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Scenario prediction of public health emergencies using infectious disease dynamics model and dynamic Bayes

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ABSTRACT

This study was aimed to discuss the predictive value of infectious disease dynamics model (IDD model) and dynamic Bayesian network (DBN) for scenario deduction of public health emergencies (PHEs). Based on the evolution law of PHEs and the meta-scenario representation of basic knowledge, this study established a DBN scenario deduction model for scenario deduction and evolution path analysis of PHEs. At the same time, based on the average field dynamics model of the SIR network, the dimensionality reduction process was performed to calculate the epidemic scale and epidemic time based on the IDD model, so as to determine the calculation methods of threshold value and epidemic time under emergency measures (quarantine). The Corona Virus Disease (COVID) epidemic was undertaken as an example to analyze the results of DBN scenario deduction, and the infectious disease dynamics model was used to analyze the number of reproductive numbers, peak arrival time, epidemic time, and latency time of the COVID epidemic. It was found that after the M1 measure was used to process the S1 state, the state probability and the probability of being true (T) were the highest, which were 91.05 and 90.21, respectively. In the sixth stage of the development of the epidemic, the epidemic had developed to level 5, the number of infected people was about 26, and the estimated loss was about 220 million yuan. The comprehensive cumulative foreground (CF) values of O1 ~ O3 schemes were -1.34, -1.21, and -0.77, respectively, and the final CF values were -1.35, 0.01, and -0.08, respectively. The final CF value of O2 was significantly higher than the other two options. The household infection probability was the highest, which was 0.37 and 0.35 in Wuhan and China, respectively. Under the measures of home quarantine, the numbers of confirmed cases of COVID in China and Wuhan were 1.503 (95% confidential interval (CI) = 1.328 ~ 1.518) and 1.729 (95% CI = 1.107 ~ 1.264), respectively, showing good fits with the real data. On the 21st day after the quarantine measures were taken, the number of COVID across the country had an obvious peak, with the confirmed cases of 24495, and the model prediction value was 24085 (95% CI = 23988 ~ 25056). The incubation period $1/q$ was shortened from 8 days to 3 days, and the number of confirmed cases showed an upward trend. The peak period of confirmed cases was advanced, shortening the overall epidemic time. It showed that the prediction results of scenario deduction based on DBN were basically consistent with the actual development scenario and development status of the epidemic. It could provide corresponding decisions for the prevention and control of COVID based on the relevant parameters of the infectious disease dynamic model, which verified the rationality and feasibility of the scenario deduction method proposed in this study.

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1. Introduction

Public health emergencies (PHEs) refer to major infectious disease outbreaks, mass diseases of unknown cause, and other events that seriously affect public health that occur suddenly and cause or may cause serious damage to the public health [1]. PHEs have the characteristics of suddenness, unexpectedness, and serious socio-economic hazards [2]. PHEs are significantly related to

the safety of people's lives and property and the development of the national economy [3]. With the rapid development of society and economy, various PHEs are frequently occurring, and effective emergency decision-making is of great significance to the development of PHEs. Scenarios are the basis and basis for emergency decision-making on PHEs of decision makers [4]. Therefore, studying the scenario representation and evolution of PHEs has important theoretical and practical significance for decision makers to make emergency decisions and conduct emergency management.

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Traditional predictive response models are difficult to cope with complex and changeable PHEs [5], so a large number of scholars have proposed scenario response models. Ayton et al. (2019) [6] elaborated on the evolution mechanism of unconventional emergencies based on the “scenario-response” emergency decision-making model. Malik et al. (2020) [7] elaborated on the methods commonly used in the performance of unconventional emergencies, and constructed the methods and steps for the selection and application of the performance of the scenarios in the various stages of the disposal process. The infectious disease dynamics model (IDD model) is an effective tool for the study of infectious diseases. It can effectively simulate the spreading mechanism and law of infectious diseases, and can provide a powerful reference value for formulating effective preventive measures. The traditional dynamic warehouse model, continuous infectious disease dynamic model, and random IDD model have played an important role in the prevention and control of infectiousness, but their assumptions about contact among individuals are equal to probability [8], which does not match the actual condition. Bayesian network is an acyclic graph composed of directed edges representing variable nodes and connection points, and has been widely used in knowledge expression and reasoning fields [9]. But it still has the uncertainty of the knowledge meta-model [10]. The dynamic Bayesian network (DBN) adds a time factor on the basis of a static Bayesian network, which can effectively maintain the continuity of events [11], but currently there are few studies on the application of DBN to PHEs scenario prediction.

In summary, there are some shortcomings for the traditional IDD model in the prediction of public health events. The DBN algorithm shows obvious advantages in the process of knowledge element expression, but there are few studies on its application in the prediction of PHEs. Therefore, based on the uncertain characteristics of PHEs, an IDD model and DBN scenario deduction model, were constructed in this study, and the scenario deduction of IDD model and DBN to PHEs was discussed, aiming to provide a reference basis for the establishment of emergency decision-making for PHEs.

2. Research methods

2.1. Analysis of the evolution path of major PHEs

Knowledge element is the smallest entity unit in which each element of an event cannot be separated. Using common knowledge elements to represent public health emergencies helps to deeply understand the evolution process of PHEs and the interrelationships among various elements [12]. For knowledge object A, the situational common knowledge can be expressed as follows:

$$K_n = (D_n, B_n, R_n) \forall n \in A \quad (1)$$

In the above equation, D_n represented the name and concept of a thing, R_n represented the relationship between the internal attributes of things, B_n referred to the quantitative or qualitative attributes of things and $B_n = B_n^I \cup B_n^S \cup B_n^O$. Of which, B_n^I , B_n^S , and B_n^O were the input attribute, state attribute, and output attribute, respectively.

If the constraint relationship among the internal attributes of a thing is $r \in R$, the knowledge meta model can be expressed as follows:

$$K_r = (C_r, B_r^I, B_r^O, F_r) \quad (2)$$

In the equation above, C_r was the mapping relationship attribute, B_r^I referred to the relationship input attribute state set,

B_r^O was the relationship output attribute state set, and F_r represented the specific mapping function of the relationship r .

The knowledge representation of the situation was the premise and basis for the evolution of the situation model and reasoning. Through the analysis of the evolution path of the situation, the development trend and influencing factors of public health events can be analyzed, and scientific and effective decision-making can be established within a limited time [13]. The situational knowledge representation model is generally composed of three parts: situational status, emergency treatment methods, and emergency goals [14]. For a PHE P , its environmental (E) and control (C) conditions were analyzed. Based on its current situational state (S), the event state (I), the event life cycle state (Elc), and the disaster-bearing body state (S) were analyzed. In addition, corresponding emergency treatment plans M1, M2, and M3 were established to achieve the corresponding emergency goals G1, G2, and G3. The specific structure of the situational knowledge representation model was shown in Fig. 1.

2.2. Establishment of scenario deduction model of PHEs based on DBN

Bayesian network is one of the most effective models in the field of uncertain knowledge expression and reasoning [15]. For the cause set H of causality in the Bayesian network, the result is expressed as I , then $H \rightarrow I$ and $H_i \in H, i = 1, 2, \dots, n$. In the Bayesian network reasoning process, the reason set for a given node is combined with its result independently [16]. Therefore, the joint probability of all nodes represented by the Bayesian network can be expressed as Eq. (3) below:

$$P(H_1, H_2, \dots, H_n) = \prod_{i=1}^n P(H_i | H_1, H_2, \dots, H_{i-1}) \\ = \prod_{i=1}^n P[H_i | \pi(H_i)] \quad (3)$$

$\pi(H_i)$ in the above equation was the set of causes of H_i in the causal relationship in the Bayesian network.

DBN was added with a time factor, which made event reasoning and development time had a high degree of continuity and consistency [17]. For an event with L event fragments, the joint probability of all nodes can be expressed as follows:

$$P(H_{11}, H_{12}, \dots, H_{L1}, H_{Lm} | I_{11}, I_{12}, \dots, I_{L1}, I_{Lm}) \\ = \frac{\prod_{i,j} P[I_{ij} | P\alpha(H_{ij})] \prod_{i,k} P[I_{ik} | P\alpha(H_{ik})]}{H_{11}, H_{12}, \dots, H_{L1}, H_{Lm} \prod_{i,j} P[I_{ij} | P\alpha(H_{i,j})] \prod_{i,k} P[I_{ik} | P\alpha(H_{ik})]} \\ i \in [1, L], j \in [1, m], k \in [1, n] \quad (4)$$

In Eq. (4) above, H_{ij} represents the j -th hidden node in the i -th time segment; I_{ij} represented the observed value; and $P(I_{ij})$ referred to the set point of cause in the causal relationship.

The scenario deduction model of PHEs based on DBN firstly determined the network node variables in the process of handling public health emergencies based on the key elements forming node variables. Then, it established the causal relationship among the node variables according to the sudden child labor and health incidents, and formed an acyclic network structure diagram. Finally, it incubated the corresponding condition probability for each node according to the Bayesian network structure. The specific PHEs processing flow based on DBN was shown in Fig. 2.

Fig. 1. The structure of the contextual knowledge representation model.

2.3. Establishment of scenario deduction model of PHEs based on IDD model

There is obvious heterogeneity in contact among individuals [18], and IDD model based on network control measures is of great significance in the scenario prediction of public health events. The final scale of epidemics and epidemic time are two important dynamic indicators for evaluating the severity of infectious diseases [19]. Due to the limitation of calculation skills and process, it is difficult to describe the epidemic time of an epidemic in a clear numerical expression [20]. For a degree-uncorrelated network whose distribution is $A(k)$, its probability generating function can be expressed as below equation:

$$P(x) = \sum_{k=0}^{\infty} A(k) x^k, \quad x \in [0, 1] \quad (5)$$

The first and second moments of the degree distribution are expressed as below equations:

$$k_1 = \sum_{k=0}^{\infty} kA(k) = P'(1) \quad (6)$$

$$k_1^2 = \sum_{k=0}^{\infty} k^2 A(k) = P'(1) + P''(1) \quad (7)$$

Then, the average field dynamics model of the SIR network can be expressed as below equations:

$$\frac{dA_k(t)}{dt} = -\chi k E_k(t) \beta_1^r(t) \quad (8)$$

$$\frac{dB_k(t)}{dt} = \chi k E_k(t) \beta_1^r(t) - \alpha B_k(t) \quad (9)$$

$$\frac{dC_k(t)}{dt} = \alpha B_k(t) \quad (10)$$

In the above equations, $E_k(t)$ represented the relative density of susceptibility values at time t and degree k ; $B_k(t)$ represented the relative density of disease values at time t and degree k ; $C_k(t)$ referred to the relative density of restored nodes at time t and degree k ; χ was the probability of contact between an infected node and a susceptible node, α represents the recovery rate; and $\beta_1^r(t)$ represented the probability of any edge connecting to the infected node at time t . In addition, $A_k(t)$, $B_k(t)$, and $C_k(t)$ satisfied $E_k(t) + B_k(t) + C_k(t) = 1$, and the calculation method of $\beta_1^r(t)$ is $\beta_1^r(t) = \frac{\sum_{k=0}^{\infty} k A_1(k) B_k(t)}{P'(1)}$.

It was assumed that the probability of an optional edge connected to a susceptible node was $\beta_1^E(t)$, and the probability of an optional edge connected to a recovery node was $\beta_1^C(t)$, then the global density of susceptible, diseased, and recovered nodes in the network were $E(t)$, $B(t)$, and $C(t)$, respectively, which can

Fig. 2. The specific PHEs processing flow based on DBN.

be calculated with below equations:

$$\begin{aligned}
 E(t) &= \sum_{k=0}^{\infty} A_1(k) E_k(t), \\
 B(t) &= \sum_{k=0}^{\infty} A_1(k) B_k(t), \\
 C(t) &= \sum_{k=0}^{\infty} A_1(k) C_k(t)
 \end{aligned} \tag{11}$$

The calculation method of the basic reproductive numbers of the mean field dynamics model of the SIR network was shown

in Eq. (12) below:

$$\Re = \frac{\chi(k^2)_1}{\alpha(k)_1} \tag{12}$$

If $\Re < 1$, it meant that the infectious disease was a small-scale outbreak; and $\Re > 1$ indicated that the infectious disease was a pandemic or a final outbreak. In order to quickly obtain the outbreak scale and epidemic time of the average field dynamics model of the SIR network, it had to be reduced in dimensionality. The mean field dynamics model of the SIR network after dimensionality reduction can be expressed as below equation:

$$\frac{d\phi_1(t)}{dt} = -\chi k \phi_1(t) \beta_1^r(t),$$

Fig. 3. The specific flow chart for establishing a multi-attribute emergency decision-making based on IDD model.

$$\begin{aligned} \frac{d\beta_1^r(t)}{dt} &= \beta_1^r(t) [\chi g_1(\phi_1(t)) - \alpha], \\ \frac{dC_k(t)}{dt} &= \alpha B_k(t) \end{aligned}$$

$$E(t) = P_1[\phi_1(t)], C(t) = 1 - E(t) - B(t) \quad (13)$$

In Eq. (13) above, $\phi_1(t)$ referred to the probability that an edge sent by the initial susceptible person had not been infected until time t , and $g_1(\phi_1(t))$ was a $\phi_1(t)$ function, which could be calculated with Eq. (14):

$$g_1(\phi_1(t)) = \frac{\phi_1^2(t) P''(1) [\phi_1(t)] + \phi_1(t) P'(1) [\phi_1(t)]}{P'(1)} \quad (14)$$

According to the algorithm restraint of the above-mentioned dimensionality reduction SIR network average field dynamics model, when $\Re < 1$, in the interval $[0, 1]$, the equilibrium point $\phi_1 = 1$, which meant that the global state was asymptotically stable; When $\Re > 1$, in the interval $[0, 1]$, the equilibrium point $\phi_1 = \phi_1^*$, which meant the global state was asymptotically stable. With time $t \rightarrow \infty$, the epidemic of infectious diseases ended. In $\phi_1(t) \rightarrow \phi_1^*$, ϕ_1^* represented the probability that after the end of the disease, there was still no infection on any of the edges. Then the final density of susceptible nodes after the end of the

infectious disease can be expressed as follows:

$$E_1^\infty \triangleq E(\infty) = \sum_{k=0}^{\infty} A_1(k) (\phi_1^*)^k = P(1) (\phi_1^*) \quad (15)$$

The scale of the epidemic outbreak based on the mean field dynamics model of the reduced-dimensional SIR network can be expressed as follows:

$$C_1^\infty \triangleq C(\infty) = 1 - E_1^\infty \quad (16)$$

It was assumed that there was an initial infected node in the network as the initial moment, and the end time when the last infected node in the network was restored after an epidemic, this period was approximated as the epidemic time [21]. Then at the initial time $t = 0$, there was only one infected node in the network. Then, the epidemic time of infectious diseases based on the mean field dynamics model of the reduced-dimensional SIR network can be expressed as below equation:

$$T_1 = \int_1^{\mu_{1*}} \frac{dt}{t [g_1(\phi_1^0) - \chi \ln t + \alpha \phi_1^0 g_1(\phi_1^0 t)]} \quad (17)$$

In Eq. (17) above, μ_{1*} represented the recovery of the last node of the infectious disease after the epidemic had spread.

In the spread of infectious diseases, at a certain moment τ , nodes with large quarantine degrees or edges of nodes with large cutting degrees were an effective intervention to reduce the risk of transmission and reduce the final scale [22]. Then, under the

Fig. 4. Diagram to show the relationship among the different elements of COVID.

full quarantine measure, the infectious disease $E_k(t^+)$ based on the dimensionality reduction SIR network average field dynamics model initially could meet the following conditions:

$$E_k(t^+) = \begin{cases} \frac{A_1(0)E_0(t^-) + \sum_{t=k+1}^{\infty} A_1(l)C_1(t^-)}{A_1(0) + \sum_{t=k+1}^{\infty} A_1(l)}, & k = 0 \\ \frac{\sum_{t=k+a_1}^{k_c} A_1(l)C_1(t^-)}{\sum_{t=k+a_1}^{k_c} A_1(l)}, & k = 1, 2, \dots, k_c \\ 0, & \text{other} \end{cases} \quad (18)$$

In Eq. (18) above, $E_k(t^+)$ and $E_0(t^-)$ represented the relative density of susceptible nodes with degree k before and after quarantine time t , respectively; and k_c indicated the maximum degree of the remaining nodes after the complete quarantine measure was taken.

Under the incomplete quarantine measure, the infectious disease based on the dimensionality reduction SIR network average field dynamics model initially could meet the following

condition:

$$E_k(t^+) = \begin{cases} \frac{A_1(0)E_0(t^-) + \sum_{t=k+1}^{\infty} A_1(l)C_1(t^-)}{A_1(0) + \sum_{t=k+1}^{\infty} A_1(l)}, & k = 0 \\ E_k(t^-), & k = 1, 2, \dots, k_c \\ 0, & \text{other} \end{cases} \quad (19)$$

Under the incomplete quarantine measure, the final scale and epidemic time of the infectious disease based on the average field dynamics model of the dimensionality reduction SIR network can be given as below equation:

$$C_2^{\infty} \triangleq 1 - \sum_{k=0}^{\infty} A_2(k)(\phi_2^*)^k = 1 - P(1)(\phi_2^*) = 1 - E_2^{\infty} \quad (20)$$

$$T_2 = \tau + \int_{\mu_2^*}^{\mu_2^*} \frac{\mu_2^* dt}{t [\mu_2^* g_1(\phi_1^* \mu_2^*) + \chi \mu_2^* \ln \mu_2^* - \chi \mu_2^* \ln t + \alpha \phi_1^* g_1(\phi_1^* t)]} \quad (21)$$

In equation above, ϕ_2^* represented the probability that the infection did not occur on any one side at the end of the infectious disease under the incomplete quarantine measure. Then, the calculation method of the quarantine time threshold with the final

Fig. 5. Probability distribution diagram of DBN scenario state.

scale can be written as below equation:

$$F(\tau) \triangleq \beta_2^E(\tau) - \beta_1^E(\tau) + g_1(\phi_2^*) - g_1(\phi_1^*) \quad (22)$$

2.4. Establishment of multi-attribute emergency decision-making plan based on IDD model

In the PHEs decision-making process, the set of factors that affect the decision-making and the degree of mutual influence between the factors and the corresponding matrix transformation have a certain impact on the formulation of the emergency plan [23]. It was assumed that the plan set of the polymorphic and multi-attribute risk PHEs emergency decision-making was $D = \{d_1, d_2, \dots, d_n\}$; the attribute set was $H = \{h_1, h_2, \dots, h_n\}$; the corresponding attribute weight was ϖ_i , $T = \{t_1, t_2, \dots, t_n\}$ referred to the feasibility plan inspection time, its corresponding time weight was δ_i , and $\sum_{i=1}^p \delta_i = 1$, then the decision matrix under time t_i can be expressed as follows:

$$J_l = [\gamma_{ij}^l(\otimes)]_{n \times m} \quad (23)$$

In Eq. (23) above, J_l represented the decision matrix, $\gamma_{ij}^l(\otimes)$ was the sample value of the effect of the scheme's attributes under time t_i , $i = 1, 2, \dots, n$, and $j = 1, 2, \dots, m$.

Cost type and benefit type are one of the common attributes of samples [24]. In order to increase comparability in the decision-making model process of dealing with public health events, the decision-making process matrix should be standardized. The related attributes can be divided to form an attribute set, and then according to the law of the development of each event within the attribute range, the correlation between the elements is greatly affected, and the sudden point of the format file is expressed in the form of a set. In the PHEs multi-attribute emergency decision-making problem, the traditional method of maximizing dispersion is most commonly used to solve the attribute

weights [25]. Under the attribute γ_j , the greater the total deviation of the correlation coefficients of all the decision schemes with respect to the positive and negative ideal schemes, the more important the effect of attribute γ_j on scheme decision-making, and the greater the weight [26]. Then the dispersion of the correlation coefficients between scheme O_i and all other schemes with respect to the positive and negative ideal schemes under attribute γ_j can be expressed as Eq. (23) below:

$$S_i^+(\varpi_j) = \sum_{k=1}^n |\delta_{ij}^+ - \delta_{kj}^+| \varpi_j, S_i^-(\varpi_j) = \sum_{k=1}^n |\delta_{ij}^- - \delta_{kj}^-| \varpi_j \quad (24)$$

$S_i^+(\varpi_j)$ and $S_i^-(\varpi_j)$ in the above equation represented the total deviations between all the decision-making plans and the correlation coefficients of other decision-making plans for the positive and negative ideal plans. Then the model optimization algorithm can be written as follows:

$$\begin{aligned} \max S(\varpi) &= \gamma S^+(\varpi_j) + (1 - \gamma) S^-(\varpi_j) \\ &= \gamma \sum_{j=1}^n \sum_{i=1}^m \sum_{k=1}^m |\delta_{ij}^+ - \delta_{kj}^+| \varpi_j \\ &\quad + (1 - \gamma) \sum_{j=1}^n \sum_{i=1}^m \sum_{k=1}^m |\delta_{ij}^- - \delta_{kj}^-| \varpi_j \\ \text{s.t. } \sum_{j=1}^n \varpi_j^2 &= 1, \varpi_j \geq 0 \end{aligned} \quad (25)$$

In the actual response to PHEs, the timelier the emergency response is, the better the loss can be prevented from spreading. How to reasonably and accurately determine the time weights of different stages of emergency response based on the existing public health event information is of vital importance to the evaluation of various emergency options and the priority of the alternatives. Therefore, the time degree can be reasonably used

Fig. 6. Analysis results of infection dynamics model indicators.

to find the time weight vector [27]. For the state S of PHEs with attribute H , it should calculate the probability in different states, establish the corresponding processing scheme O according to the state S and probability P , and process the scheme information into a curved interval as the amount of data in the decision-making process. The specific process of establishing multi-attribute emergency decision-making for PHEs based on IDD model was shown in Fig. 3.

2.5. Simulation analysis parameters of the model

The topological structure of the network and the basic reproductive numbers and final scale of the outbreak and epidemic of heterogeneous infectious diseases have a great influence on the characteristics of infectious diseases. When a uniform Poisson degree distribution (P) or a heterogeneous power rate distribution (L) is assigned to each sub-network, 4 coupling networks (PP , LP , PL , and LL) are obtained.

According to the cumulative foreground (CF) theory, the foreground value of the emergency decision plan for PHEs is correlated with the value function [28]. The calculation method of the value function was given in below equation:

$$V(\Delta y_i) = \begin{cases} (\Delta y)^\alpha, & \Delta y \geq 0 \\ -\chi(-\Delta y)^\beta, & \Delta y < 0 \end{cases} \quad (26)$$

In Eq. (25) above, Δy was the state of loss or gain of the decision-making plan relative to the decision maker at the reference point, $\Delta y \geq 0$ meant gain, and $\Delta y < 0$ meant loss; α , β , and χ referred to the risk aversion coefficient, the risk preference coefficient, and the comparative gain, respectively.

2.6. Application of the model in COVID data

The COVID data used in this study came from the specific data reported by the National Health Commission of China (NHCC). As of September 2020, it has reported a total of 85,022 confirmed cases, a total of 80,126 cured and discharged cases, and a total of 4,634 deaths in China. The number of national statistical cases is used as the data of the PHEs scenario deduction study. According to the development characteristics of COVID, the relevant processing methods were adopted to provide a basis for judgment, the scene of the epidemic was divided to extract the key elements that affected the development of the epidemic to facilitate the deduction of its development trend, which is more conducive to analyzing and judging the correlation between the elements. According to the development process of the epidemic situation,

the situation status is mainly divided into five scenarios: citizen health, fever, positive nucleic acid test, citizen and family quarantine observation, and infection in the associated area of the citizen. In addition, corresponding emergency measures will be given according to different scenarios. The specific scenario elements of the epidemic situation were shown in Fig. 4.

According to the interrelationship among the elements of the COVID situation, the element structure of the situational knowledge can be expressed as $K = \{S, M, G\}$. Three decision-making methods were initially established to solve the emergency decision-making problem. Option 1 ($O1$) is to dispatch a medical team and an emergency ambulance; Option 2 ($O2$) is to add a medical expert and corresponding emergency medical equipment on the basis of $O1$; and Option 3 ($O3$) is to send a medical emergency protection team on the basis of $O2$. The effectiveness of the options was evaluated based on the health status of the patients, the number of rescuers, the cost of rescue equipment and manpower.

The data was analyzed using Wuhan COVID data as an emergency decision plan. The clustering coefficient O was used to characterize the quarantine intensity of household quarantine measures in the COVID outbreak. The greater the intensity of the quarantine measure, the greater the O value. According to national statistics, domestic quarantine is mainly divided into 10 categories under the domestic quarantine measure [29]. When each family was completely isolated, the clustering O of the network can be expressed as Eq. (25) below:

$$O = \frac{3 \sum_{k=3}^{10} O_k^3 F_k}{\sum_{k=3}^{10} M_k^3 F_k} = \frac{\sum_{k=3}^{10} \binom{3}{k} F_k}{2 \sum_{k=3}^{10} \binom{3}{k} F_k} = 0.5 \quad (27)$$

In the equation above, F_k was the number of households with k family members, O referred to the number of combinations, and M represented the number of permutations.

3. Results

3.1. Result analysis of scenario deduction based on DBN

After corresponding emergency measures were adopted in each situation, it had to judge whether the corresponding result was true or not. The probability in different states was calculated according to the probability calculation equations of the Bayesian scenario deduction model. At the same time, according to the correlation between the knowledge element structure of the scenario mode, the probability distribution diagram of the DBN

scenario state was established (Fig. 5). The target values obtained by taking corresponding emergency measures under different conditions showed great differences. After the M1 measure was used to process the S1 state, the state where the result was true (T) showed the highest probability and over probability, which were 91.05 and 90.21, respectively.

3.2. Analysis of the loss value of the plan based on the IDD model

The statistical analysis was performed on the level of the epidemic, the number of infections, and the loss of the plan at different stages of the development of the epidemic, and the results were given in Fig. 6. In the face of the continuous development of the epidemic, the level of the epidemic had become more and more serious, and the number of infections and the value of the meta loss had also shown a clear upward trend. In the sixth stage of the development of the epidemic, the epidemic had reached level 5, and the number of infections per person was about 26. The maximum loss value was estimated to be around 220 million yuan.

3.3. Analysis of CF value of emergency plan based on IDD model

The same scheme (O1 ~ O3) was adopted for each stage of the epidemic development, and the CF values of different schemes were calculated and analyzed according to the CF decision algorithm (Fig. 7). The comprehensive CF values of O1 ~ O3 were -1.34 , -1.21 , and -0.77 , respectively, and the corresponding final CF values were -1.35 , 0.01 , and -0.08 , respectively. The final CF value of O2 was higher obviously than that of the other two options.

3.4. COVID case data analysis

The number and distribution of patient cases in the first 28 days of the COVID outbreak were statistically analyzed, and the statistical results were shown in Fig. 8 A. As time went by, the number of COVID pathological patients in Wuhan and across the country had shown an obvious upward trend. At the 28th day of the outbreak, the number of confirmed cases nationwide was 5895, of which number of patients in Wuhan accounted for more than 95%. Under the quarantine measure, statistical analysis was performed on the infection probability of 10 different types of patients according to the family distribution of the National Bureau of Statistics [30], and the results (Fig. 8B) suggested that the household infection probability was the highest, which was 0.37 and 0.35 in Wuhan and China, respectively.

3.5. Analysis of model fitting results

The model established in this study was used to iterate 10,000 times to perform a fitting analysis on the number of confirmed COVID cases. As illustrated in Fig. 9, under the measures of home quarantine, the number of confirmed COVID cases in China and Wuhan showed a good fitting result with the real data. According to the fitting results, the reproductive numbers of Wuhan and China were 1.503 (95% confidential interval (CI) = $1.328 \sim 1.518$) and 1.729 (95% CI = $1.107 \sim 1.264$), respectively.

3.6. COVID feature prediction

The data of confirmed COVID cases was analyzed based on the model, and the results were shown in Fig. 10. The model predicts that on the 4th day after one cycle (10 days) after the quarantine measure was taken, there was a clear peak in Wuhan COVID outbreak cases. The peak value of confirmed cases was

Fig. 7. Comparison on CF values of emergency plans under different options.

7996 cases, and the model predicted a value of 7822 cases (95% CI = $7167 \sim 8255$). Across the country, there was a clear peak of COVID outbreak cases on the 11th day 10 days after the adoption of quarantine measures. The peak value of confirmed cases was 24495, and the model prediction value was 24085 (95% CI = $23988 \sim 25056$).

3.7. Sensitivity analysis of the model

To verify the effectiveness of emergency measures, the key parameter incubation period $1/q$ that reflected the detection intensity was analyzed, as revealed in Fig. 11. After effective quarantine measures were taken, when the incubation period $1/q$ was shortened from 8 days to 3 days, the number of confirmed cases showed an upward trend, and the peak period of confirmed cases was advanced, shortening the overall epidemic time.

4. Discussion

PHEs have had a serious impact on the global public health and economy, and have seriously hindered the development of human society. Scenarios are the fundamental basis for establishing public health emergency decision-making [30]. Predicting PHEs in a complex environment and establishing corresponding emergency decision-making are of great significance to the management and development of public health incidents [31]. In this study, a DBN scenario prediction model was established based on the evolution of public health event scenarios and their main factors. The development of the COVID epidemic was undertaken as an example to analyze the process and key technologies of the scenario deduction of the COVID epidemic. The suddenness of PHEs leads to the complicated and changeable evolution process, and it is impossible to establish an effective case library in a short period of time. Therefore, the expert evaluation scoring method should be the main method, and the average value of the evaluation results of multiple experts should be used as the final result [32]. Based on historical data and expert knowledge, the conditional probability of each node variable was determined, and the probability distribution diagram of the state deduction in different states was analyzed. It was found that the target value obtained by taking corresponding emergency measures in different states showed great differences. After the M1 measure was used to process the S1 state, the state where the result

Fig. 8. COVID case data statistics. (A: Data of confirmed COVID cases nationwide and Wuhan; B: Nodes distribution in the country and Wuhan after quarantine measures were adopted)

Fig. 9. Analysis of fitting results of confirmed COVID cases.

was true (T) showed the highest probability and over probability, which were 91.05 and 90.21, respectively. Deduction of the probability distribution map based on the state can predict the development trend of the epidemic, and make reasonable

adjustments and optimizations, which can make the situation and state emergency measures more ideal [33], and can effectively block the development and spread of the epidemic.

Fig. 10. Time series chart of cumulative confirmed COVID cases.

Fig. 11. Sensitivity analysis of the model. (A: The relationship between the cumulative confirmed cases nationwide and the incubation period; B: The relationship between the cumulative confirmed cases in Wuhan and the incubation period)

COVID can infect humans across populations, and its clinical symptoms mainly include cough, fever, and dyspnea, and its respiratory tract infection lasts in the range of 2–14 [34]. Under normal circumstances, the establishment of a public emergency

response strategy model requires the analysis of the characteristics, mechanism, dynamics, and other parameters and variables of the spread of infectious diseases; the parameters can be estimated based on actual data and model fitting, so as to determine the basic reproductive numbers of infectious diseases, peak scale,

peak time, final scale, and epidemic time. Factors such as the number of medical staff, the number of infected people, and the scope of the area all exert great impacts on the emergency decision-making of public health events [35], so it is necessary to collect statistics on epidemic-related data, and analyze the related data sets based on these data. The results in the article showed that with the continuous development of the epidemic, the level of the epidemic had become more and more serious, and the number of infected persons and the value of yuan loss had also shown a significant upward trend; in the sixth stage of the development of the epidemic, the epidemic reached level 5. The number of infections per person was about 26, and the estimated loss was about 220 million yuan. The comprehensive CF values of O1 ~ O3 were -1.34 , -1.21 , and -0.77 , respectively, and the final CF values were -1.35 , 0.01 , and -0.08 , respectively. The final CF value of O2 was significantly higher than the other two solutions. Such results suggest that the O2 shows obvious advantages compared with the other two options. The results of this study proved that after effective quarantine measures were taken, when the incubation period $1/q$ was shortened from 8 days to 3 days, the number of confirmed cases showed an upward trend, and the peak period of confirmed cases was advanced, shortening the overall epidemic time. Therefore, effective suggestions can be provided for the prevention and control of COVID based on latency time.

5. Conclusion

In this study, a scenario deduction model of DBN was established based on DBN and PHEs scenario evolution law, and an IDD model was established based on SIR network; some parameters such as epidemic scale, epidemic time, and thresholds were determined and applied to the development and scenario prediction of the COVID epidemic. It was found that the prediction result of scenario deduction based on DBN was basically consistent with the actual development scenario and development status of the epidemic, and it could provide corresponding decisions for COVID prevention and control based on the relevant parameters of the IDD model. However, there were some shortcomings in this study. It failed to further analyze the stability of the established model and compare it with other models. In future work, it will continue to analyze the stability of the two established models and compare them with other public health event scenario deduction models. In short, the PHEs scenario deduction model established in this study was reasonable and feasible, which provided a reference basis for the establishment of PHEs decision-making programs.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

- [1] M. Palacios Cruz, E. Santos, M.A. Velázquez Cervantes, M. León Juárez, COVID-19, a worldwide public health emergency, *Rev. Clin. Esp. (Barc)*

- 221 (1) (2021) 55–61, <http://dx.doi.org/10.1016/j.rceng.2020.03.001>, Epub 2020 Apr 21. PMID: 33998479; PMCID: PMC7173827.
- [2] Y. Khan, T. O'Sullivan, A. Brown, S. Tracey, J. Gibson, M. Gnreux, B. Henry, B. Schwartz, Public health emergency preparedness: a framework to promote resilience, *BMC Public Health* 18 (1) (2018) 1344, <http://dx.doi.org/10.1186/s12889-018-6250-7>, PMID: 30518348; PMCID: PMC6280369.
- [3] L.O. Gostin, E.A. Friedman, S.A. Wetter, Responding to Covid-19: How to navigate a public health emergency legally and ethically, *Hastings Cent. Rep.* 50 (2) (2020) 8–12, <http://dx.doi.org/10.1002/hast.1090>, Epub 2020 Mar 26. PMID: 32219845; PMCID: PMC7228225.
- [4] Y. Cao, J. Shan, Z. Gong, J. Kuang, Y. Gao, Status and challenges of public health emergency management in China related to COVID-19, *Front. Public Health* 8 (May) (2020) 250, <http://dx.doi.org/10.3389/fpubh.2020.00250>, PMID: 32574311; PMCID: PMC7273973.
- [5] M.C. van Schalkwyk, N. Maani, M. McKee, Public health emergency or opportunity to profit? The two faces of the COVID-19 pandemic, *Lancet Diabetes Endocrinol.* 9 (2) (2021) 61–63, [http://dx.doi.org/10.1016/S2213-8587\(21\)00001-2](http://dx.doi.org/10.1016/S2213-8587(21)00001-2), Epub 2021 Jan 5. PMID: 33417836.
- [6] A. Ayton, A. Ibrahim, Obesity is a public health emergency, *BMJ* 366 (Sep) (2019) 15463, <http://dx.doi.org/10.1136/bmj.15463>, PMID: 31519652.
- [7] Y.S. Malik, S. Sircar, S. Bhat, K. Sharun, K. Dhama, M. Dadar, R. Tiwari, W. Chaicumpa, Emerging novel coronavirus (2019-nCoV)-current scenario, evolutionary perspective based on genome analysis and recent developments, *Vet Q* 40 (1) (2020) 68–76, <http://dx.doi.org/10.1080/01652176.2020.1727993>, PMID: 32036774; PMCID: PMC7054940.
- [8] H. Heesterbeek, R.M. Anderson, V. Andreasen, S. Bansal, D. De Angelis, C. Dye, K.T. Eames, W.J. Edmunds, S.D. Frost, S. Funk, T.D. Hollingsworth, T. House, V. Isham, P. Klepac, J. Lessler, J.O. Lloyd-Smith, C.J. Metcalf, D. Morrison, L. Pellis, J.R. Pulliam, M.G. Roberts, C. Viboud, Isaac Newton Institute IDD Collaboration, Modeling infectious disease dynamics in the complex landscape of global health, *Science* 347 (6227) (2015) 44339, <http://dx.doi.org/10.1126/science.aaa4339>, PMID: 25766240; PMCID: PMC4445966.
- [9] O.N. Bjrnstad, K. Shea, M. Krzywinski, N. Altman, The SEIRS model for infectious disease dynamics, *Nature Methods* 17 (6) (2020) 557–558, <http://dx.doi.org/10.1038/s41592-020-0856-2>; *Nature Methods* 18 (3) (2021) 321, PMID: 32499633 (erratum).
- [10] Y.H. Jin, Q. Huang, Y.Y. Wang, X.T. Zeng, L.S. Luo, Z.Y. Pan, Y.F. Yuan, Z.M. Chen, Z.S. Cheng, X. Huang, N. Wang, B.H. Li, H. Zi, M.J. Zhao, L.L. Ma, T. Deng, Y. Wang, X.H. Wang, Perceived infection transmission routes, infection control practices, psychosocial changes, and management of COVID-19 infected healthcare workers in a tertiary acute care hospital in Wuhan: a cross-sectional survey, *Mil. Med. Res.* 7 (1) (2020) 24, <http://dx.doi.org/10.1186/s40779-020-00254-8>, PMID: 32393381; PMCID: PMC7211983.
- [11] Y. Guo, Z. Zhong, C. Yang, J. Hu, Y. Jiang, Z. Liang, H. Gao, J. Liu, Epi-CTBN: an approach of epistasis mining based on genetic Tabu algorithm and Bayesian network, *BMC Bioinform.* 20 (1) (2019) 444, <http://dx.doi.org/10.1186/s12859-019-3022-z>, PMID: 31455207; PMCID: PMC6712799.
- [12] T. Norri-Sederholm, H. Paakkonen, J. Kuroki, K. Saranto, Situational awareness and information flow in prehospital emergency medical care from the perspective of paramedic field supervisors: a scenario-based study, *Scand. J. Trauma Resusc. Emerg. Med.* 23 (Jan) (2015) 4, <http://dx.doi.org/10.1186/s13049-014-0083-x>, PMID: 25591664; PMCID: PMC4299807.
- [13] P. Jia, W. Dong, S. Yang, Z. Zhan, L. Tu, S. Lai, Spatial lifecourse epidemiology and infectious disease research, *Trends Parasitol.* 36 (3) (2020) 235–238, <http://dx.doi.org/10.1016/j.pt.2019.12.012>, Epub 2020 Feb 7. PMID: 32044243; PMCID: PMC7172117.
- [14] X. Ni, H. Zhou, W. Chen, Addition of an emotionally stable node in the SOSa-SPSa model for group emotional contagion of panic in public health emergency: Implications for epidemic emergency responses, *Int. J. Environ. Res. Public Health* 17 (14) (2020) 5044, <http://dx.doi.org/10.3390/ijerph17145044>, PMID: 32674259; PMCID: PMC7400402.
- [15] D.G. Ahn, H.J. Shin, M.H. Kim, S. Lee, H.S. Kim, J. Myoung, B.T. Kim, S.J. Kim, Current status of epidemiology, diagnosis, therapeutics, and vaccines for novel coronavirus disease 2019 (COVID-19), *J. Microbiol. Biotechnol.* 30 (3) (2020) 313–324, <http://dx.doi.org/10.4014/jmb.2003.03011>, PMID: 32238757.
- [16] Z. Guo, S. Wu, M. Ohno, R. Yoshida, Bayesian algorithm for retrosynthesis, *J. Chem. Inf. Model.* 60 (10) (2020) 4474–4486, <http://dx.doi.org/10.1021/acs.jcim.0c00320>, Epub 2020 Oct 13. PMID: 32975943.
- [17] M. Abbasinia, O. Kalatpour, M. Motamedzadeh, A. Soltanian, I. Mohammad-fam, Dynamic human error assessment in emergency using fuzzy Bayesian CREAM, *J. Res. Health Sci.* 20 (1) (2020) e00468, <http://dx.doi.org/10.34172/jrhs.2020.03>, PMID: 32814689; PMCID: PMC7585760.
- [18] M. Baguelin, G.F. Medley, E.S. Nightingale, K.M. O'Reilly, E.M. Rees, N.R. Waterlow, M. Wagner, Tooling-up for infectious disease transmission modelling, *Epidemics* 32 (Sep) (2020) 100395, <http://dx.doi.org/10.1016/j.epidem.2020.100395>, Epub 2020 May 13. PMID: 32405321; PMCID: PMC7219405.

- [19] L.O. Gostin, E.A. Friedman, S.A. Wetter, Responding to Covid-19: How to navigate a public health emergency legally and ethically, *Hastings Cent. Rep.* 50 (2) (2020) 8–12, <http://dx.doi.org/10.1002/hast.1090>, Epub 2020 Mar 26. PMID: 32219845; PMCID: PMC7228225.
- [20] E. Hunter, B. Mac Namee, J. Kelleher, An open-data-driven agent-based model to simulate infectious disease outbreaks, *PLoS One* 13 (12) (2018) e0208775, <http://dx.doi.org/10.1371/journal.pone.0208775>; *PLoS One* 14 (1) (2019) e0211245, PMID: 30566424; PMCID: PMC6300276 (erratum).
- [21] N. Zhang, H. Huang, M. Duarte, J.J. Zhang, Dynamic population flow based risk analysis of infectious disease propagation in a metropolis, *Environ. Int.* 94 (Sep) (2016) 369–379, <http://dx.doi.org/10.1016/j.envint.2016.03.038>, Epub 2016 Apr 20. PMID: 27107973.
- [22] G. Chowell, R. Rothenberg, Spatial infectious disease epidemiology: on the cusp, *BMC Med.* 16 (1) (2018) 192, <http://dx.doi.org/10.1186/s12916-018-1184-6>, PMID: 30333024; PMCID: PMC6193292.
- [23] M.L. Ndeffo-Mbah, V.S. Vigliotti, L.A. Skrip, K. Dolan, A.P. Galvani, Dynamic models of infectious disease transmission in prisons and the general population, *Epidemiol. Rev.* 40 (1) (2018) 40–57, <http://dx.doi.org/10.1093/epirev/mxx014>, PMID: 29566137; PMCID: PMC5982711.
- [24] H. Cao, D.X. Yan, A. Li, Dynamic analysis of the recurrent epidemic model, *Math. Biosci. Eng.* 16 (5) (2019) 5972–5990, <http://dx.doi.org/10.3934/mbe.2019299>, PMID: 31499748.
- [25] W. Garira, The research and development process for multiscale models of infectious disease systems, *PLoS Comput. Biol.* 16 (4) (2020) e1007734, <http://dx.doi.org/10.1371/journal.pcbi.1007734>, PMID: 32240165; PMCID: PMC7156109.
- [26] P. Derjany, S. Namila, D. Liu, A. Srinivasan, Multiscale model for the optimal design of pedestrian queues to mitigate infectious disease spread, *PLoS One* 15 (7) (2020) e0235891, <http://dx.doi.org/10.1371/journal.pone.0235891>, PMID: 32645057; PMCID: PMC7347216.
- [27] S. Bin, G. Sun, C.C. Chen, Spread of infectious disease modeling and analysis of different factors on spread of infectious disease based on cellular automata, *Int. J. Environ. Res. Public Health* 16 (23) (2019) 4683, <http://dx.doi.org/10.3390/ijerph16234683>, PMID: 31775236; PMCID: PMC6926909.
- [28] G. Li, Y. Dong, Dynamic modelling of the impact of public health education on the control of emerging infectious disease, *J. Biol. Dyn.* 13 (1) (2019) 502–517, <http://dx.doi.org/10.1080/17513758.2019.1639835>, PMID: 31288612.
- [29] N. Wale, M.A. Duffy, The use and underuse of model systems in infectious disease ecology and evolutionary biology, *Am. Nat.* 198 (1) (2021) 69–92, <http://dx.doi.org/10.1086/714595>, Epub 2021 May 20. PMID: 34143716.
- [30] K.M. Bubar, K. Reinholt, S.M. Kissler, M. Lipsitch, S. Cobey, Y.H. Grad, D.B. Larremore, Model-informed COVID-19 vaccine prioritization strategies by age and serostatus, *Science* 371 (6532) (2021) 916–921, <http://dx.doi.org/10.1126/science.abe6959>, Epub 2021 Jan 21. PMID: 33479118; PMCID: PMC7963218.
- [31] A.J. Kucharski, T.W. Russell, C. Diamond, Y. Liu, J. Edmunds, S. Funk, R.M. Eggo, Centre for mathematical modelling of infectious diseases COVID-19 working group. Early dynamics of transmission and control of COVID-19: a mathematical modelling study, *Lancet Infect Dis.* 20 (5) (2020) 553–558, [http://dx.doi.org/10.1016/S1473-3099\(20\)30144-4](http://dx.doi.org/10.1016/S1473-3099(20)30144-4), Epub 2020 Mar 11; *Lancet Infect Dis.* (Mar) (2020) PMID: 32171059; PMCID: PMC7158569 (erratum).
- [32] R.K. Rai, P.K. Tiwari, Y. Kang, A.K. Misra, Modeling the effect of literacy and social media advertisements on the dynamics of infectious diseases, *Math. Biosci. Eng.* 17 (5) (2020) 5812–5848, <http://dx.doi.org/10.3934/mbe.2020311>, PMID: 33120578.
- [33] W.J. Wiersinga, A. Rhodes, A.C. Cheng, S.J. Peacock, H.C. Prescott, Pathophysiology, transmission, diagnosis, and treatment of coronavirus disease 2019 (COVID-19): A review, *JAMA* 324 (8) (2020) 782–793, <http://dx.doi.org/10.1001/jama.2020.12839>, PMID: 32648899.
- [34] P. Dashraath, J.L.J. Wong, M.X.K. Lim, L.M. Lim, S. Li, A. Biswas, M. Choolani, C. Mattar, L.L. Su, Coronavirus disease 2019 (COVID-19) pandemic and pregnancy, *Am. J. Obstet. Gynecol.* 222 (6) (2020) 521–531, <http://dx.doi.org/10.1016/j.ajog.2020.03.021>, Epub 2020 Mar 23. PMID: 32217113; PMCID: PMC7270569.
- [35] P. Dashraath, J.L.J. Wong, M.X.K. Lim, L.M. Lim, S. Li, A. Biswas, M. Choolani, C. Mattar, L.L. Su, Coronavirus disease 2019 (COVID-19): current status and future perspectives, *Int. J. Antimicrob. Agents* 55 (5) (2020) 105951, <http://dx.doi.org/10.1016/j.ijantimicag.2020.105951>, Epub 2020 Mar 29. PMID: 32234466; PMCID: PMC7139247.