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The effects of population mobility on Chinese HIV epidemics in spill-over and influx risks perspectives: a spatial epidemiology analysis

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Abstract

Investigating the spatial effects of population mobility on Human Immunodeficiency Virus (HIV) epidemics provides valuable insights for effective disease control. Data on the incidence and prevalence of HIV and socioeconomic factors from 2013 to 2022 across 31 provinces in China were collected. The Baidu migration index was employed to construct inter-provincial population migration matrices for spatial lag models to evaluate spatial spill-overs and influx risks associated with HIV epidemics macroscopically. This study also analysed the impacts of socioeconomic variables, conducted robustness tests for validation, and performed subgroup analysis stratified by HIV incidence levels. Significant spatial autocorrelation of HIV morbidity was confirmed by finding a positive Moran's *I*. The spatial lag model indicated that when a given province had a 1-unit increase in HIV incidence, its average outflow would cause a 0.7068-unit incidence rate increment in other destination provinces, while every unit increase of HIV incidence in other provinces would induce a 0.7013-unit HIV average incidence rise in the original one when it played the role of destination on average. Furthermore, higher population density and lower educational attainment were associated with elevated HIV incidence ($p<0.001$). The robustness of the findings was verified, and subgroup analysis indicated that reasons besides population mobility should be given priority consideration in regions with higher HIV incidence. The risks of population mobility related to the HIV epidemic were quantified, highlighting the necessity of developing effective and acceptable HIV prevention and control strategies specifically tailored for migrant populations.

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Introduction

Human Immunodeficiency Virus (HIV) and Acquired Immune Deficiency Syndrome (AIDS) have remained significant global public health challenges for decades, consistently ranking among the top ten disease burdens worldwide. According to estimates from the Joint United Nations Programme on HIV/AIDS (UNAIDS), 37.7 million people were living with HIV in 2020, leading to 680,000 AIDS-related deaths globally (Rajasingham *et al.*, 2022). The HIV prevention situation in China is worrisome, with the number of new infections rising annually and transmission from high-risk groups to the general population increasing.

Considering the growing severity of the HIV transmission, numerous studies sought to examine its spatiotemporal patterns (Yuan *et al.*, 2021). To achieve these objectives, Moran's *I*, local Getis-Ord G*I statistics, and Bayesian spatiotemporal models have been commonly employed (Otiende *et al.*, 2020), with Moran's *I* and Local Getis-Ord G*I statistics used to demonstrate the spatial autocorrelation and agglomeration of HIV epidemics (Dos Reis *et al.*, 2022). The Bayesian spatiotemporal model is generally applied to estimate spatially structured and unstructured random effects, time trends, and spatiotemporal interactions, with results indicating that HIV exhibits significant regional heterogeneity, positive spatial correlation, and clear spatial clustering effects (Otiende *et al.*, 2020). Additionally, the challenges in HIV prevention and control have been shown to be associated with income, education level (Bidzha *et al.*, 2024), urbanization rate (Fang *et al.*, 2020), population density and medical accessibility (Espoir *et al.*, 2021).

Nevertheless, current studies exhibit notable limitations. Most models employ the spatial adjacency matrix as the weight matrix (Qian *et al.*, 2014), positing that only directly adjacent regions can exert mutual influence (Anselin, 1988), which diverges significantly from real-world transmission routes. HIV, being primarily sexually transmitted (Teng *et al.*, 2011), necessitates direct contact between individuals (Das *et al.*, 2019). Therefore, the frequency of interaction between regions cannot be approximated based solely on geographic proximity. Additionally, advancements in transportation mitigate barriers to population movement, amplifying the risk of disease outbreaks (Nouvellet *et al.*, 2021). Consequently, when analysing the spatial effects of HIV epidemics, the influence of population mobility must be integrated (Borkowski *et al.*, 2021). On the other hand, research has been conducted to quantify the impacts of population mobility on the transmission of HIV, albeit from a non-spatial standpoint (Camlin *et al.*, 2018; Cassels, 2020). However, the majority of corresponding studies have been restricted to small groups of high-risk populations over a limited follow-up period, lacking provincial evidence on such impacts (Carvalho *et al.*, 2012; Klabbers *et al.*, 2024). Furthermore, it is imperative that the consistency of the influence of population mobility on regions with different levels of HIV prevalence be quantified further to develop tailored policies.

Given the limitations of previous research, this study employed web-crawling to obtain the provincial-level Baidu Migration Index data. Based on these data, specific spatial population mobility weight matrices were calculated and integrated into spatial models to quantify the impacts of population mobility on HIV epidemics at the provincial level. Furthermore, subgroup analysis was conducted, particularly in areas experiencing high and low rates of HIV, to examine the impact heterogeneity of population mobility on HIV spread.

Materials and Methods

Overview of the modelling frameworks

The analytical modelling framework is graphically summarized in Figure 1. First, spatial population mobility weight matrices were calculated from both spill-over and influx risk perspectives. Spatial autocorrelation was then assessed using Moran's *I*, while hot/cold spot analysis employed Local Getis-Ord Gi* statistics. Subsequently, spatial econometric models quantified population mobility effects on HIV epidemics from both risk perspectives. The robustness of these effects was tested using conventional spatial adjacency and distance matrices. Finally, subgroup analyses stratified by HIV incidence levels were performed. Detailed methodological specifications follow.

Spatial population mobility weight matrices

This study employed Baidu Migration Big Data (https://qianxi.baidu.com/#/) to quantify interprovincial population mobility (Huang *et al.*, 2017), with its validity supported by prior research (Yao *et al.*, 2017). The migration data were crawled from the web on January 5, 2024, and included migration scale indexes and migrant Origin-Destination (OD) share matrices, covering the period from January 1, 2021, to December 31, 2023.

The annual mean migration scale indexes, including population outflow and inflow indices for each province, were obtained to present horizontal comparable population outflux and influx scales. Similarly, the migrant OD share matrix was categorized into population outflow and inflow OD share matrices. The outflow share matrix was composed with 31*31 elements, and each element o_{ij} presented the share of population mobility flowing from origin-region *i* to destination-region *j* in the total outflow from region *i*. And the matrix element q_{ij} for inflow OD share matrix demonstrated the proportion of population inflow from origin-region *j* to destination-region *i* in total influx of region *i*. Consequently, for a given region *i*, the spill-over and influx volumes of population mobility were analysed separately.

The outflow scale index multiplied by the outflow share matrix yields the horizontal comparable population outflow from region *i* to region *j*, and the interaction between the weight matrix with the HIV incidence of origin-region *i* provides an average indication of how the HIV epidemic in region *i* affects destination region *j*. This spill-over of HIV presence from a given region to another is referred as the "spill-over risk". With regard to population influx, the corresponding calculation shows how the presence of HIV in region *j* impacts the destination region *i* with the influence now referred to as the "influx risk". The spatial outflow and inflow weight matrices satisfied the premise assumptions of spatial dependence, non-negativity, and first law of geography (LeSage *et al.*, 2008; Tobler, 1970).

Spatial autocorrelation

Moran's *I* is a statistical measure for assessing spatial autocorrelation of geographic data, indicating whether similar values cluster or disperse with a range from -1 to 1. The Moran scatter plot visually represents this by plotting individual observation values against their neighbouring averages, where points in the first and third quadrants indicate positive autocorrelation, while those in the second and fourth reflect negative autocorrelation. In addition, the Local Getis-Ord Gi* statistic identifies hotspots and coldspots based on spatial data. It measures the clustering of high or low values in localized areas by comparing observed values to expected values under random distribution. Thus, a significant positive Gi* value indicates a hotspot, where high values are concentrated, while a significant negative Gi* value signifies a coldspot, where low values are clustered.

Spatial econometric models

This study utilized the spatial lag model (SLM), Equation (1) and the spatial error model (SEM), Equation (2) to analyse the effect of spatial spill-over of HIV due to population mobility (Bivand, 2015). The model expressions are as follows (Anselin, 1988):

$$y_{it} = \rho \sum_{j=1}^{N} \omega_{ij} y_{jt} + x_{it}\beta + \lambda_t + \mu_i + \varepsilon_{it}, i = 1, \dots, N; t = 1, \dots, T; \qquad (1)$$

$$\begin{cases} y_{it} = x_{it}\beta + \lambda_t + \mu_i + \varphi_{it} \\ \varphi_{it} = \nu \sum_{j=1}^{N} \omega_{ij} \varphi_{jt} + \varepsilon_{it} \end{cases}, i = 1, \dots, N; t = 1, \dots, T; \qquad (2)$$

where, y_{it} is the dependent variable of region *i* at year *t*; $W = (\omega_{ij})$ the given spatial population mobility weight matrix; ρ the spatial autoregressive coefficient; ε_{it} and φ_{it} the error terms, v the spatial autocorrelation coefficient of the residual term. x_{it} presents the p−dimensional explanatory vector; β is the p−dimensional unknown parameter vector; λ_t and μ_i denote temporal and spatial effects. The spatial lag and error tests with the robust Lagrange Multiplier (LM) were carried to determine the optimal models from SLM and SEM.

The dependent variables in this study were the annual incidence of newly diagnosed HIV (IH, referred to as HIV incidence model) and the annual number of newly diagnosed HIV (NH, referred to as HIV prevalence model). The independent variables were represented by comprehensive indicators derived using entropy methods (Ding *et al.*, 2005), including Socioeconomic Factors (SF; a composite of the Gross Domestic Product (GDP) per capita, the proportion of the tertiary sector and the disposable income per capita); Population Density (PD; calculated from urbanization rate and population density); Health Resource Factors (HRF; based on the number of doctors and nurses per 1,000 people, the number of hospital beds per 1,000 people and the number of hospitals); and Education Level (EL; measured by education expenditure and the proportion of the population with tertiary education). All variables were log-transformed (ln) to mitigate potential issues related to multicollinearity and heteroscedasticity, e.g., lnIH, lnNH, lnSF, lnPD, lnHRF, and lnEL.

Robustness test and subgroup analysis

This study constructed spatial econometric models using the traditional spatial adjacency (adjacency perspective) and spatial distance (distance perspective) weight matrices for the purpose of evaluating the robustness of spatial models utilizing the spatial population mobility weight matrices. Furthermore, according to the results of the hotspots/coldspots analysis, subgroup analysis for hotspot-regions, coldspot-regions, and the remaining regions was conducted to estimate the spatial autoregressive coefficients after adjusting for the aforementioned socioeconomic variables to quantify the impacts of population mobility on regions with different levels of HIV prevalence.

Data sources

The variables used in this study were obtained from the China Notifiable Infectious Diseases Network Reporting System (https://www.phsciencedata.cn/Share/index.jsp), China Statistical Yearbooks, China Health Statistical Yearbooks and the Baidu Migration Big Data database. Missing data were handled by the "mice" package in R (version 4.0.5), which used multivariate imputation by chained equations with a linear regression model, and a 5-fold validation bootstrap was employed. Choropleth maps were generated by ArcMap software (version 10.8). Statistical analyses regarding spatial econometric modelling were conducted in Stata (version 14.0) utilizing the "spatwmat" package and key Stata commands, including "xtcd2", "xtcdf", "pescadf", "xtmoran", "spregxt", and "xsmle" packages.

Results

Population mobility and HIV incidence

The average annual population outflow and inflow indices for each province in mainland China are presented in Figure S1, demonstrating significant regional heterogeneity in population mobility. High-density migration was concentrated along the south-eastern coast of China, while population mobility in the western and north-eastern regions remained relatively limited. The incidence of HIV per 100,000 people is depicted in Figure S2. Overall, the epidemiology of HIV in China exhibited distinct spatial heterogeneity, with a higher incidence in the Southwest and lower prevalence in the northern regions. Provinces with a high incidence of HIV and significant population outflow included Sichuan, Chongqing, Guangxi, Hunan, and Guangdong. In contrast, Beijing, Jiangsu, Hebei, and Anhui were found to have relatively lower HIV incidence despite a higher volume of population inflow.

Spatial autocorrelation and hotspot analysis

The spatial autocorrelations of the dependent variables were assessed by estimating the Moran's I from 2013 to 2022 (*Table S1, Figures S3 and S4*). From both the spill-over and influx risk perspectives, the significant spatial autocorrelations of lnIH and lnNH were confirmed, as indicated by non-zero Moran's I (p<0.001).

The results of the Local Getis Gi* statistic for hotspots and coldspots of lnIH and lnNH are presented in Figures 2 and 3, respectively. In general, the hotspots of HIV incidence were concentrated in Sichuan, Chongqing, Yunnan, Guizhou, and Guangxi, whereas significant coldspots were seen in Inner Mongolia, Jilin, Liaoning, Beijing, and Hebei (Figure 2). For the number of people living with HIV, the hotspots with 95% significance level were located in the south-western region, while the northern region emerged as a region with notable coldspots (Figure 3). These results revealed clear spatial autocorrelation and heterogeneity in HIV distribution.

Cross-sectional dependency and stationary

Prior to establishing the spatial models, it was essential to prevent potential errors. To this end, we employed the Pesaran (Pesaran, 2015) cross-sectional dependence (CD) test (Table S2), which revealed significant CD concerns. Consequently, the traditional first-generation unit root tests were not applicable. Instead, the adjusted Im-Pesaran-Shin (CIPS) test (Im *et al.*, 2003) and the co-integrated augmented Dickey-Fuller (CADF) test (Dickey *et al.*, 1979) were utilized, and the stationarity of each variable was confirmed (*Table S2)*.

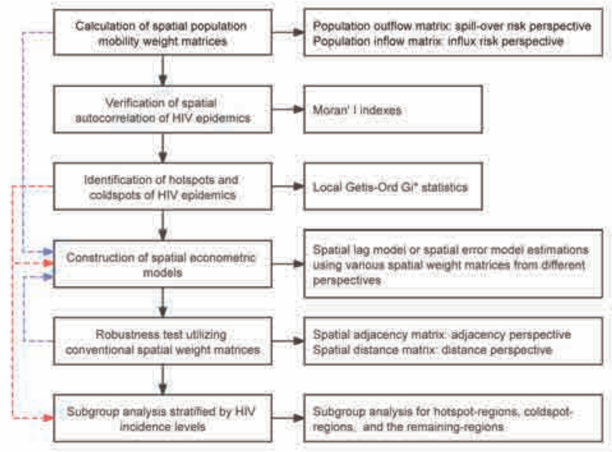

Figure 1. Flow diagram of the modelling framework.

Estimation results of spatial lag models

Based on the results of the LM and the robust LM tests (Table S3), the spatial lag models were ultimately selected with statistical significance set at the 0.001 level. The estimation results from both spatial spill-over and influx risk perspectives are shown in Table 1.

The Hausman test (Hausman, 1978), a statistic assisting the choice between different estimators in econometrics panel data analysis, was used to determine whether unique errors were correlated with the regressors. A positive outcome of this test indicates that the random effects estimator is inconsistent, which means that the fixed effects estimator should be preferred. Here, it indicated that random effect was appropriate for HIV incidence model, while

Table 1. Estimation outcomes of spatial lag models.

	Spill-over risk perspective		Influx risk perspective	
	IH Result (SE)	NH Result (SE)	IH Result (SE)	NH Result (SE)
MAIN				
Intercept	-0.3441** (0.1515)	/	-0.3567** (0.1514)	/
lnSF	0.0181 (0.0847)	0.0736 (0.0845)	0.0226 (0.0845)	0.0812 (0.0842)
lnPD	0.1239*** (0.0421)	0.1536*** (0.0414)	0.1246*** (0.0420)	0.1548*** (0.0412)
lnHRF	0.3146*** (0.0481)	0.3261*** (0.0479)	0.3147*** (0.0479)	0.3267*** (0.0477)
lnEL	-0.1695*** (0.0578)	-0.1660*** (0.0574)	-0.1624*** (0.0576)	-0.1563*** (0.0573)
SPATIAL				
ρ	0.7068*** (0.0480)	0.7417*** (0.0433)	0.7013*** (0.0474)	0.7360*** (0.0428)
LLH	270.2796	363.8884	271.5862	365.2544
Hausman	3.5900	24.6000***	2.9600	24.4400***

IH = HIV incidence model; NH = HIV prevalence model; SE = standard error: lnSF = socioeconomic factors; lnPD = population density; lnHRF = health resource factors; lnEL = education level; ρ = spatial autoregressive coefficient; LLH = log-likelihood; *p<0.1; **p<0.05; ***p<0.001.

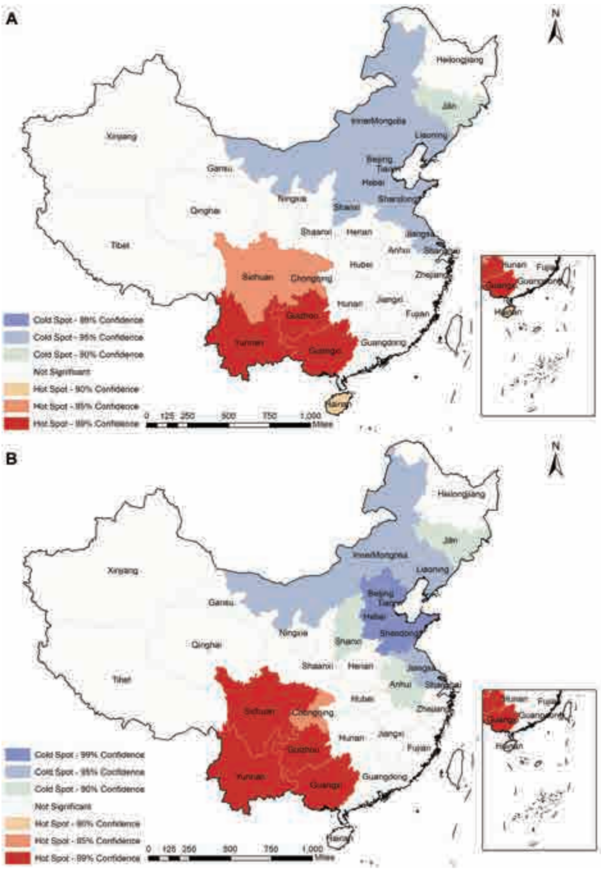

Figure 2. Hotspots of HIV incidence largely concentrated in the south-western provinces with coldspots located in the northern provinces. Statistical approach: local Getis Gi*. **A**) 2013; **B**) 2022.

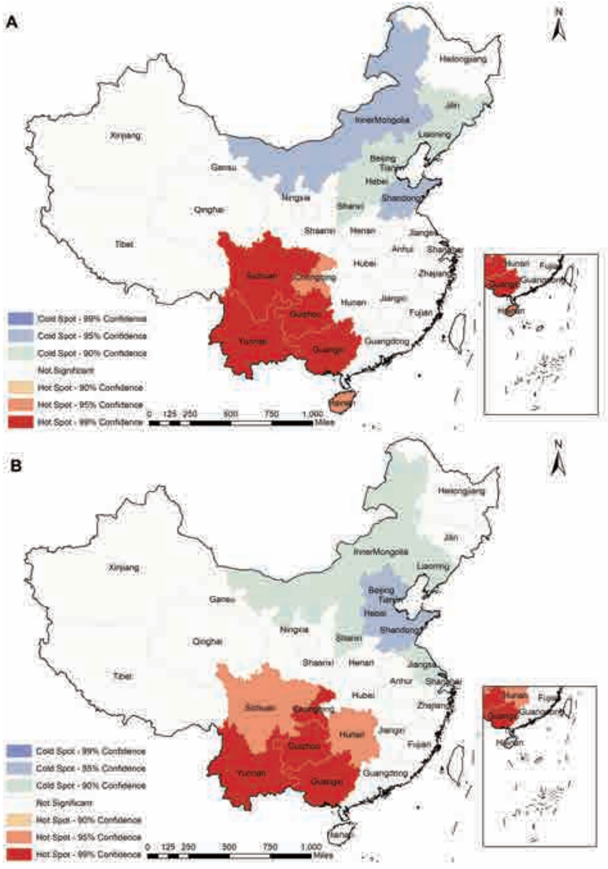

Figure 3. Hotspots of HIV prevalence largely concentrated in the south-western provinces with coldspots located in the northern provinces. Statistical approach: local Getis Gi*. **A**) 2013; **B**) 2022.

fixed effect was identified for HIV prevalence model. From the spill-over risk perspective, the spatial autoregression coefficient for HIV incidence model was 0.7068 ($p<0.001$), indicating that for each unit rise in HIV incidence in a province with large-scale population outflow, the average incidence in the destination provinces surged by 0.7068 units (logarithmic transformation applied to all variables). The HIV prevalence model also demonstrated a significant spatial spill-over effect, with a spatial autoregression coefficient of 0.7417 ($p<0.001$). From the influx risk perspective, one unit increase of HIV incidence in the province of origin significantly impacted such values in destination provinces (=0.7013, $p<0.001$). Specifically, a one-unit growth in the number of people living with HIV in the province of origin resulted in a corresponding rise of 0.7360 in the number of people living with HIV in the destination provinces. For a specific province *i*, when serving as the origin of population mobility with a 1-unit increase in HIV incidence, the resultant outflow contributes to an average unit, resulting in an increment of 0.7068 among the destination provinces. Conversely, when a province *i* functions as a destination, each unit increase in HIV incidence in other originating provinces would lead to an average unit rise of 0.7013 in *i*. This explanation is equally applicable to the HIV prevalence model.

The lnSF, obtained using the entropy method (Ding *et al.*, 2005), exhibited a positive but statistically insignificant effect on the HIV epidemic. In contrast, the linear effects of lnPD, lnHRF and lnEL were statistically significant at the 0.001 level. From the spill-over risk perspective, the elastic lnPD coefficients implied that for each unit increase in population density, the HIV incidence increased by 0.1239, assuming all other conditions remaining constant. In both the spill-over and influx perspectives, the negative lnEL coefficients suggested that a higher level of education was associated with lower HIV data.

Decomposition of spatial effects

The decomposition of spatial influences was presented in *Table S4*. The direct, spill-over, and total lnSF effects on the HIV levels were positive but statistically insignificant. In contrast, lnPD exhibited statistically significant positive, direct spill-over effects suggesting that an increase in population density in a given region not only exacerbated its own HIV epidemic but also contributed to a more severe HIV prevalence in other migration destination provinces. lnEL was negative and highly significant at the 0.001 level, both with respect to spill-over and influx risk, indicating that increased investment in education in a given region should not only be able to effectively reduce its own HIV epidemic, but also the infection rates in neighbouring provinces with frequent population mobilities.

Spatial lag models and subgroup analysis

In both the adjacency and distance perspectives (Table 2), the estimation results of the spatial coefficients were consistent with those in the spill-over and influx risk perspectives thereby initially confirming the robustness of the base SLMs.

The results of subgroup analysis for hotspot-regions (Sichuan, Chongqing, Guizhou, Yunnan, Guangxi, and Hunan), coldspot-regions (Inner Mongolia, Jilin, Liaoning, Beijing, Tianjin, Hebei, Shaanxi, and Jiangsu) and the remaining regions, *i.e.* the other 17 provinces, are presented in Table 3. In each scenario, the estimated values for the hotspot-regions ranged from 0.2457 to 0.2832, indicating that the spatial spill-over effects caused by population mobility in areas with more serious HIV epidemics were noticeably lower than in the overall situation. Meanwhile, the spatial autocorrelation coefficients for the coldspot-regions and the remaining regions ranged from 0.5301 to 0.7008, exhibiting comparable results to the overall situation, with only slight differences. This indicates that south-western China has its own unique drivers for becoming HIV hotspot areas. In addition to population mobility, rampant drug use (Li *et al.*, 2014), frequent commercial sex (Drake *et al.*, 2016), low levels of economic development and the increasing proportion of ceratain high-risk groups, such as Men who have Sex with Men (MSM) (Liu *et al.*, 2013) may be the possible reasons.

Discussion

This study revealed significant spatial spill-over effects and influx risks caused by population mobility against the background of HIV epidemics. Notably, Sichuan, Chongqing, Hunan, and Guangdong were identified as areas facing severe HIV epidemics coupled with high levels of population outflow. In contrast, regions such as Beijing, Jiangsu, Shanghai, and Anhui exhibited relatively

Table 2. Robustness analysis from adjacency and distance perspectives.

	Adjacency perspective		Distance perspective	
	IH Result (SE)	NH Result (SE)	IH Result (SE)	NH Result (SE)
MAIN				
Intercept	-0.3165** (0.1555)	/	-0.2943 (0.1505)	/
lnSF	0.0288 (0.0868)	0.0739 (0.0863)	0.0447** (0.0828)	0.0897 (0.0811)
lnPD	0.1182*** (0.0430)	0.1464*** (0.0422)	0.1048*** (0.0410)	0.1397*** (0.0398)
lnHRF	0.3266*** (0.0490)	0.3395*** (0.0489)	0.2862*** (0.0470)	0.3019*** (0.0461)
lnEL	-0.1526*** (0.0595)	-0.1462** (0.0589)	-0.1886** (0.0561)	-0.1601*** (0.0550)
SPATIAL				
ρ	0.5726*** (0.0438)	0.6157*** (0.0403)	0.7802*** (0.0451)	0.8077*** (0.0395)
LLH	262.0693	355.0350	281.0926	380.1507
Hausman	1.5700	31.1000***	2.5300	28.8400***

IH = HIV incidence model; NH = HIV prevalence model; SE = standard error; lnSF = socioeconomic factors; lnPD = population density; lnHRF = health resource factors; lnEL = education level; ρ = spatial autoregressive coefficient; LLH = log-likelihood; *p<0.1; **p<0.05; ***p<0.001.

mild HIV prevalence but experienced substantial population inflow. Given the correlation of HIV and population mobility, it is essential to implement tailored policies.

HIV epidemics from the population mobility perspective

Currently, numerous studies have demonstrated significant spatial spill-over effects and spatial clustering in HIV prevalence (Mosnier *et al.*, 2019; Qian *et al.*, 2014), as evidenced by Moran's *I* (Yuan *et al.*, 2023), Local Getis Gi* statistics (Peng ZH, 2011; Wang *et al.*, 2016), and spatial autoregression coefficients results (Das *et al.*, 2019). In studies addressing population mobility, Hu *et al*. (2020) collected 85 days of data from a social networking app for MSM in mainland China, finding that five mobility centres (Guangdong, Beijing, Shanghai, Zhejiang, and Jiangsu) accounted for 57.2% of the total population flow of MSM in China, highlighting regional migration heterogeneity within this high-risk HIV group. Utilizing the network model based on transmission and molecular chain characterization, Yuan *et al.* (2023) concluded that even after diagnosis, HIV patients continued to travel frequently across cities and provinces, thereby contributing strongly to the spread of the HIV virus. Duncan et al. combined self-reported spatial mobility data of MSM with real GPS location data and concluded that MSM were more likely to engage in sexual activity in areas different from their places of residence, suggesting that the spatial mobility of high-risk groups may be one of the factors driving the increasing rates of HIV in the destination regions (Duncan *et al.*, 2020).

Treatment for prevention

It would be useful to promote a "treatment as prevention" strategy that includes early diagnosis and timely treatment to reduce community viral load (Nguyen *et al.*, 2011) and ensure that healthcare facilities provide accessible medical services for migrant populations. Offer necessary economic support to migrant populations, such as transportation subsidies and reductions in medication costs are needed to ensure they can consistently access treatment. Development of a robust data collection system would help to regularly assess the implementation effectiveness and coverage of the "treatment as prevention" strategy, ensuring that the health needs of migrant populations are met. This approach should also utilize data analysis to identify high-risk groups within the migrant population and make timely adjustments to intervention strategies based on these findings.

Recommended policies

Consequently, policies implemented with respect to population mobility should be useful and customized counselling and testing services should be developed to meet the needs of migrant populations, ensuring that these services are accessible and culturally sensitive (Obeagu *et al.*, 2023). There is a need for conduct-targeted health education initiatives aimed at increasing awareness among migrant populations regarding HIV transmission routes, preventive measures and treatment options and the use of self-testing tools to empower individuals in migrant populations to easily access HIV testing and status awareness should be promoted. It would also be essential to adhere strictly to privacy protection regulations when providing services and establish transparent feedback mechanisms to involve migrant populations in service design and evaluation. Finally, structural barriers to service access must be eliminated to ensure that migrant populations have equitable access to HIV treatment and prevention services regardless of their residency status (Körner, 2007). Policymakers should solicit the views of migrant populations broadly to ensure that policies are fair, just and respectful of each individual's rights (Ibrahim *et al.*, 2008).

Further, integrated public health strategies that promote interprovincial cooperation should be instituted to provide ongoing HIV care and support for migrant populations (Pai *et al.*, 2018). When implementing such policies, improper collection and use of data could lead to breaches of privacy, adversely affecting the safety and freedom of migrant populations. Adherence to strict data protection standards when collecting personal health data is needed to ensure transparency regarding how this information will be used, thereby enabling migrant populations to understand the implications of sharing their information.

Limitations

The Baidu Migration Index only provided macro-level horizontal comparable data, and the conjoint-analysis of micro-level population mobility patterns, especially among the high-risk groups, may facilitate a more precise assessment. However, research into the quantification and utilisation of such population mobility patterns, both from macro and micro perspectives remains deficient. Furthermore, the dataset has only been available online for a limited period, which may have led to an overestimation of the overall level of population mobility when applying the spatial weighting matrix. The temporal attributes of the data precluded the analysis of population mobility on HIV epidemics specific during

Table 3. Subgroup analysis of Hotspot-, Coldspot-, and Remaining-regions.

	IH ρ (SE)	NH ρ (SE)
Spill-over risk perspective		
Hotspot-regions	0.2457*** (0.1223)	0.2820** (0.1214)
Coldspot-regions	0.5301*** (0.0940)	0.6000*** (0.0847)
Remaining-regions	0.6423*** (0.0651)	0.7008*** (0.0580)
Influx risk perspective		
Hotspot-regions	0.2469** (0.1225)	0.2832** (0.1216)
Coldspot-regions	0.5314*** (0.0937)	0.6034*** (0.0820)
Remaining-regions	0.6248*** (0.0635)	0.6852*** (0.0570)

Note: IH = HIV incidence model; NH = HIV prevalence model; SE = standard error; the adjusted covariates were lnSF (socioeconomic factors), lnPD (population density), lnHRF (health resource factors), and lnEL (education level); ρ = spatial autoregressive coefficient; *p<0.1; **p<0.05; ***p<0.001.

a certain holiday. Finally, the impact of undocumented populations may have further contributed to estimation bias in the models.

Conclusions

The study demonstrated that, from a spill-over perspective, each increase of HIV incidence in the original province resulted in a unit average incidence rate increment of 0.7068 in destination provinces. Furthermore, analogous statistically significant effects of population mobility on local HIV epidemics were identified from influx perspectives, and the impact of this mobility on HIV epidemics was found to be inconsistent when examined through subgroup analyses of hotspots and coldspots. In consideration of these findings, the development of bespoke, accessible services in a culturally sensitive and migrant-specific manner would be useful. Finally, the implementation of a comprehensive “treatment as prevention” strategy, and the removal of structural barriers to equitable service access irrespective of residency status may be considered as feasible policies for HIV prevention from a population mobility perspective.

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Online supplementary materials

Table S1. Moran's I of lnIH and lnNH in spill-over and influx risk perspectives.

Table S2. The cross-sectional dependency test and panel unit root analysis.

Table S3. Model selection test results of panel data models.

Table S4. Decomposition of spatial effects.

Figure S1. The spatial distribution of average population mobility indexes. A) population outflow indexes; B) population inflow indexes.

Figure S2. The spatial distribution of HIV incidence. A) 2013; B) 2022.

Figure S3. Moran's I scatterplot in spillover risk perspective.

Figure S4.Moran's I scatterplot in influx risk perspective.