BHD and CBFM in a network consisting of links of the same weight(Figure2(a)) did not reveal any differences between the two methods. However, for the weighted network, the quarantine

efficiency between BHD and CBFM differed; i.e., the ratio of quarantine by CBFM was higher than that using BHD in that either the modularity or the quarantine coverage was lower.

2. Structure of scale-free network

The outbreak of HPAI in Korea spread in a short time in a densely populated area because of undirected contact among moving people. The spread of HPAI, caused by the H5N1 virus, resulted in a high infective rate and fatality in Korea. The outbreak of HPAI occurred in a one-year

Table 1. Binary logistic regression result to determine HPAI-related factors.

With 4 association			With 3 association		
OR	s.e. OR	p-value	OR	s.e. OR	p-value
-2.781	0.804	0.001	-2.216	19.025	0.000
2.191	0.783	0.005	2.382	9.405	0.002
0.867	0.838	0.302			
1.795	0.671	0.007	1.877	7.972	0.005
2.322	0.773	0.003	2.384	9.141	0.003

period after 2000; however, beginning in 2008, the rate at which HPAI spread changed and it rapidly spread in a short period of time. The area of HPAI outbreak was concentrated in the area surrounding the cities of Gimje and Jeongeup, traditional markets near a large city in pursuance of distributing poultry, where 68% of the poultry farms and poultry are located within 2 km of these two cities. The contact between farms and clients formed about 97% of all the contacts, whereas the contact among farms formed about 3% of the total.The data used in this study were received from the national veterinary research and quarantine service in Korea based on an epidemiological survey of the outbreak of HPAI in Korea in 2008.

The data were structured according to the condition of the farm, whether the farm was infected, time of infection, farm location, and the way of contact between the farm and client. We implemented binary logistic regression using the farm and client to calculate the factors affecting the spread of HPAI. In addition, the kind of farm and client was also specified, i.e., poultry-related farm, shipment business, medicine business, feed business, and poultry-waste treatment business. The result of the binary logistic regression showed that poultry-waste treatment businesses, for which the p-value was determined to be 0.300, were not responsible for spreading HPAI.

We calculated the factor related to the spread of HPAI by determining the contact between the farm and shipment business, medicine business, and feed business(Table 1). A network that re-enacted the occurrence of the spread of HPAI in Korea in 2008 was constructed based on a heterogeneity network and included the following nodes: farms and clients, where the weight of the links(edges) was calculated by the kind of contact between the farm and client. The weight of the links(edges) was the quantitative value of the probability of the influence of HPAI spreading among the nodes, and this influence was calculated by using the method of binary logistic regression. The entire HPAI spread network was constructed by using 266 nodes and 734 links (edges), where the value of the weight of the links(edges) was between 0.725 and 0.316(Figure 3).

We calculated the centrality of the farm node in the HPAI spread network and compared the result with the centrality values obtained for infected and non-infected farms to enable us to estimate the validity of the HPAI spread network. The centrality method of degree, betweenness, and closeness was used, allowing us to estimate the validity of the HPAI spread network. The centrality of infected nodes is known to be higher than that of non-infected nodes(Lee et al., 2013). The ratio of infected to non-infected farms was found to be over 0, with a ratio over 1 indicating that the centrality of infected nodes was higher than that of non-infected nodes, which confirmed the validity of the HPAI spread network. The validity of the structure of the network that was constructed in this study was estimated, the ratio of degree was 1.556, the ratio of betweenness was 2.444, and the ratio of closeness was 1.250(Table 2). IP and NIP are the average of the centrality calculated based on infected and non-infected farms, respectively. IP/NIP is the ratio between the centrality of infected and non-infected farms. IP/NIP calculated by the betweenness in the method of centrality was 2.444, which is the highest in the method of centrality.

3. Effectiveness test

We compared the efficiency of a quarantine strategy based on CBFM and the centrality method for the HPAI spread network in Korea in 2008 to validate the implementation of CBFM. The results compared the HPAI spread blocking ratio and showed that the quarantine strategy based on CBFM was more efficient to prevent

Table 2. Comparison between centrality values of infected and non-infected farms.

Rank	HPAI Spread Network		
	Degree	Betweenness	Closeness
IP	0.014	0.022	0.010
NIP	0.009	0.009	0.008
IP/NIP	1.556	2.444	1.250

HPAI spread. A quarantine simulation was used to generate the HPAI outbreak in the network and then to use the different strategies to prevent the spread of HPAI. The sequence of the HPAI outbreak was decided by the dates on which this actually happened, and the simulation of the HPAI spread was terminated at the node connecting infected and non-infected communities.

The quarantine procedure was determined by values calculated to have higher centrality and CBFM, and the blocking ratio of HPAI spread was calculated to increase the quarantine range for a network of the same structure(Table 3, Figure4). The value of the index based on CBFM was 14% higher than for the centrality method, the difference value of the index was highest at 0.875 for 10% quarantine, the ratio of the index was highest at 0.170 for 15% quarantine. The blocking ratio of the quarantine strategy based on CBFM was about 15% higher than the strategy based on centrality without a quarantine

Table 3. Index of HPAI outbreak prevention between infected and non-infected farms determined by carrying out a quarantine simulation.

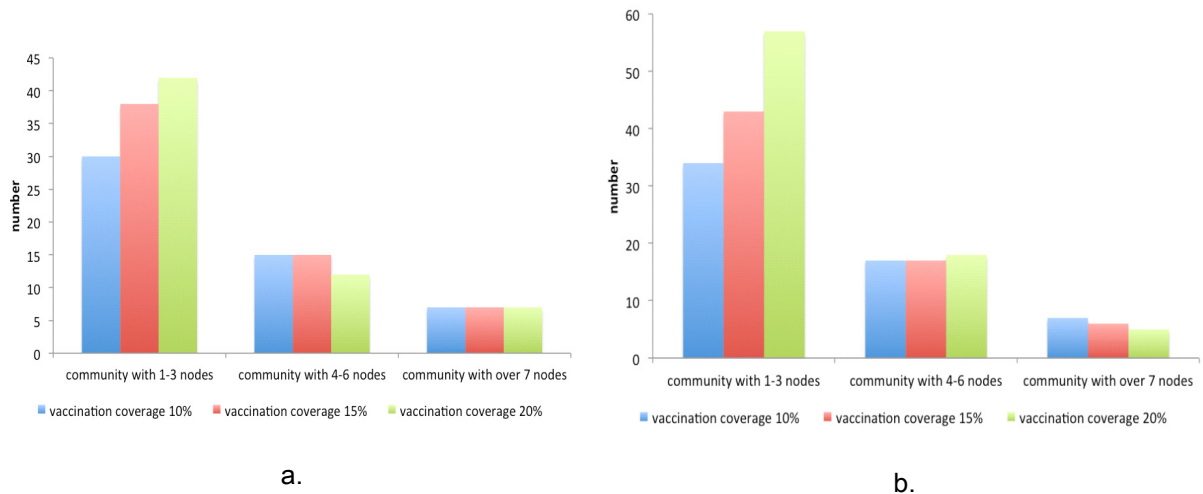|	Top 10% quarantined		Top 15% quarantined		Top 20% quarantined	
	CBFM	Centrality	CBFM	Centrality	CBFM	Centrality
# of non-infected farms	47	40	49	41	50	44
# of quarantined farms	8	8	14	14	20	20
Outbreak prevention index	5.875	5.000	3.500	2.929	2.500	2.200

a.

b.

Figure 4 Structural change in HPAI spread network according to the quarantine simulation based on CBFM and centrality. The graph shows the number variation in the community according to the size of the network. The size of the community was divided into three: 1 to 3 nodes, 4 to 6 nodes, and over 7 nodes. a. The structural change of the HPAI spread network according to the simulation of quarantine based on centrality. The number of communities under quarantine including 1 to 3 nodes was 30 (i.e., 10% of the total), and the number of these communities increased by 30% for stronger quarantine. The number of communities under quarantine including 4 to 6 nodes was 13 (i.e., 10% of the total), and the number of these communities decreased for stronger quarantine. b. Structural change of the HPAI spread network according to the simulation of quarantine based on CBFM. The number of communities under quarantine including 1 to 3 nodes was 34 (i.e., 10% of the total), and the number of these communities increased by about 40% for stronger quarantine. The number of communities under quarantine including 4 to 6 nodes was 16 (i.e., 10% of the total), and the number of these communities increased for stronger quarantine.

range. We compared the extent to which the structure of the network was changed by the quarantined node in the network by using a strategy based on CBFM and centrality. As a result, the number of communities including 1 to 3 nodes was 10% higher using the quarantine strategy of CBFM compared to that of centrality. The number of communities including more than seven nodes was reduced when the community bridge node was increasingly quarantined by a strategy based on CBFM.

IV. Conclusions

This study led to an improved method to calculate the community bridge finder in networks. The method is based on an application of the modularity of network theory and uses a quantitative calculation to find the bridge node in a weighted network.

CBFM, an improvement of CBF, was compared with the BHD in a simulation that was used to calculate the community bridge node in a network describing epidemic spread. This enabled the validity of the CBFM to be measured, and as a result, the difference of the quarantine effectiveness between CBFM and BHD in a non-weighted network was found to be about 3% without tendency, whereas the difference of the quarantine effectiveness between CBFM and BHD in a weighted network was about 10% with a tendency, which was the lower of modularity or disease prevention.

The HPAI spread network was constructed based on data obtained during an epidemiological survey in Korea in 2008 to measure the validity of the CBFM. The method of validity was the index based on centrality, the value of which was over 1 in the case of a well-constructed network. The result of the validity assessment was that the index based on degree was about 1.556, the index based on betweenness was 2.444, and the index based on closeness was about 1.250.

We expected the use of the CBFM to improve the quarantine strategy. However, a study of the implementation of CBFM for small-sized networks with weighted links(edges) is needed to improve the capability of the CBFM. Furthermore, a method to calculate the factor related to farms of complex is required to construct

a network to enable find areas to be determined more accurately.

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