Estimation of HIV Incidence Rate in Thailand Using the Bayesian Hierarchical Approach

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ABSTRACT

HIV infection remains a major public health problem in Thailand. Disease mapping and statistical modeling of incidence/prevalence plays important roles in epidemiology to display the spatial risks on a map and explain the causal pattern between disease outcomes and potential risk factors. The Bayesian hierarchical method was proposed to fit with the HIV mapping data and to cope with the HIV modeling incidence among risk factors. The aim of the study was to estimate the HIV incidence rate in disease mapping application using the Bayesian hierarchical model. A useful source of informative data was retrieved from the NAP (National AIDS Program), collected by the National Health Security Office (NHSO) in Thailand 2017. The best fitted model was the interaction effect model. The top five provinces with the highest risk (incidence rate >8.9%) comprised Samut Prakarn (35.83%), Nakhon Nayok (26.28%), Pathumthani (13.20%), Phuket (12.38%) and Chumphon (12.28%), respectively. The Bayesian model could analyze HIV infection rate well among different areas. Several risk factors were able to explain the high risk areas with the relative risk estimates for HIV infection.

Keywords: HIV infection, disease mapping, HIV incidence rate, bayesian hierarchical model, Interaction effect model

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Introduction

HIV remains a major public health problem. In 2016, an estimated 36.7 million people worldwide were living with HIV. Of these, 1.8 million people were new HIV cases, decreasing from 2.1 million in 2015. Similarly, in Thailand, an estimated 450,000 people were living with HIV and 6,400 people new HIV cases. About 90% of all new HIV cases are caused by unsafe sex and unsafe injecting drug use is the second cause. The main populations at risk are men who have sex with men (MSM), male and female sex workers and injecting drug users including spouses in these populations. Around 50% of all new HIV infection cases involved men who have sex with men (including male sex workers and transgender people).[1] Accordingly, the HIV epidemic is still ongoing. Changing social and economic conditions as well as the expansion of the city are factors influencing the incidence or prevalence of HIV infection. The provinces are filled with entertainment venues, hotels, brothels, pubs, cafes, massage parlors and karaokes linked to economic prosperity and tourists in provinces.[2] These places often host many vulnerable populations, resulting in a higher incidence or prevalence of HIV than other provinces.

Visualization of disease distribution is an important procedure in understanding disease occurrence. The use of maps in the context of disease distribution has developed rapidly in the public health sector.[3] Disease mapping studies have become a routine application within geographical epidemiology and are typically analyzed within a Bayesian hierarchical model formulation. Bayesian analysis is an investigation of unknown parameters of statistical models using probability that consists of a likelihood function based on observed data and prior distribution based on previous data. All parameters of the model are random quantities that depend on the previous event parameter. The Bayesian hierarchical model is a statistical model for multiple levels (hierarchical form) using the Bayesian method. The Bayesian hierarchical model constructs the parameter estimation of each analytical unit by borrowing data from all analytical units. For over-dispersion cases, the classical regression model describes the variance slightly but the unexplained variance is defined as heterogeneity effects or spatial correlation effects for the Bayesian hierarchical model. The study of Zhao used Bayesian model to predict the incidence of cervical cancer in Songkhla, Thailand. The results showed that the incidence declined at the province level. The trend of cervical cancer varies according to the relevant factors of each district and estimated incidence of the Bayesian approach was more stable.[4] For chronic infectious diseases like HIV/AIDS,

Mohebbi introduced Bayesian techniques as a suitable method for the smooth analysis for HIV/AIDS because data involve complex and hierarchical structures.[5] Lange N., et al. conducted a fully Bayesian analysis of the progression of HIV incidence using longitudinal CD4 T-cell numbers with a high-dimensional hierarchical model. They found that the hierarchical Bayes modeling framework together with the stochastic relaxation method of the Gibbs sampler was a highly flexible environment within to pose, adapt, and help resolve many of the interdependent scientific questions arising from very different sources of knowledge and expertise in areas.[6]

In this study, we placed the risk factors associated with HIV in the model using the Bayesian hierarchical approach to explain the HIV infection rate in Thailand and showed the distribution of the HIV incidence rate using disease mapping.

Method

1. Data and source of data

This study was reviewed and approved according to the Standard Operating Procedures of Ethics Review Committee for Human Research, Faculty of Public Health, Mahidol University 22 January 2018, number 10/2561.

In this study, HIV/AIDS data for 2017 from the NAP database support, under the NHSO in cooperation with the MOPH-CDC (Thai Ministry of Public Health and Collaboration Center for Disease Control and Prevention, USA) were used.

The information consisted of the number of people receiving blood tests and those first diagnosed as HIV positivefor each province totaling 77 provinces. Data included HIV information by risk factor such as the sociodemographic factors including age and sex, type of people receiving medical examination such as MSM, sex workers, people who inject drugs (PWID), husbands of a pregnant woman infected with HIV, partners of sero discordance, prisoners, people born to HIV positive mothers, pregnant women (ANC), suspected HIV infection/symptoms of HIV, risk behavior factors such as unsafe sex, mother-to-child transmission, exposure to blood or secretions containing HIV and sharing needle.

2. Bayesian hierarchical modeling

Let y_i and N_i represent the number of HIV cases and population at risk having blood tests in a province i, (i=1,2,3,...,77), respectively. We assume that y_i is conditional on μ_i and the Poisson distribution with mean μ_i where $\mu_i = N_i \exp(\psi_i)$ is written as

$$y_i \mid \mu_i \sim \text{Poisson}(N_i \exp(\psi_i)) \quad (1)$$

where $\psi_i = X_i'\beta + v_i$, X_i' represents the vector of area-specific covariates for HIV, β as a vector of coefficients that are obtained

by regression, v_i as a random effect with apprehending residual in province *i*, which is the unstructured heterogeneity that compiles the effect of covariates in an unknown province. The province *i* has the relative risk as $r_i = \exp(\psi_i)$. Then specification of the log-link function is

$$\log(\mu_i) = X_i'\beta + v_i + \log(N_i) \quad (2)$$

where $\log(N_i)$ is an offset term.

3. Parameters estimation

Parameters estimation using the Bayesian hierarchical approach was an important step of data analysis, requiring the prior distribution of parameter β denoted by $P(\beta)$ and the Poisson likelihood function based on the observed counts, leading to the posterior mean at last and the prior distribution for *v* (notation as P(*v*)). We supposed $P(\beta)$ as the normal distribution with mean 0 and variance τ_β^2, P(*v*) as the normal distribution with mean 0 and variance τ_v^2, which τ_v^2 as inverse-gamma distribution. thus, we derived the posterior distribution as

$$P(\beta, v, \tau_\beta^2, \tau_v^2 \mid y, N, r) \propto P(y, N, r \mid \beta, v, \tau_\beta^2, \tau_v^2) P(\beta) P(v). \quad (3)$$

The Bayesian model for these data comprised

$$\log(\mu_i) = \beta_0 + \beta_k X_{ik}' + v_i + \log(N_i) = \beta_k X_{ik}' + \tau_i + \log(N_i), \quad (4)$$

$$\beta_0, \beta_1, \ldots, \beta_k \sim N(0, \sigma^2) \quad (5)$$

$$\tau_i \sim \text{i.i.d. } N(\beta_0, \sigma_{\text{id}}^2) \quad (6)$$

$$\sigma_{\text{id}}^2 \sim \text{InvGamma}(alpha, beta). \quad (7)$$

The model had three main parameters of interest: regression coefficients β_0, β_k and variance components σ_{id}^2. β_0 was actually a hyperparameter because it constituted the mean parameter of the prior distribution for random effect τ_i. The province random effects τ_i were considered nuisance parameters. We used normal prior for regression coefficients and group level identified by id variable and the inverse-gamma prior for the variance parameter. We used Markov Chain Monte Carlo method (MCMC) via Metropolis-Hastings algorithm for parameters estimation.

We used the deviance information criterion (DIC) for the Bayesian model selection. DIC was applied to determine the impact of the complex form or the hierarchical model with a high dimension because to calculate and interpret the Bayes factors was difficult. The DIC was based on the deviance posterior mean, $\bar{D} = E_{\mu|y}(D)$. It represented the sum of the deviance posterior mean and proficient number of parameters, p_D, and could be written as $DIC = \bar{D} + p_D$ where $p_D = E_{\mu|y}(D) - D(E_{\mu|y}(\mu))$,

$D(E_{\mu|y}(\mu))$ as the evaluation of deviance at the posterior mean.[7] The lowest DIC value was indicated for the best fitted model.

Results

The observed counts of newly diagnosed HIV incidence based on the 77 provinces totaled 33,845 individuals of the number of people receiving medical examinations with blood tests of 952,123 persons, about a 3.55% incidence rate. In all, 23,333 males and 10,512 females were HIV positive. The most common were aged 25 to 49, 20 to 24 and 50 and above at 22,280, 5,126 and 4,064 individuals, respectively.

We conducted a screening of potential risk factors or covariates using univariate mixed effect Poisson regression, see Table 1. Covariates in this study were not directly affected at the individual level, but instead on the provincial level, so the required variables in the model were established at a p-value <0.15. We found that the significant variables were being male, age groups, MSM, PWID, husband of a pregnant woman with HIV, prisoners, pregnant women (ANC), unsafe sex, mother-to-child transmission, exposure to blood or secretions containing HIV and sharing needles. The remaining variables such as sex worker, partner of sero discordance and people born to HIV positive mothers were excluded from the analysis.

Table 1 Screening of covariates using univariate mixed effect Poisson regression

Covariates	z	p-value
Sex (male)	46.95	0.000
Age (20-24 years)	15.73	0.000
Age (25-49 years)	34.66	0.000
Age (50 years and above)	-11.02	0.000
MSM	1.45	0.140
Sex workers	0.43	0.671
PWID	2.96	0.003
Husbands of a pregnant woman with HIV	4.34	0.000
Partners of sero discordance	0.68	0.498
Prisoners	1.74	0.081
People born to HIV positive mothers	0.46	0.648
Pregnant women (ANC)	5.41	0.000
Unsafe sex	14.98	0.000
Mother-to-child transmission	3.14	0.002
Exposure to blood or secretions containing HIV	2.12	0.034
Sharing needles	2.65	0.008

We proceeded to identify significant variables while forming the initially additive model (main effect model). We were aware of synergism and antagonism types of interaction effect terms and attempted to build multiplication effects among all predictors using both significant and no significant variables in the candidate models. The candidate fitting models were compared using the DIC. We found that the interaction effect model could fit data better than the additive model with lower values of DIC (5911.830). Due to the limited numbers of printing spaces, the additive model and the interaction effect model showed the comparison of candidate models; see details in Table 2.

Table 2 Comparison of the additive and the interaction effect models

Model	σ_v^2	DIC
Additive model		
$\log(\mu_i) = \beta_0 + \beta_1 gender_i + \beta_2 age2_i + \beta_3 age3_i + \beta_4 age4_i + \beta_5 MSM_i + \beta_6 PWID_i + \beta_7 husband_i + \beta_8 prisoner_i + \beta_9 ANC_i + \beta_{10} unsafe_i + \beta_{11} mtc_i + \beta_{12} contact_i + v_i + \log(N_i)$	0.0919	6120.656
Interaction effect model (final model)		
$\log(\mu_i) = \beta_0 + \beta_1 gender_i + \beta_2 age2_i + \beta_3 age3_i + \beta_4 age4_i + \beta_5 MSM_i + \beta_6 PWID_i + \beta_7 husband_i + \beta_8 prisoner_i + \beta_9 ANC_i + \beta_{10} unsafe_i + \beta_{11} mtc_i + \beta_{12} contact_i + \beta_{13} SW_i + \beta_{14} gender_i * age2_i + \beta_{15} gender_i * age3_i + \beta_{16} gender_i * age4_i + \beta_{17} prison_i * PWID_i + \beta_{18} MSM_i * unsafe_i + \beta_{19} SW_i * age2_i + \beta_{20} SW_i * age3_i + \beta_{21} SW_i * age4_i + v_i + \log(N_i)$	0.0802	5911.830

Note gender = variable of sex, *age2* = variable of aged 20-24 years, *age3* = variable of aged 25-49 years, *age4* = variable of aged 50 years and above, *PWID* = variable of people who inject drugs (PWID), *husband* = variable of husband of a pregnant woman with HIV, *prisoner* = variable of prisoners, *ANC* = variable of pregnant women (ANC), *unsafe* = variable of unsafe sex, *mtc* = variable of mother-to-child transmission, *contact* = variable of exposure to blood or secretions containing HIV, *needle* = variable of sharing needles, *MSM* = variable of men who have sex with men (MSM) and *SW* = variable of sex workers

The null model could predict the heterogeneity variance as a value equal to 0.4766. However, when the additive model was considered with many covariates indicating causal relationships with outcomes, the heterogeneity variance significantly decreased to 0.0919, about 80.7% from null model. Similarly, the interaction effect model could reduce the heterogeneity variance of mean to 0.0802, about 83.2% from the null. Therefore, the heterogeneous situation still existed and appeared among the covariates and heterogeneity was confirmed with a heterogeneity variance greater than zero.

The incidence relative rate (IRR), MCMC standard error (MCSE) and 90% credible interval of IRR are presented in Table 3. The estimated HIV infection rate for males was 1.8153 times higher than that of females, holding other predictors constant. Regarding age groups, the estimated HIV incidence rates for individuals aged 25 to 49 years and 20 to 24 years were 2.1748 and 1.1417 times higher than those aged 0 to 19 years respectively, whereas the estimated HIV infection rate for those aged 50 years and above was 0.9192 times lower than those aged 0 to 19 years. The estimated HIV incidence rates for MSM, PWID, sex workers and the prisoners were 1.0014, 1.0007, 1.0049 and 1.0005 times higher than those of the other groups respectively. Likewise, for the husband of a pregnant woman with HIV, unsafe sex, mother-to-child transmission and exposure to blood or secretions containing HIV groups had estimated HIV incidence rates of about 1.0026, 1.1906, 1.0262 and 1.0102 times higher than those of the other groups, respectively. On the other hand, the estimated HIV infection rate for pregnant women (ANC) group was 0.9973 times lower than those of the other groups.

Additionally, the estimated HIV incidence rates for males aged 25 to 49 years, males aged 20 to 24 years and males aged 50 years and above groups were 3.6536, 2.8464 and 1.1912 times higher than that of males aged 0 to 19 years' group, respectively. Sex workers aged 25 to 49 years and sex workers aged 20 to 24 years' groups had estimated HIV incidence rates at about 2.1932 and 1.1472 times higher than those of sex workers aged 0 to 19 years' group, respectively. However, the estimated HIV incidence rates for sex workers aged 50 years and above were 0.9259 times lower than those of sex worker aged 0-19 years. Furthermore, the estimated HIV incidence rate for PWID, prisoners and MSM in the unsafe sex groups were 1.0009 and 1.1918 times higher than those of other groups.

Table 3 Incidence rate ratio (IRR), MCMC standard error (MCSE) and 90% credible interval of IRR for risk factors from the interaction model (final model)

Risk Factors	IRR	MCSE	90% Credible Interval of IRR
Sex			
- Male	1.8153	0.00010	(1.8143, 1.8163)
- Female	1	-	-
Age			
- 0-19 years	1	-	-
- 20-24 years	1.1417	0.00005	(1.1412, 1.1422)
- 25-49 years	2.1748	0.00012	(2.1732, 2.1765)
- 50 years and above	0.9192	0.00010	(0.9183, 0.9200)
MSM	1.0014	0.00025	(0.9996, 1.0028)
PWID	1.0007	0.00025	(0.9991, 1.0026)
Sex worker	1.0049	0.00004	(1.0047, 1.0051)
Husband	1.0026	0.00014	(1.0016, 1.0034)
Prisoner	1.0005	0.00014	(0.9994, 1.0016)
Pregnant woman (ANC)	0.9973	0.00004	(0.9971, 0.9978)
Unsafe sex	1.1906	0.00005	(1.1901, 1.1909)
Mother-to-child transmission	1.0262	0.00014	(1.0252, 1.0269)
Exposure to blood or secretions containing HIV	1.0102	0.00018	(1.0088, 1.0114)
Sex*Age			
- Male*0-19 years	1	-	-
- Male*20-24 years	2.8464	0.00024	(2.8445, 2.8483)
- Male*25-49 years	3.6536	0.00028	(3.6517, 3.6555)
- Male*50 years and above	1.1912	0.00008	(1.1906, 1.1918)
Sex worker*Age			
- Sex worker *0-19 years	1	-	-
- Sex worker *20-24 years	1.1472	0.00003	(1.1469, 1.1474)
- Sex worker *25-49 years	2.1932	0.00008	(2.1923, 2.1941)
- Sex worker *50 years and above	0.9259	0.00004	(0.9253, 0.9265)
PWID*Prisoner	1.0009	0.000003	(1.0008, 1.0009)
MSM*Unsafe sex	1.1918	0.000026	(1.1916, 1.1920)

We found the top five provinces with the highest risk (incidence rate >8.9%) were Samut Prakarn (incidence rate = 35.83%), Nakhon Nayok (incidence rate = 26.28%), Pathumthani (incidence rate = 13.20%), Phuket (incidence rate = 12.38%) and Chumphon (incidence rate = 12.28%). Disease mapping was based on estimated HIV infection rate. We considered disease mapping in Figure 1; dark red indicated the province with the highest risk, while orange and green provided a decreased rate.

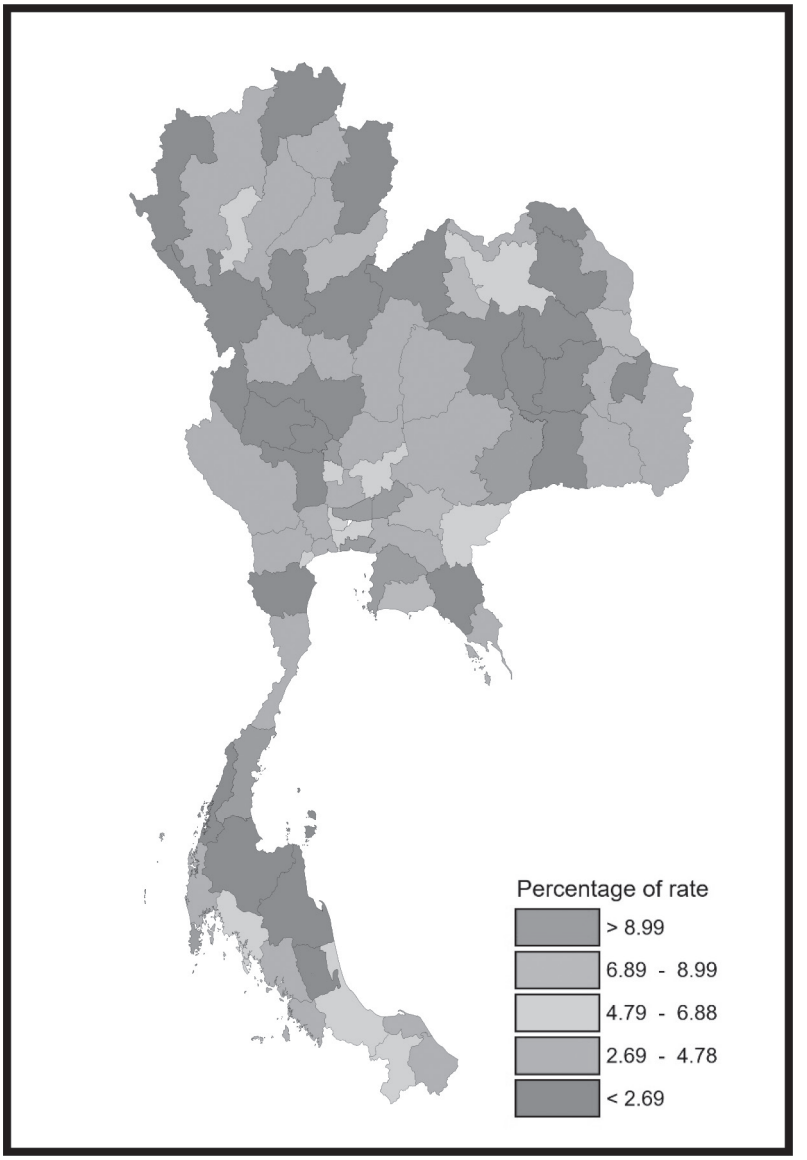

Figure 1 Map of percentage of incidence rate for HIV in Thailand, 2017

Discussion

The Bayesian model could analyze HIV incidence rates in different areas and provided reliable models with fine estimated values. Although the results showed the highest HIV rates of provinces from this study may be similar but unlike the reports of the Bureau of Epidemiology in Thailand, they showed the behavioral risk factors at the individual level, not area level. Some different results may have been due to quite different measurements, different data and data sources, different target populations and different duration of data collection. Sources of data in this study provided information concerning newly diagnosed HIV individuals (incidence) of the people who came to receive medical treatments with blood test examination in health care centers. However, the Bureau of Epidemiology used the accumulated people with HIV (prevalence) in the midyear population.

The estimated HIV incidence rate for males (1.8153 times) was greater than that of the female group. Regarding age group, the highest estimated HIV incidence rate was that of those aged 25 to 49 years (2.1748 times) and those aged 20 to 24 years (1.1417 times) when compared with those aged 0 to 19 years. However, those aged 50 years and above had an estimated HIV incidence rate (0.9192 times) lower than that of those aged 0 to 19 years. New HIV and sexually transmitted infections increased among those aged 25 to 49 and 20 to 24 years. Likewise, males aged 25 to 49 years, males aged 20 to 24 years and males aged 50 years and above had estimated HIV incidence rates (3.6536, 2.8464 and 1.1912 times, respectively) higher than those of males aged 0 to 19 years. MSM, PWID, sex workers and prisoner groups had high estimated HIV incidence rates (1.0014, 1.0007 and 1.0049 times) when compared with other groups, because these groups were in key affected populations. The estimated HIV incidence rate for MSM was 1.1918 times higher than other unsafe sex groups. The high vulnerability to HIV in the MSM group was because unprotected anal sex carries a higher risk of transmission than vaginal sex.

The top five provinces with the highest risk (incidence rate >8.9%) were Samut Prakarn (incidence rate = 35.83%), Nakhon Nayok (incidence rate = 26.28%), Pathumthani (incidence rate = 13.20%), Phuket (incidence rate = 12.38%) and Chumphon (incidence rate = 12.28%) respectively. Some provinces had fewer people who came to receive medical treatments with blood test examination but detected HIV status was found among those few people with blood tests, so the higher HIV incidence rate was inflated above those of provinces with a high HIV incidence rate.

Recommendations

The recommendations for further study emphasize issues as described below.

1. In this study, we used the dependent variable as incidence rate with Poisson distribution with offset terms. The alternative dependent variable may be the standardized infection rate with normal distribution, for a more comparable study.

2. Placing the spatial variable in the model for a more comprehensive and reliable estimate should be considered.

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การประมาณอัตราการติดเชื้อเอชไอวีในประเทศไทยโดยใช้วิธีการลำดับชั้นแบบเบย์

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บทคัดย่อ

การติดเชื้อเอชไอวียังคงเป็นปัญหาสาธารณสุขที่สำคัญในประเทศไทย การทำแผนที่โรค และการสร้างแบบจำลองทางสถิติของอุบัติการณ์/ความชุก มีบทบาทสำคัญในด้านการระบาดวิทยา เพื่อแสดงความเสี่ยงเชิงพื้นที่บนแผนที่โรคและอธิบายถึงรูปแบบเชิงสาเหตุระหว่างผลลัพท์ของโรคที่มีปัจจัยเสี่ยงที่อาจเกิดขึ้น วิธีการลำดับชั้นแบบเบย์ได้รับการเสนอให้เหมาะสมกับข้อมูลเอชไอวีและการสร้างแบบจำลองอุบัติการณ์ของเอชไอวีวัตถุประสงค์ของการศึกษาเพื่อประมาณค่าอัตราการติดเชื้อเอชไอวีโดยใช้แบบจำลองลำดับชั้นเบย์ (Bayesian hierarchical model) ซึ่งใช้แหล่งข้อมูลจากโปรแกรมสำหรับการบันทึกข้อมูลการให้บริการดูแลรักษาผู้ติดเชื้อเอชไอวีและผู้ป่วยเอดส์ (National AIDS Program) เก็บรวบรวมโดยสำนักงานหลักประกันสุขภาพแห่งชาติ (สปสช) พ.ศ. 2560 แบบจำลองที่ดีที่สุด คือ แบบจำลองแบบมีอิทธิพลร่วม (Interaction effect model) โดยจังหวัดที่มีความเสี่ยงที่สุด 5 อันดับแรกของอัตราอุบัติการณ์การติดเชื้อเอชไอวี ได้แก่ จังหวัดสมุทรปราการ (35.83%) นครนายก (26.28%) ปทุมธานี (13.20%) ภูเก็ต (12.38%) และชุมพร (12.28%) ตามลำดับ แบบจำลองแบบเบย์สามารถวิเคราะห์อัตราอุบัติการณ์การติดเชื้อเอชไอวีได้ในพื้นที่ที่แตกต่างกันได้ ซึ่งมีปัจจัยเสี่ยงหลายประการที่สามารถอธิบายเกี่ยวกับพื้นที่ที่มีความเสี่ยงสูงด้วยการประมาณค่าความเสี่ยงสัมพัทธ์สำหรับการติดเชื้อเอชไอวีได้

คำสำคัญ: การติดเชื้อเอชไอวี การทำแผนที่โรค อัตราอุบัติการณ์การติดเชื้อเอชไอวี แบบจำลองลำดับชั้นแบบเบย์ แบบจำลองแบบมีอิทธิพลร่วม

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