Analysis of the Geographic Transmission Differences of COVID-19 in China Caused by Population Movement and Population Density

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Abstract
The coronavirus disease (COVID-19) has led to a global pandemic and caused huge healthy and economic losses. Non-pharmaceutical interventions, especially contact tracing and social distance restrictions, play a vital role in the control of COVID-19. Understanding the spatial impact is essential for designing such a control policy. Based on epidemic data of the confirmed cases after the Wuhan lockdown, we calculate the invasive reproduction numbers of COVID-19 in the different regions of China. Statistical analysis indicates a significant positive correlation between the reproduction numbers and the population input sizes from Wuhan, which indicates that the large-scale population movement contributed a lot to the geographic spread of COVID-19 in China. Moreover, there is a significant positive correlation between reproduction numbers and local population densities, which shows that the higher population density intensifies the spread of disease. Considering that in the early stage, there were sequential imported cases that affected the estimation of reproduction numbers, we classify the imported cases and local cases through the information of epidemiological data and calculate the net invasive reproduction number to quantify the local spread of the epidemic. The results are applied to the design of border control policy on the basis of vaccination coverage.

Keywords Reproduction number · Population density · Population movement · Regional differences

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1 Introduction

In this ongoing epidemic of COVID-19, the implementation of non-pharmaceutical interventions (NPIs) can help to curb the spread of the epidemic, even if vaccines are available. NPIs include early case identification and isolation, banning public gatherings, personal contact restrictions, social alienation measures and personal protection actions. Many countries have implemented full or partial blockade measures to restrict gathering activities (Block et al. 2020; Ferguson et al. 2020; Gatto et al. 2020). Because Wuhan was the first city in China where the epidemic occurred, to prevent the further spatial spread of COVID-19 in China, Wuhan started to lockdown on January 23, 2020 (Tian et al. 2020). Afterward, all provinces started to implement prevention and control measures such as inter-city travel restrictions and encouraging the public to wash their hands, wear masks. China has implemented a series of public health and medical measures, such as building Fangcang Shelter Hospitals, reasonably allocated medical resources and achieved complete treatment for patients.

Data analysis and mathematical modeling can help to understand the spread of COVID-19 and provide important theoretical supports and decision-making basis for epidemic prevention and control. After the outbreak of COVID-19, compartment models are established (Zhao and Feng 2020; Huang et al. 2020; Roda et al. 2020; Song et al. 2020; Tang et al. 2020a, c; Yu et al. 2020; Zhang et al. 2020a) to estimate important parameters, such as the basic reproduction number ($R_0$), epidemic time, number of cases (Huo et al. 2021) and the final size. As an important indicator to characterize the spread of infectious diseases, $R_0$ is defined as the average number of new infections caused by a typical individual (Dietz 1974; Hethcote 2000; van den Driessche and Watmough 2002). Li et al. (2020) fit the initial case data in Wuhan and estimated that the basic reproduction number is 2.2 (1.4–3.9). Many studies have evaluated the control effect of NPIs on COVID-19 (Gatto et al. 2020; Ge et al. 2020; Jia et al. 2020; Luo et al. 2021; Tang et al. 2020d; Xue et al. 2021), such as the effect of building Fangcang Shelter Hospitals (He et al. 2021), wearing masks (Eikenberry et al. 2020). In terms of monitoring and evaluation research on prevention and control strategies, many articles have given valuable results (Fang et al. 2020; Huang et al. 2020). Moreover, Tang et al. (2020b) and Wang et al. (2020) analyzed the best time to resume work in Wuhan.

Population movement has a strong risk to diffuse the spread of the epidemic. Chen et al. (2020) studied the distribution of cases of the early epidemic in Wuhan and its relationship with population movement. Ye et al. (2020) analyzed the trend of the epidemic situation in Guangdong Province based on population movement. In addition, there is a strong positive correlation between the number of case and the number of population outflow from Zhang et al. (2020c) and Zhou et al. (2020).

To the best of our knowledge, most of researches focus on the establishment of a dynamic model in a fixed area and very few works have considered the spatial effects of COVID-19 transmission. Indeed, before the lockdown of Wuhan, approximately 5 million people flowed to other regions of China due to Chinese New Year (https://news.163.com/20/0126/22/F3ROV3FU00018990.html) and caused the epidemic outbreaks in these sites. Notice that input numbers of migrants from Wuhan were different for different cities and provinces. Furthermore, the local population
densities (PD) vary greatly in different regions. These spatial differences may result in different epidemic risks, because each individual in a region with a higher PD probably has a larger social network with each other and sites near the epidemic center are easier to get more infectious inflows, which means more infectious contacts. Therefore, it is important to consider how the population migration and population density contribute to the outbreaks of COVID-19.

In the present paper, based on the reported epidemic data before the lockdown of Wuhan, we estimate the reproduction numbers of COVID-19 for the provinces and cities of China. Through correlation analysis and multiple linear regression, we reveal the relation between the reproduction numbers and population densities, and the relation between the reproduction numbers and population migrations. These results are helpful for the formulation of prevention and control measures.

The organization of the remaining paper is set as follows. Section 2 presents data collection and analysis. Section 3 introduces the main methods, including reproduction number and data smoothing method. In Sect. 4, we calculate the invasive reproduction numbers and show the correlation analysis results. We also analyze the spread of the local epidemic through the net invasive reproduction number. The paper ends with a brief discussion.

2 Data Collection and Analysis

The daily epidemic report data of 31 provinces (municipalities and autonomous regions) in China are obtained from the website of Chinese Center for Disease Control and Prevention (http://2019ncov.chinacdc.cn/2019-nCoV/global.html). The epidemic data of each city in Hubei Province are obtained from the Health Commission of Hubei Province (http://wjw.hubei.gov.cn/fbjd/dtyw/). The data for calculating population movement sizes come from Baidu Migration website (https://qianxi.baidu.com/2020/).

Notice that the Spring Festival travel season began on January 10, 2020, and Wuhan started to lock down at 10 a.m. on January 23, 2020. We select the time period of data from January 10 to January 24, 2020, a total of 15 days. The population flows among the regions except for Wuhan are ignored because the dispersal individuals were susceptible and had little influence on disease transmissions and local population densities. Thus, we focus only on the emigration flows of Wuhan. The specific formula for computing the population input size (PIS) of each site (province or large city), coming from Wuhan during this period, is given by

\[ PIS = \sum_{i} IP_i \times \frac{\text{index}_i}{\sum_{i} \text{index}_i} \times N_{\text{total}}. \]

Here, IP$_i$ represents the inflow proportion from Wuhan on the $i$th day, index$_i$ represents the migration index in Wuhan on the $i$th day, reflects the scale of migration population, which can be horizontally compared between cities, $i = 1, \ldots, 15$, $N_{\text{total}}$ represents the total number of migrants from Wuhan, which is 5 million (https://news.163.com/20/0126/22/F3ROV3FU0001899O.html).
Table 1  The PIS from Wuhan and PD at provincial level in China

| Region      | PIS   | PD  | Region      | PIS   | PD  |
|-------------|-------|-----|-------------|-------|-----|
| Anhui       | 113,921 | 451 | Jiangsu     | 73,842 | 751 |
| Beijing     | 44,544  | 1313| Jiangxi     | 106,634 | 278 |
| Chongqing   | 63,249  | 376 | Jilin       | 8461   | 144 |
| Fujian      | 45,271  | 325 | Liaoning    | 16,595 | 295 |
| Gansu       | 17,501  | 62  | Ningxia     | 4228   | 104 |
| Guangdong   | 95,756  | 631 | Shaanxi     | 36,249 | 188 |
| Guangxi     | 40,099  | 207 | Shandong    | 55,151 | 636 |
| Guizhou     | 28,261  | 204 | Shanghai    | 33,914 | 3823|
| Hainan      | 18,667  | 264 | Sichuan     | 29,857 | 237 |
| Hebei       | 47,177  | 400 | Tianjin     | 62,244 | 172 |
| Heilongjiang| 14,010  | 80  |              | 7641   |     |
| Henan       | 283,921 | 575 | Xinjiang    | 10,440 | 15  |
| Hunan       | 174,886 | 326 | Yunnan      | 26,756 | 123 |
| Inner Mongolia | 8964  | 21  | Zhejiang    | 54,315 | 564 |

PIS, population input size, person; PD, population density, person/km²

![Fig. 1 Geographic distribution of Wuhan’s population outflow sizes from January 10 to January 24, 2020](Color figure online)
Table 2 The PIS from Wuhan and PD at prefecture-level cities in Hubei Province

| Region   | PIS   | PD   | Region   | PIS   | PD   |
|----------|-------|------|----------|-------|------|
| Enshi    | 66,405| 141  | Suizhou  | 110,313| 230  |
| Ezhou    | 140,353| 676  | Tianmen  | 72,295| 485  |
| Huanggang| 459,650| 364  | Xiangyang| 137,432| 286  |
| Huangshi | 132,239| 539  | Xianning | 176,204| 258  |
| Jinmen   | 114,832| 234  | Xiantao  | 102,915| 449  |
| Jinzhou  | 228,290| 396  | Xiaogan  | 479,663| 552  |
| Qianjiang| 39,730 | 482  | Yichang  | 100,065| 197  |
| Shiyan   | 66,902 | 144  |          |       |      |

PIS, population input size, person; PD, population density, person/km²

The numbers of PIS at provincial level are shown in Table 1. Figure 1 shows the geographic distribution of population movements. Outside Hubei Province, there were large differences in the size of population movements. Henan, Hunan and Anhui, which are the neighboring provinces of Hubei, ranked the top three in PIS, while Ningxia, Qinghai and Tibet, which are far away from Wuhan, were in the bottom of PIS rank. In addition, in order to describe the geographic distribution of population mobility on a smaller scale, we further focus on the cities in Hubei Province. Before the lockdown of Wuhan, nearly 70% of the total migrant population in Wuhan flowed into the prefecture-level cities in Hubei Province every day, and the corresponding PISs at prefecture-level cities in Hubei Province are shown in Table 2. The three prefecture-level cities with the largest inflows were Xiaogan, Huanggang and Jingzhou, whereas Shiyan City, Enshi Prefecture, Qianjiang City and Shennongjia Forest Region had relatively small inflows.

The PD of each province or city comes from the 2019 Statistical Yearbook (National Bureau of statistics 2020), which lists the population numbers of the regions at the end of 2018 and the areas of the administrative divisions of China. The results are shown in Tables 1 and 2, where the PD is the ratio of population numbers to area in the unit of person/km².

3 Method

3.1 Lotka–Euler equation

Our objective is to use the data of daily reported cases to estimate the reproduction numbers of COVID-19 in the regions of China. As usual, we consider the case that the daily counts of new cases in the initial phase increase exponentially at a rate \( r \). Let \( b(t) \) be the total number of infectious inputs and local new infections at time \( t \). Under the assumption that the infection process is stationary, we have

\[
b(t) = b(t - a)e^{ra}
\]
for $a > 0$.

If $F(a)$ is the infection rate and $S(a)$ is the proportion of infectious individuals at time $a$ since local infection or arrival time for an infectious immigrant, then $F(a)S(a)$ is the expected rate of secondary cases at time $a$. It follows from Wallinga and Lipsitch (2007) that

$$b(t) = \int_0^\infty b(t-a)F(a)S(a)\,da.$$ 

In view of (1), we get the Lotka–Euler renewal equation

$$1 = \int_0^\infty e^{-ra}F(a)S(a)\,da. \quad (2)$$

Let us define the invasive reproduction number $R_0$ by

$$R_0 = \int_0^\infty F(a)S(a)\,da.$$ 

The invasive reproduction number is an appropriate quantity to measure the transmission risk as the number of new cases increases exponentially with a rate $r > 0$ when $R_0 > 1$, and decline exponentially with a rate $r < 0$ when $R_0 < 1$. In addition, it includes the influences of continuous infectious inputs, whereas the classical basic reproduction number considers only the local new transmissions. More importantly, it can be estimated by direct fitting the data of daily reported cases. Indeed, the rate $F(a)S(a)$ can be normalized to a distribution $g(a)$:

$$g(a) = \frac{F(a)S(a)}{\int_0^\infty F(a)S(a)\,da} = \frac{F(a)S(a)}{R_0}.$$ 

This is a distribution of serial interval, which is defined as the mean duration between the time of infection of a secondary infector and the time of infection of its primary infector (Wallinga and Lipsitch 2007). Substituting this expression into (2), we get

$$\frac{1}{R_0} = \int_0^\infty e^{-ra}g(a)\,da.$$ 

Note that the right-hand side of this equation is the Laplace transform of function $g(a)$. If $M(z) = \int_0^\infty e^{za}g(a)\,da$, which is the moment generating function of the distribution $g(a)$, it follows from Wallinga and Lipsitch (2007) that the invasive reproduction number $R_0$ can be computed by

$$R_0 = \frac{1}{M(-r)}. \quad (3)$$
3.2 Distribution of Serial Interval

The estimation of the reproduction number under a given growth rate depends on the specific distribution of the serial intervals (Wallinga and Lipsitch 2007). The gamma distribution is rich in shape and is very effective in fitting the data of serial interval of COVID-19 (Li et al. 2020; Zhang et al. 2020b). Thus, we fix the distribution of serial interval as a gamma distribution. The probability density function is

\[ g(x) = \frac{\beta^\alpha}{\Gamma(\alpha)} x^{\alpha-1} e^{-\beta x}, \]

where \( \alpha \) is the shape parameter, and \( \beta \) is the scale parameter. Exponential distribution and chi-square distribution are special cases of the gamma distribution. The corresponding moment generating function of gamma distribution is

\[ M(t) = \frac{\beta^\alpha}{\Gamma(\alpha)} \int_0^\infty x^{\alpha-1} e^{(t-\beta)x} dx. \] (4)

For \( t < \beta \), by the transformation \( v = (\beta - t)x \) we obtain

\[ M(t) = \frac{\beta^\alpha}{(\beta - t)^\alpha \Gamma(\alpha)} \int_0^\infty v^{\alpha-1} e^{-v} dv = \left( \frac{\beta}{\beta - t} \right)^\alpha. \] (5)

Fixing \( t = -r \) in (5), one obtains the formula of the invasive reproduction number

\[ R_0 = \frac{1}{M(-r)} = \left( \frac{\beta + r}{\beta} \right)^\alpha. \] (6)

3.3 Exponential Growth Rate

We estimate the exponential growth rate \( r \) from the time series of daily confirmed cases \((t_i, x_i), i = 0, \ldots, n - 1\). For the region like Guangdong Province, the epidemic data in the early stage are well fitted by an exponential curve. Figure 2 shows the fitting graph of the confirmed cases of Guangdong Province, where January 22 of 2020, the date of the first reported case in Guangdong Province, is fixed as the initial date for fitting.

For cities or provinces with a small number of cases, the fitting effect of exponential growth is poor. This may result from the stochastic effects such as the errors of data reports, the variation of infection progressions and environmental perturbations. In order to filter the stochastic fluctuations, we ask the techniques of Earn et al. (2020) and Ma et al. (2013) where a logistic model is first used to simulate the increase in cumulative cases and the modified daily cases are extracted from the cumulative cases. More specifically, we assume that \( c(t) \) (the total number of cases at \( t \)) satisfies
Fig. 2  a Daily confirmed data in Guangdong Province and b fitting graph of exponential growth rate of Guangdong Province (Color figure online)

Fig. 3  a Daily confirmed data and smoothed data in Guangxi Province and b fitting graph of exponential growth rate of Guangxi Province (Color figure online)

a Logistic equation:

$$\frac{dc(t)}{dt} = r_c c(t) \left[ 1 - \frac{c(t)}{K} \right], \quad (7)$$

where $r_c$ is the intrinsic growth rate of the epidemic and $K$ represents the final scale of the epidemic. After that, we fix $x(t_i) = c(t_i) - c(t_{i-1})$ and then fit the filtered data by an exponential curve. Take Guangxi Province as an example, the actual data fluctuate largely because the sizes of new cases are small, as shown in Fig. 3a. Through the filtration, the random fluctuation of data is eliminated to get a better exponential fit, as shown in Fig. 3b.
3.4 Statistical Analysis

Shapiro–Wilk test is used to test the normality of the PD, PIS and reproduction number. If variables obey the normal distribution, then Pearson correlation coefficient is selected. Otherwise, Spearman correlation coefficient is selected. Multiple linear regression is selected to explore the relationships among $R_0$, PD and PIS. Results are considered as statistically significant when the $p$ value is less than 0.05.

4 Results

In the epidemic spread, a considerable part of the cases were imported at the initial phase and the cases due to local transmissions occurred over time. Notice that the confirmed data do not distinguish the imported cases from the local cases. Therefore, we define the invasive reproduction number on the basis of confirmed data as $R_0$, and the reproduction number from the local case data as the net invasive reproduction number ($R_{0}^{net}$), which describes the local transmission risk of the epidemic after the arrival of imported cases.

4.1 The Invasive Reproduction Number

First, we use the data of confirmed cases in the early stage of COVID-19 spread from January 20, 2020, to February 20, 2020, to fit the exponential growth rate of each region. Second, based on the data of 425 cases in Wuhan, we previously used the maximum likelihood method to estimate the gamma distribution of serial interval, and our results in Hu et al. (2020) are in good agreement with Li et al. (2020) and Zhang et al. (2020b). Taking the estimated parameters $\alpha = 5.3183$, $\beta = 0.6010$ in Hu et al. (2020), by (6) we obtain the calculation formula for invasive reproduction number:

$$R_0 = \left(1 + \frac{r}{0.601}\right)^{5.3183}.$$ 

Table 3 shows the results of invasive reproduction numbers at provincial level in China. Similarly, we also obtain the reproduction numbers at prefecture-level cities in Hubei Province, which are shown in Table 4. On the whole, the reproduction numbers in the early stage of the epidemic transmissions in the regions (cities) are between 2.0 and 6.6. Therefore, there was a high risk of epidemic outbreak.

In order to reveal how population movement and local population size influence the risk of COVID-19 outbreaks, we conduct the correlation analysis between invasive reproduction number and PIS, and the correlation analysis between invasive reproduction number and PD. After the test of normality, we find that the Pearson correlation is selected for the first one, and the Spearman correlation is appropriate for the second case. These correlation analyses show that the invasive reproduction number of a province (city) in China (except Hubei Province) has a significant correlation with the PIS (the correlation coefficient $r = 0.628$, $P < 0.0001$) and has also a significant correlation with the local PD ($r = 0.650$, $P < 0.0001$). Furthermore, in Hubei...
Table 3  Estimations of invasive reproduction numbers and their 95% confidence interval (CI) at provincial level in China

| Region    | $R_0$   | 95% CI       | Region       | $R_0$   | 95% CI       |
|-----------|---------|--------------|--------------|---------|--------------|
| Anhui     | 4.16    | (3.65, 4.73) | Jiangxi*     | 3.65    | (3.02, 4.38) |
| Beijing   | 3.69    | (3.29, 4.14) | Liaoning     | 3.39    | (1.84, 4.01) |
| Fujian    | 2.90    | (2.32, 3.60) | Inner Mongolia| 2.54   | (1.88, 3.38) |
| Gansu     | 2.65    | (2.21, 3.16) | Ningxia      | 2.46    | (2.23, 2.69) |
| Guangdong*| 4.80    | (4.25, 5.40) | Shandong*    | 3.66    | (3.27, 4.08) |
| Guangxi   | 2.57    | (2.24, 2.93) | Shanxi       | 3.76    | (3.16, 4.44) |
| Guizhou   | 3.16    | (2.67, 3.72) | Shaanxi      | 3.36    | (2.74, 4.09) |
| Hainan    | 2.85    | (2.55, 3.17) | Shanghai*    | 3.91    | (3.39, 4.50) |
| Hebei     | 3.42    | (3.13, 3.73) | Sichuan*     | 2.95    | (2.67, 3.25) |
| Henan*    | 4.53    | (3.98, 5.13) | Tianjin      | 3.24    | (3.01, 3.47) |
| Heilongjiang* | 3.55 | (3.06, 4.11) | Xinjiang     | 2.58    | (2.39, 2.80) |
| Hunan*    | 4.11    | (3.55, 4.76) | Yunnan*      | 3.40    | (2.72, 4.23) |
| Jilin     | 3.38    | (2.55, 4.41) | Zhejiang*    | 4.10    | (3.24, 5.14) |
| Jiangsu*  | 3.56    | (3.17, 3.99) | Chongqing    | 2.70    | (2.36, 3.08) |
| Hubei     | 5.81    | (5.76, 5.86) |              |         |              |

The province with * means its $R_0$ is computed by raw data, the others are calculated by filtered data.

Table 4  Estimations of invasive reproduction numbers and their 95% CI at prefecture-level cities in Hubei Province

| Region   | $R_0$   | 95% CI       | Region   | $R_0$   | 95% CI       |
|----------|---------|--------------|----------|---------|--------------|
| Enshi    | 2.29    | (2.04, 2.57) | Suizhou* | 4.03    | (3.28, 4.91) |
| Ezhou*   | 4.29    | (4.01, 4.59) | Tianmen  | 3.62    | (3.33, 3.93) |
| Huanggang*| 3.65 | (3.13, 4.23) | Xiangyang| 3.49    | (2.69, 4.47) |
| Huangshi*| 3.62    | (2.95, 4.41) | Xianning | 2.32    | (2.18, 2.46) |
| Jinmen   | 3.58    | (3.31, 3.86) | Xiantao  | 3.42    | (2.91, 4.01) |
| Jinhua*  | 4.54    | (4.20, 4.89) | Xiaogan* | 4.73    | (4.13, 5.30) |
| Qianjiang| 3.02    | (2.84, 3.20) | Yichang* | 3.69    | (3.08, 4.40) |
| Shiyan*  | 3.26    | (2.90, 3.65) | Wuhan*   | 6.26    | (5.99, 6.54) |

The city with * means its $R_0$ is computed by raw data, the others are calculated by filtered data.

Though the above-mentioned correlations are statistically significant, the scatter plots indicate that the linear correlations are weak, which are shown in Fig. 4. This should be the case because a variety of control measures were adopted to reduce social activities in China from the beginning. In addition, people were urged to wear surgical masks for protection. These NPIs decreased the correlations.
With the development of epidemics, the vaccination program (Kaur and Gupta 2020) and the border reopening measures (Nali et al. 2021) are implemented, which cause a variety of influences on PD and PIS. First, the PD of susceptible population becomes lower because the vaccination of COVID-19 provides a barrier for those vaccinated individuals. In addition, the border reopened policy results in the increase in PIS. In order to figure out how much the PD and PIS contribute to the disease transmission risk, we fit the values of $R_0$ by the PD and PIS. Notice that the disease transmissions in one site are attributed to local transmission and infectious contacts with imported individuals. We select

$$R_0 = a \times PD + b \times PIS \times PD$$  \hspace{1cm} (9)
Table 5  Parameter estimations of regression model

| Model   | Unstandardized coefficients | Standardized coefficients | t  | P  |
|---------|-----------------------------|---------------------------|----|----|
|         | B                          | Standard error            |    |    |
| PD      | $1.632 \times 10^{-3}$     | $6.310 \times 10^{-4}$   | 0.344 | 2.588 | 0.013 |
| PIS*PD  | $2.498 \times 10^{-8}$     | $6.964 \times 10^{-9}$   | 0.477 | 3.587 | 0.001 |

PIS population input size, PD population density
* $F = 24.897$, $R^2 = 0.548$

to fit the data, where $a$ and $b$ are constants to measure the intensities of local transmission and the transmission with imported individuals, respectively. Using the data in Tables 1, 2, 3 and 4 and multiple linear regression, we obtain the regression model, in which $R_0$ is the dependent variable, and the two indicators (PD and PIS) are explaining variables. Table 5 shows the results of the parameter estimation of the regression model, including regression coefficients, standard errors, standardized coefficients and the results of hypothesis test.

We consider a scenario where PIS varies from 1 to $10^5$ and PD varies from 1 to 1000. Then numerical computations of invasive reproduction number on the basis of (9) and Table 5 yield Fig. 5a where the green plane corresponds to $R_0 = 1$. This figure indicates that suitable sizes of PIS and PD can drive the reproduction number below unity to control the epidemic disease. To demonstrate this, we let the vaccination ratio be $\alpha$ and assume that the vaccine is 100% effective. Then the susceptible PD is $(1 - \alpha) * PD$ and (9) become

$$R_0 = a * (1 - \alpha) * PD + b * (1 - \alpha) * PIS * PD.$$  

If PD = 1000 and $\alpha = 0.6$, we get a relation between $R_0$ and PIS, which is shown in Fig. 5b. From this function, we see that $R_0 < 1$ when PIS < 23,170. This means that the daily input number should be less than 23,170/15 ≈ 1544 to control the epidemic. In other words, the control strategy should be selected from the green region in Fig. 5b.

Let us fix $R_0 = 1$ in (10). Then the blue surface in Fig. 5c shows the surface of critical vaccination ratio as PIS and PD vary, that is, if the vaccination ratio is above this surface, the epidemic is controlled because $R_0 < 1$. In order to consider border reopening scenario under vaccination, we fix PD = 800 and $R_0 = 1$. Then we get a curve in the surface to describe the critical relation between the vaccination ratio and PIS, which is marked by red color in Fig. 5c. To be clearer, we present Fig. 5d to show the curve in the PIS-$\alpha$-plane, in which the green region means that the epidemic is controlled. It reveals that only when vaccination ratio exceeds a certain critical value (here is 23.4% in this scenario, see blue pentagram in Fig. 5d), can the border be reopened, and a higher vaccination ratio leads to the more openness.
4.2 The Net Invasive Reproduction Number

Since there were sequential inputs of imported cases in the early stage of COVID-19 spread, which affect the estimation of invasive reproduction numbers, we classify the imported cases and local cases through the information of epidemiological data and calculate the net invasive reproduction number to quantify the local spread of the epidemic. The cities or provinces with the full epidemiological information include Shanghai, Yunnan, Guizhou, Shaanxi, Beijing, Liaoning, Sichuan and Henan. The daily reported epidemiological data of these regions are collected through the websites of the Health Commissions or from the literature (Cheng et al. 2020b; Liu et al. 2020). The infected persons are divided as imported cases and local cases. An imported case is defined as a patient who had a history of living in Hubei Province within 14 days before the onset of illness. Otherwise, it is classified as a local case (Cheng et al. 2020a).
Table 6 The net invasive reproduction numbers and their 95% CI

| Region  | $R_{0}^{net}$ | 95% CI    | Region  | $R_{0}^{net}$ | 95% CI    |
|---------|---------------|-----------|---------|---------------|-----------|
| Shanghai | 4.48          | (3.65, 5.45) | Sichuan | 2.23          | (2.07, 2.44) |
| Yunnan  | 1.65          | (1.53, 1.79) | Beijing | 2.78          | (2.42, 3.19) |
| Guizhou | 3.23          | (2.53, 4.08) | Liaoning | 2.99         | (2.45, 3.61) |
| Shaanxi | 3.12          | (2.57, 3.76) | Henan   | 3.39          | (2.80, 4.08) |

Based on the data of local cases and (8), the net invasive reproduction numbers are shown in Table 6. Compared with Table 3, the net invasive reproduction number in most areas is less than the total invasive reproduction number. This means that the reproduction number decreases with the removal of imported cases. Hence, the total invasive reproduction number could cause an overestimation of local disease transmission risk. Especially, this is the case for a city or a province with the strict prevention measures or the lower PD, such as Southwest China, Beijing and Liaoning.

However, an attention should be paid to Shanghai’s net invasive reproduction number $R_{0}^{net} = 4.48$ (95%CI 3.65–5.45), which is larger than the invasive reproduction number and indicates the risk of local spread of the epidemic in Shanghai is relatively higher. This weird paradox may be caused by the following reasons. In early 2020, similar to other provinces and cities, the outbreak of COVID-19 in Shanghai originated from the imported cases in Wuhan. Approximatively, the spread of disease could be roughly divided into two stages: imported case transmission and local case transmission. As an international large city, Shanghai had the ability to quickly identify and isolate these imported cases through information means to block their transmission. This reduced the invasive reproduction number in the period of imported case transmission. However, for the stage of local transmission, the local asymptomatic individuals and local exposed individuals contributed much more than the imported members, but they could not be isolated as rapidly as the imported individuals because there was no massive nucleic acid test during that time. This, together with the highest population density in China, intensified the net reproduction number.

Furthermore, the $R_{0}^{net}$ in Yunnan and Henan dropped significantly because of geographic reasons or control measures. In fact, Yunnan is far from Wuhan, the center of the epidemic, and has a relatively small PD. Henan took the lead in adopting prevention and control measures in the early stage of the epidemic because it neighbors Wuhan, which had a greater advantage in preventing the spread of COVID-19.

5 Discussion

In this paper, we have calculated the invasive reproduction number in each province (large city) of China, studied the relationship between the reproduction numbers and PIS, and the relations between the reproduction number and local PD. These results reveal how the population migration and PD contribute to the outbreaks of COVID-19 in China, which are important for guiding the policy of NPIs. First, since there
is a significant correlation between PD and reproduction number, it is crucial to take more stringent prevention measures, such as reduction of vaccination hesitancy (Razai et al. 2021), home isolation and community control measures, for the region with the higher PD. Second, since the PIS intensifies the reproduction number, it is important to conduct the lockdown policy to curb the spread of COVID-19, and it is necessary to strengthen import and export quarantine when the border is reopened. Moreover, we have calculated the net invasive reproduction numbers based on local cases and analyzed the characteristics of local transmission of COVID-19, which indicates that the total invasive reproduction number in most cases, could cause an overestimation of local disease transmission risk.

Though this paper has obtained some results in the assessment of the transmission capacity of COVID-19, there are some limitations. First, the lack of understanding of COVID-19 in the early stage and the limited detection capabilities have led to large fluctuations in the number of daily reports. And there are asymptomatic infections and incubation cases, which affects the estimation of reproduction number. Second, the Lotka–Euler equation is used to calculate the reproduction number for the phase of early epidemic growth. It is interesting to consider how the geographic differences affect the outcomes of COVID-19 spread in the later stage when a variety of intervention measures are used. Third, the epidemic of COVID-19 is still prevalent all over the world. A variety of mutant viruses have occurred, such as $\alpha$-virus in British (Davies et al. 2021), $\beta$-virus in South Africa (Tegally et al. 2020), $\gamma$-virus in Brazil (Faria et al. 2021), $\delta$-virus in India (Campbell et al. 2021) and the latest Omicron-virus (Karim and Karim 2021). Various researches show that these variants have the ability to weaken the efficacy of vaccination. Therefore, it might be an attractable study to investigate how the mutations influence the vaccination and further impact the reproduction numbers. We leave these as future research.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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