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# Predicting influenza in China from October 1, 2023, to February 5, 2024: A transmission dynamics model based on population migration



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# **ABSTRACT**

Introduction: Since November 2023, influenza has ranked first in reported cases of infectious diseases in China, with the outbreak in both northern and southern provinces exceeding the levels observed during the same period in 2022. This poses a serious health risk to the population. Therefore, short to medium-term influenza predictions are beneficial for epidemic assessment and can reduce the disease burden.

Methods: A transmission dynamics model considering population migration, encompassing susceptible-exposed-infectious-asymptomatic-recovered (SEIAR) was used to predict the dynamics of influenza before the Spring Festival travel rush.

Results: The overall epidemic shows a declining trend, with the peak expected to occur from week 47 in 2023 to week 1 in 2024. The number of cases of A (H3N2) is greater than that of influenza B, and the influenza situation is more severe in the southern provinces compared to the northern ones.

Conclusion: Our method is applicable for short-term and medium-term influenza predictions. As the spring festival travel rush approaches. Therefore, it is advisable to advocate for nonpharmaceutical interventions (NPIs), influenza vaccination, and other measures to reduce healthcare and public health burden.

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# 1. Introduction

Influenza, an acute respiratory infectious disease, is caused by influenza viruses classified into four types: A, B, C, and D based on differences in surface antigenicity. Among these, the influenza A and B viruses are known to stir severe

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# Abbreviations

influenza-like illness rate (ILI%) Baidu Influenza Search Index (BISI) Sceptible-exposed-infectious-asymptomatic-recovered (SEIAR) Infection attack rate (IAR)

manifestations and contribute to seasonal outbreaks [\(World Health Organization, 2023\)](#page-9-0). The epidemiological patterns of influenza are driven by climatic conditions, with temperate regions experiencing seasonal outbreaks predominantly during the winter and spring seasons. In contrast, tropical regions exhibit diverse patterns of influenza prevalence, including yearround or semiannual cyclic patterns of prevalence, as well as perennial circulation ([Newman et al., 2018](#page-9-1)). In China, seasonal influenza commonly peaks in the winter and spring seasons, but southern regions may experience potential peaks during the summer seasons. Meanwhile, the number of infections is generally higher in the South than in the North. [\(China NICC, 2024](#page-9-2)) The subtype distribution of influenza reveals that the epidemic intensity of influenza A typically exceeds that of influenza B, yet a contrasting trend is noted in specific regions and years [\(Yang et al., 2018\)](#page-10-0). Therefore, the prediction of influenza based on the characteristics of virus epidemic subtypes, and regional and temporal changes is very meaningful for prevention and control.

In the realm of public health, the transmission and impact of influenza remain a focal point of concern. It is estimated that globally, approximately one billion individuals contract influenza annually, of which roughly 3 to 5 million cases are classified as severe, culminating in approximately 500,000 fatalities due to influenza infection ([Iuliano et al., 2018;](#page-9-3) [World Health](#page-9-0) [Organization, 2023](#page-9-0)). Influenza has imposed a significant disease burden in China which ranks third in both reported incidence and reported mortality among Class C infectious diseases in China [\(China NICC, 2024\)](#page-9-2). Mainland China has an influenza hospitalization rate of 73.0 per 100,000 individuals, while in Hong Kong, this rate is 35.7 per 100,000 individuals [\(Paget et al.,](#page-9-4) [2023\)](#page-9-4). Moreover, China has a relatively low influenza vaccine coverage rate compared to the global ave ([Palache et al.;](#page-9-5) [Yang](#page-9-6) [et al.](#page-9-6)) which may be due to exacerbate the challenges faced by China in addressing the increasing number of influenza cases during the flu season.

Influenza prevalence patterns have been influenced during the COVID-19 pandemic, with a reduction in the intensity of the influenza epidemic and a delayed peak observed in most countries ([Achangwa et al., 2022](#page-9-7); [Cowling et al., 2020](#page-9-8); [Lampejo,](#page-9-9) [2022\)](#page-9-9). After discontinuing nonpharmaceutical interventions associated with COVID-19, influenza incidence increased rapidly in China in February 2023, predominantly characterized by influenza A (H1N1), exceeding the levels observed in natural epidemic years ([Zeng et al., 2023\)](#page-10-1). Since November, a co-circulation pattern of A (H3N2) and influenza B, which are the main contributors to the number of cases reported in infectious disease surveillance in China. [\(China NICC, 2024,\)](#page-9-2) From April 2023 to December, a total of 3058 outbreaks of influenza-like disease (ILI) cases were reported, with case numbers in both northern and southern provinces exceeding the levels reported during the same period in 2022, indicative of increased severity in the influenza situation in China. ([China NICC, 2024,](#page-9-2)) In summary, the disease burden of influenza cannot be overlooked. As China is currently in the midst of the influenza season, the surveillance, forecasting, and development of effective control and prevention strategies for seasonal influenza are of paramount importance in safeguarding public health and mitigating the socioeconomic impact.

Accurate prediction of influenza outbreaks is pivotal for the effective prevention and control of the virus, holding significant importance for governmental entities in implementing proactive measures, allocating pharmaceuticals and medical resources, and alleviating the disease burden on the populace, as well as curbing the dissemination of the infection. Currently, the prevalent models for influenza prediction encompass mathematical models such as compartmental models, time-series analyses, and statistical approaches including machine learning algorithms and neural network models, as well as epidemic propagation dynamics models. It has been observed that simpler mathematical constructs are insufficient to precisely forecast the epidemiological dynamics and incidence rates of influenza [\(Chretien et al., 2014\)](#page-9-10). A study utilized a compartment model combined with the Kalman filter algorithm to forecast influenza activity in the southern and northern regions of China from March to September 2023, the COVID-19 epidemic. However, the predictive accuracy has not been refined to individual provinces, and no predictions were made for the winter influenza season of 2023. Given the significant differences in population size and mobility among provinces, which influence the spread of influenza and the evolution of outbreaks, it is imperative to conduct predictive analyses for influenza epidemics across individual provinces in mainland China. Therefore, our study adopts a compartmental epidemiological model that incorporates population mobility to provide a more detailed description of disease transmission within populations, which is then applied to predict influenza incidence rates, peak periods, and developmental trends in various provinces in southern and northern China from October 1, 2023, to February 5, 2024.

# 2. Methods

## 2.1. Data collection

Data on influenza positivity rate and influenza-like illness rate (ILI%) were obtained from the National Influenza Center of China [\(https://ivdc.chinacdc.cn/cnic/\)](https://ivdc.chinacdc.cn/cnic/), which covers the first week of 2014 to the first week of 2024. The ILI  $+$  index was calculated to represent the influenza infection situation, which is defined as multiplying the ILI% by the influenza test positivity rate [\(Yang et al., 2015\)](#page-9-11). Furthermore, data from the Baidu Influenza Search Index (BISI) were collected from January 1, 2014, to January 14, 2024, from (<https://index.baidu.com/v2/index.html#/>). And the search keywords included influenza, influenza A, influenza B, nasal congestion, and fever. The Baidu Migration Index data were obtained from ([https://qianxi.](https://qianxi.baidu.com#/) [baidu.com#/\)](https://qianxi.baidu.com#/), with the total population for each province obtained from respective statistical yearbooks. We grouped the provinces according to the standards of the Chinese Center for Disease Control and Prevention (CDC) for the northern and southern provinces.

We partitioned the human population by regions and disease stages of susceptible-exposed-infectious-asymptomaticrecovered (SEIAR) and modeled the migration and transmission dynamics in ordinary differential equations. After the model is calibrated with observed surveillance data, each influenza subtype is provincially predicted from October 1, 2023 to February 5, 2024. We performed correlation analyses using contemporaneous ILI  $+$  data with the predicted data to verify the accuracy of the predicted results.

#### 2.2. Disease transmission model

Let  $S, E, I, A, R \in \mathbb{R}^{n \times 1}$  be the region-wise population size of susceptible, exposed, symptomatic infectious, asymptomatic infectious and removed, respectively. The specific details are as follows. The detailed collection of model parameters' specific meaning and value is provided in Supplementary 1. The transmission occurring within regions is formularized by the following ordinary differential disease transmission model:

$$
\frac{d}{dt}\begin{bmatrix} S \\ E \\ I \\ H \\ R \end{bmatrix} = \begin{bmatrix} -\beta \odot S \odot (I + \kappa A) \\ \beta \odot S \odot (I + \kappa A) - (1 - p)\omega E - p\omega' E \\ (1 - p)\omega E - \gamma I \\ p\omega' E - \gamma' A \\ \gamma I + \gamma' A \end{bmatrix}
$$
(1)

where the  $\odot$  denotes the entry-wise multiplication.

To introduce human migration, let  $\pmb{M}\!\in\!\mathbb{R}^{n\times n}$  be the migration data matrix whose ij-th entry denotes the migration rate from the i-th region to the j-th region and further assumes that individual migration behavior is not impacted by disease stages. The derivative according to migration is obtained by:

$$
\frac{dS}{dt} = -M1 \odot \left(\frac{S}{N}\right) + M^T \left(\frac{S}{N}\right) \tag{2}
$$

where the right-hand-side is an adjustment for  $\frac{dS}{dt'}$  and it will be similar for  $E,I,A,R;$  1 is the vector of ones with compatible size;  $\odot$  and  $\oslash$  represent entry-wise multiplication and division respectively.

#### 2.3. Observation model

The observation model assumes that the browser search index is corrupted by a measurement with constant delay and misreports:

$$
y_t = \alpha((1-p)\omega\mathbf{E}(t-\tau)) + C
$$
\n(3)

where  $y_t$  is the searching rate for specific region at time t; the amplifier  $\alpha$  is constants for each region;  $\tau$  is the delay effect of observation, which is a simplification of observation blur  $\int g(s)E(t-s)ds$ ; constant term C represent the minimum searching rate, represent the circumstances that constant searching without disease prevalence.

The initial value estimates for each compartment in Beijing will be used as an example.

(1) A recent study estimated that the infection attack rate (IAR) of the influenza wave between October 9, 2022, and October 1, 2023, as 18.51% (95% CI: 0.00%, 37.78%) in northern China and 28.30% (95% CI: 14.77%, 41.82%) in southern China [\(Du et al., 2023\)](#page-9-12). Then we collected the population of Beijing N, and multiplied by the IAR in northern China. The enlargement factor  $\alpha$  of Beijing is calculated as:

$$
\alpha = \frac{\sum y_t}{N \times IAR} \tag{4}
$$

where  $\sum y_t$  is the sum of BISI between October 9, 2022, and October 1, 2023.

(2) We assume that the BISI lagged ILI + by 2-3 weeks, and ILI + lagged daily new infections by 1-2 weeks, therefore,  $\tau$ was set to  $4-5$  weeks. The initial value of the exposed population E can be derived from the observation model above:

$$
E_0 = \frac{y_{t+\tau}}{\alpha(1-p)\omega} \tag{5}
$$

(3) Accordingly, the initial value of symptomatic infections  $I_0$  is set to  $\frac{y_{t+\tau}}{\alpha} - \frac{y_{t+\tau}}{\alpha(1-p)\omega} \gamma$ , which is the same order of magnitude as  $E_0$ .  $A_0$  is set to  $\frac{p}{(1-p)}I_0$ . And we assume that 30% of tot compartment R  $(R_0)$  is set to 0.3  $\times$  N. Finally,  $S_0 = N - E_0 - I_0 - A_0 - R_0$ .

# 2.4. Computation of effective reproduction number  $(R_{\text{eff}})$

The effective reproduction number ( $R_{\text{eff}}$ ) is defined as the expectation of secondary cases produced by one infected individual in a population exposed to public health and social measures, during its lifespan as infectious. [Guo et al. \(2022\)](#page-9-13) For each infected individual x, we start from the initial compartment of x and compute the probability  $P(x)$  that x attains each infectious compartment. For the SEIAR model, we have:

$$
\mathbb{P}(\mathbf{x}\in A) = \mathbb{P}(\mathbf{x}\in A|\mathbf{x}\in E)\mathbb{P}(\mathbf{x}\in E) = \frac{p\omega'}{p\omega' + (1-p)\omega}
$$
(6)

$$
\mathbb{P}(\mathbf{x}\in I) = \mathbb{P}(\mathbf{x}\in I|\mathbf{x}\in E)\mathbb{P}(\mathbf{x}\in E) = \frac{(1-p)\omega}{p\omega' + (1-p)\omega}
$$
\n(7)

where  $P(x \in I | x \in E)$  denote the conditional probability of  $x \in I$  when  $x \in E$  is known.

For all infectious compartments  $[U_1,U_2,...,U_r]$  that x might attain, compute the newly infection rate for the case that x in  $U_i$ .  $i = 1,2,...,r$ , by letting  $U_i$  equals 1, and other  $U_i, j \neq i$  equals zero in the term of newly infection (e.g.,  $\beta S f(U_1, U_2,...,U_r)$ , where f is a multi-variable function). For the SEIAR model, letting  $(I, A) = (1, 0)$  and  $(0, 1)$  respectively, one obtains the secondary infection produced by x per unit time, for two bracnch when x becomes asymptomatic infectious  $(A)$  or symptomatic infectious (I):

$$
Q(x) = \begin{cases} \kappa \beta S, & \text{if } x \in A \\ \beta S, & \text{if } x \in I \end{cases}
$$
 (8)

Compute the time duration  $T(x)$  that x will stay in each infectious compartment using compartment removing rate (fatality of the disease, recovery rate, and natural death rate, usually set to be constants). For the SEIAR model:

$$
T(x) = \begin{cases} \frac{1}{\gamma'}, & \text{if } x \in A \\ \frac{1}{\gamma}, & \text{if } x \in I \end{cases}
$$
 (9)

Assuming that the disease is currently at an initial stage of development, the number of infected takes only a small portion of the total population. This assumption implies  $Q(x)$  remains constant during the time interval  $T(x)$ .

Taking expectations to eliminate the stochasticity of different infectious compartments that  $x$  might develop into, the effective reproduction number is obtained by:

$$
R_{\text{eff}} = \sum_{\text{all infections } State_i} P(x \in State_i) Q(x \in State_i) T(x \in State_i)
$$
\n(10)

For the SEIAR model:

$$
R_{eff} = \mathbb{P}(x \in A) Q(x \in A) T(x \in A) + \mathbb{P}(x \in I) Q(x \in I) T(x \in I)
$$
  
= 
$$
\frac{\beta S}{p\omega' + (1 - p)\omega} \cdot \left[ \frac{\kappa p\omega'}{\gamma'} + \frac{(1 - p)\omega}{\gamma} \right]
$$
 (11)

# 3. Results

<span id="page-4-0"></span>Table 1

Comparing the period from January 29, 2024, to February 5, 2024 (past seven days) with the upcoming period from February 6, 2024, to January 12, 2024 (next seven days), new cases in China for the next seven days are anticipated to reach 8,804,450 which have decreased by 13.08%. In particular, new cases in all provinces exhibit a declining trend in the future. Among them, the Guangdong, Shandong, Sichuan and Henan provinces are expected to rank among the top four in the country for the number of new cases in the following week. There were generally fewer new cases in the northern provinces compared to the southern provinces. The provinces of Tibet, Hainan, Ningxia Hui Autonomous Region and Zhejiang exhibited the most significant decrease in the incidence of new cases when compared to the preceding seven-day period ([Table 1](#page-4-0)). All of which, the number of cases of influenza A in the forthcoming seven-day period is 5,906,375, representing a 27.00% decline in new cases compared to the preceding seven-day period. The provinces of Guangdong, Jiangsu, and Shandong have the highest incidence of influenza A cases in the country, with all other provinces exhibiting a downward trend. It is anticipated that the prevalence of Influenza B will surpass that of Influenza A over the course of the next seven days, establishing itself as the dominant subtype (Supplementary 2).



Short-term forecast results for new influenza cases.

Note: the predicted regions do not include Taiwan province, Hong Kong, and Macau.

<span id="page-5-0"></span>

Fig. 1. Influenza predicted results from October 1, 2023, to February 5, 2024. A shows the predicted results of influenza in the southern provinces, and B shows the predicted results in the northern provinces.

In the fifth week of 2024 before the spring festival travel rush, the midterm forecast results [\(Fig. 1\)](#page-5-0) indicate that the peak weeks for influenza are expected to fall between week 47 in 2023 and week 1 in 2024. The Ningxia Hui autonomous region is expected to peak earliest in the 47th week, with most southern provinces peaking later than northern provinces (weeks 50–52 vs. weeks 48–50). All regions have peaked by January 1, 2024 ([Table 1\)](#page-4-0). In most provinces, influenza B shows a plateau trend during its peak, with fewer new cases compared to influenza A. Severe influenza outbreaks persist in the provinces of Sichuan, Hunan, Guangdong, Shandong, and Hubei. The peak week of influenza A is consistent with, or one week earlier than the overall peak of influenza in that city. In 2023, influenza A peaked between weeks 47 and 52, with the Jilin and Ningxia Hui Autonomous Region peaking earlier, at week 47. The overall peak of influenza B occurs later than that of influenza A, with most cities peaking in the first to fourth week of 2024. The number of cases caused by influenza B at the peak of the pandemic was lower than the number of cases of influenza A, which was about 1/2 of the number of people infected with influenza A (Supplementary 3).

Considering that the COVID-19 pandemic disrupted the seasonality of influenza, a delay analysis between BISI and  $ILI+$ was performed. Our analysis result revealed that before the COVID-19 pandemic, BISI lagged ILI + by  $2-3$  weeks. During the pandemic, BISI exhibited a 5 to 6-week delay behind ILI+. Post-pandemic, BISI consistently aligned with ILI + trends without a delay effect. Consequently, we used the ILI  $+$  index as validation data for the predicted results [\(Fig. 2-A, 2-B](#page-6-0)). ILI  $+$  validation in the southern and northern provinces ([Fig. 3\)](#page-7-0) shows a significant alignment with the predicted cases ( $P < 0.05$ ). [\(Table. 2](#page-8-0))

# 4. Discussion

Our research findings reveal that in the early stages of the epidemic, historical Baidu search indices lagged behind ILI by 2–3 weeks. However, previous studies have indicated that Baidu search indices lead surveillance data reported by the Centers for Disease Control and Prevention (CDC) at  $1-2$  weeks [\(Dai](#page-9-14) & [Han, 2023\)](#page-9-14). This discrepancy may stem from the different indicators we employed  $ILI<sub>+</sub>$ , which compared to  $ILI\%$  and positivity rate, demonstrates greater real-time accuracy and representativeness [\(Shaman et al., 2013;](#page-9-15) [Yang et al., 2014](#page-9-16)). Additionally, existing literature suggests that the surge in public sentiment data begins after a substantial accumulation of cases, lending further validation to our results. BISI for 2023 exhibits no delay compared to ILI+, possibly attributed, which may be due to the COVID-19 pandemic creating a short-lived increase in awareness of disease prevention in the population [\(He et al., 2022\)](#page-9-17). There is increasing attention to respiratory diseases such

<span id="page-6-0"></span>

Fig. 2. Lag analysis of influenza surveillance data ILI $+$  and Baidu influenza search index.

as COVID-19 and influenza, with some demographics engaging in early searches for medications and stockpiling behaviors. However, adhering to historical patterns,  $ILI<sub>+</sub>$  is more sensitive and accurate than BISI in terms of setting alert thresholds and warning cycles.

Our study predicts that the influenza outbreak will persist for more than four months, a period that coincides with previous influenza pandemic cycles [\(Diamond et al., 2022](#page-9-18)), with the peak occurring from week 47 in 2023 to week 1 in 2024, preceding the peak observed during the COVID-19 pandemic [\(China NICC, 2024](#page-9-2)). The overall forecast indicates a declining trend, potentially attributed to the decline of children and adolescents which are the main contributors to influenza. In many provinces of China, kindergartens and primary schools have started their winter vacation period, during which, compared to regular daily contact, there is a 50% reduction in interactions ([Litvinova et al., 2019](#page-9-19)). This disruption in routine contact breaks the influenza transmission chain, decreasing influenza spread [\(Qiao et al., 2024](#page-9-20)).

The predictions for A (H3N2) and Influenza B are not entirely identical, with Influenza A having a higher number of cases and epidemiological cycles than those for Influenza B, and peaking earlier than Influenza B, which is consistent with historical trends ([Yang et al., 2018](#page-10-0)). This discrepancy in transmission dynamics could be attributed to the extended incubation period of influenza A (H3N2), which is approximately 0.8 days longer than that of influenza B. This prolonged period potentially offers a broader temporal window for viral dissemination. What's more the basic reproduction number for A (H3N2) ranges from 1.3 to 1.8 [\(Park](#page-9-21) & [Ryu, 2018\)](#page-9-21), signifying a superior transmissibility compared to influenza B. Therefore, A (H3N2) has a greater potential for transmission within the population and poses a more significant public health threat to individuals. Our findings highlight that the current influenza epidemic is predominantly characterized by influenza A, with a subsequent shift towards influenza B subtypes in the later phase of the epidemic. This suggests that public health authorities should place a greater emphasis on the surveillance and preventive measures for influenza A during the flu season while remaining vigilant to the potential emergence of influenza B outbreaks.

The incidence of the northern province of Henan, as well as the southern cities of Guangdong, Shandong, Sichuan, and Jiangsu, have a relatively higher incidence of influenza. This phenomenon may be attributed to two factors. First, these provinces have large population bases and frequent interpersonal interactions, which provide more opportunities for virus transmission, resulting in a higher number of primary infections. Second, population migration significantly influences the spread of influenza ([Bedford et al., 2010](#page-9-22)). Some of these provinces are tourist destinations, where the influx of people far exceeds the outflow, leading to intense population mobility. This not only facilitates the exchange of viral strains between different regions but also accelerates the rapid spread of the virus. Tourist cities typically have a higher proportion of external visitors, who may originate from various areas and carry different viral strains, thereby increasing the diversity and transmission risk of local influenza viruses so that enhances the opportunities for exposure and infection. Therefore, public health departments should implement more stringent surveillance and control measures in these areas to effectively reduce the risk of influenza virus transmission.

As the spring festival travel rush approaches, the increase in interpersonal contact during this period increases the probability of influenza transmission. Therefore, during the Spring Festival travel rush period, especially in provinces with significant population mobility, the implementation of NPIs is still advisable. Among these measures, wearing masks on public transport is sanded out as an effective protective measure, capable of reducing infection risk by 45% ([Liang et al., 2020](#page-9-23)). Despite the downward trend of influenza A, its mainstream status cannot be ignored and influenza vaccination remains the cornerstone of influenza prevention. However, China's influenza vaccination coverage is currently low with a rate of only 2.47% in 2022 [\(Zhao, Peng, Ni et al., 2022](#page-10-2)). Intensifying efforts to promote influenza vaccination for influenza A and influenza B is crucial to reducing the number of infections during the influenza season, consequently alleviating the burden on healthcare systems and mitigating economic implications. Influenza B epidemics have not yet peaked in many provinces, making close monitoring of the epidemic and the establishment of an early warning system particularly important. Prevention and control

<span id="page-7-0"></span>

Fig. 3. ILI + data validates trends in predicted outcomes. A indicates validated trends in the southern provinces, and B indicates validated trends in the northern provinces.

#### <span id="page-8-0"></span>Table 2

Influenza peak forecast results.



Note: 1. the predicted regions don't include Taiwan province, Hong Kong, and Macau.

2.\* denotes weeks in 2024.

efforts should be strengthened in crowded places such as schools, and high-risk groups should be encouraged to get vaccinated to reduce the risk of influenza B transmission.

Although we predict influenza trends before the Spring Festival travel rush, this model can be applied to the short-term prediction of influenza and other respiratory infectious diseases, facilitating enhanced preparedness and previous interventions in public health scenarios. Some limitations remain and first, Large fluctuations in population flow and the complexity of the epidemic trend make it challenging for the model to predict the influenza trends during the Spring Festival travel rush, so we did not forecast influenza during this period. Furthermore, due to the mechanism of the current influenza surveillance system, the ILI  $+$  used for validation does not represent the real incidence of influenza, merely validating the modeled trend of influenza. Third, there are differences in influenza transmissibility among provinces. Our study did not collect provincial-level analyses of influenza natural history parameters, which may affect the regional specificity of influenza forecasts.

# 5. Conclusion

Following the advent of the global pandemic caused by the SARS-CoV-2 virus, the prevalence of influenza has exceeded that observed in the contemporaneous period. It was predicted that influenza would persist for a period exceeding four months during the current winter epidemic, with the peak expected to occur between weeks 47 of 2023 and week 1 of 2024. The prevalence intensity of A (H3N2) is greater than that of Influenza B, and the prevalence in the southern regions is greater than that in the northern regions. It is anticipated that within the next seven days, the number of cases of influenza B will exceed those of influenza A. Therefore, it is imperative to call on the public to adopt NPIs and receive influenza vaccination and it is essential to establish an early warning system for influenza B to reduce the healthcare burden. Furthermore. While our method demonstrates efficacy for short to medium-term influenza predictions, further in-depth research is warranted, incorporating multiple data sources for the validation and calibration of influenza models.

#### CRediT authorship contribution statement

Huimin Qu: Writing - review & editing, Writing - original draft, Software, Resources, Methodology, Investigation, Formal analysis, Conceptualization. Yichao Guo: Writing  $-$  review & editing, Writing  $-$  original draft, Software, Methodology,

Investigation, Formal analysis, Data curation. Xiaohao Guo: Writing  $-$  review & editing, Supervision, Software, Methodology, Formal analysis, Data curation. Kang Fang: Writing – review & editing, Software, Resources, Methodology. Jiadong Wu: Writing  $-$  review & editing, Validation, Formal analysis. **Tao Li:** Validation, Formal analysis, Data curation. **Jia Rui:** Validation, Supervision. Hongjie Wei: Supervision, Methodology, Data curation. Kun Su: Data curation, Conceptualization. Tianmu Chen: Funding acquisition, Data curation, Conceptualization.

## 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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#### Supplementary data

Supplementary data to this article can be found online at [https://doi.org/10.1016/j.idm.2024.09.007.](https://doi.org/10.1016/j.idm.2024.09.007)

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