

Original Article

Asian Pacific Journal of Tropical Medicine

doi: 10.4103/apjtm.apjtm_248_26

Bayesian spatial modelling and landscape correlates of snakebite risk in Fuzhou, China, 2021–2025

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ABSTRACT

Objective: To evaluate whether combining Bayesian spatial modelling with landscape-ecological analysis could identify high-risk townships and account for their spatial clustering in Fuzhou, Fujian Province, China.

Methods: In this retrospective study, patients with clinically confirmed venomous snakebite treated at a single provincial tertiary referral centre in Fuzhou between January 2021 and December 2025 were included in descriptive demographic, temporal, and taxonomic analyses. In addition, patients with concordant township-level residence and bite location were included in spatial analyses. Five-year cumulative incidence per 100 000 population was calculated for each of 141 townships. A Besag-York-Mollié 2 (BYM2) model was used to obtain smoothed relative risks, and Global Moran's I and Getis-Ord G_i^* statistics assessed spatial clustering and hotspots. Associations between landscape metrics and township-level case counts were examined using negative binomial regression with log population included as an offset.

Results: A total of 741 patients were eligible for this retrospective analysis, and 560 of them were included in spatial analyses. Viperidae accounted for 589 of 741 cases (79.49%); patients aged 40–79 years accounted for 85.02% of cases, with a modest male predominance (1.28:1). Bayesian-smoothed incidence showed significant spatial clustering (Moran's $I=0.322$, $P=0.001$), and Getis-Ord G_i^* analysis identified 13 hotspot townships, with smoothed relative risks ranging from 3.40 to 22.16. Forest connectivity (COHESION $IRR=3.37$, 95% CI 1.72–6.59) was positively, and forest patch isolation (ENN_MN $IRR=0.59$, 95% CI 0.49–0.72) inversely, associated with incidence; cropland shape complexity (LSI $IRR=1.48$, 95% CI 1.22–1.80) was also positively associated. These landscape covariates accounted for the spatial structure identified

by BYM2, with no significant residual autocorrelation in model residuals (Moran's $I=-0.110$, $P=0.968$).

Conclusions: Landscape configuration, particularly forest connectivity and cropland edge complexity, is statistically associated with the spatial distribution of snakebite risk in Fuzhou and appears statistically sufficient to account for the clustering identified by Bayesian spatial smoothing. These findings, while ecological and correlational rather than causal, offer a replicable framework for prioritising township-level snakebite prevention resources.

KEYWORDS: Snakebite; Spatial epidemiology; Bayesian spatial modelling; Landscape ecology; Risk assessment

Summary

Question: Can Bayesian spatial modelling combined with landscape ecological analysis identify high-risk areas and explain spatial variation in snakebite risk?

Findings: In this retrospective observational study of 741 clinically confirmed snakebite cases in Fuzhou, China, Getis-Ord G_i^* analysis of Bayesian-smoothed incidence identified 13 hotspot townships, and landscape configuration was significantly associated with township-level snakebite risk.

Meaning: Integrating Bayesian spatial modelling with landscape ecology may improve fine-scale snakebite risk assessment and support targeted prevention strategies.

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How to cite this article: Gao G, Zhu QT, Zhao YM, Chen YL, Wang SJ. Bayesian spatial modelling and landscape correlates of snakebite risk in Fuzhou, China, 2021–2025. Asian Pac J Trop Med 2026; 19(11): 486–496.

Article history: Received 11 May 2026 Revision 23 September 2026
Accepted 13 October 2026 Available online 16 October 2026

1. Introduction

Snakebite envenoming remains a major global public health challenge and was classified as a neglected tropical disease by the World Health Organization (WHO) in 2017. Approximately 5.4 million snakebites occur worldwide annually, causing 1.8–2.7 million envenomings and 81 000–137 000 deaths, alongside permanent disability, chronic health consequences, and substantial socioeconomic burden[1–4]. The WHO global strategy for snakebite prevention and control emphasises identifying high-risk populations and developing targeted, localised prevention[5].

China harbours high snake diversity, and snakebite remains an important public health concern in southern regions[6,7]. Existing Chinese studies have largely characterised clinical features, epidemiological patterns, and patient outcomes[8–11], while the spatial structure of risk and the ecological mechanisms that may generate it remain insufficiently examined. Because prevention is implemented at local administrative levels, fine-scale risk assessment is essential; yet snakebite is a rare, sporadic event, and crude incidence rates calculated for small geographic units are often unstable due to random variation[12]. Bayesian spatial models address this problem directly, incorporating spatial dependence and uncertainty to yield more reliable small-area risk estimates[13,14].

Identifying where risk concentrates; however, is only the first step; effective prevention also requires understanding why risk varies across locations. Snakebite arises from the spatial overlap between snake habitats and human activity[15–18]. Prior risk studies have largely examined macro-environmental factors such as climate and topography, which capture broad-scale patterns but offer limited insight at the administrative scales relevant to intervention. At

finer scales, the configuration of local habitats such as availability, fragmentation, connectivity, shape complexity, and edge structure may more directly shape where snakes and people are likely to encounter one another[15,16,19,20]. Landscape ecology offers a natural intermediate lens for this problem, linking habitat structure to human-modified environments without treating ecological and human factors as separate domains[21–25].

This study therefore uses Fuzhou, Fujian Province, China, as a case study to operationalise an integrated fine-scale framework linking these two steps. Combining clinical snakebite records from 2021–2025 with Bayesian spatial risk estimation and landscape metrics, we aimed to (1) identify township-level high-risk areas and (2) evaluate how much of this spatial variation is statistically accounted for by landscape configuration. The aim is not to establish causal ecological pathways, but to test whether a landscape-ecological perspective can help explain fine-scale snakebite risk and support more targeted local prevention, a framework intended to be transferable beyond this single case study.

2. Methods

2.1. Data collection

2.1.1. Study area and population data

Fuzhou (25°15′–26°39′ N, 118°08′–120°31′ E), located in eastern Fujian Province along the Taiwan Strait (Figure 1), has a subtropical monsoon climate and supports venomous snake species of medical importance belonging to the families Viperidae and Elapidae[26]. For seasonal analyses, spring, summer, autumn, and winter were

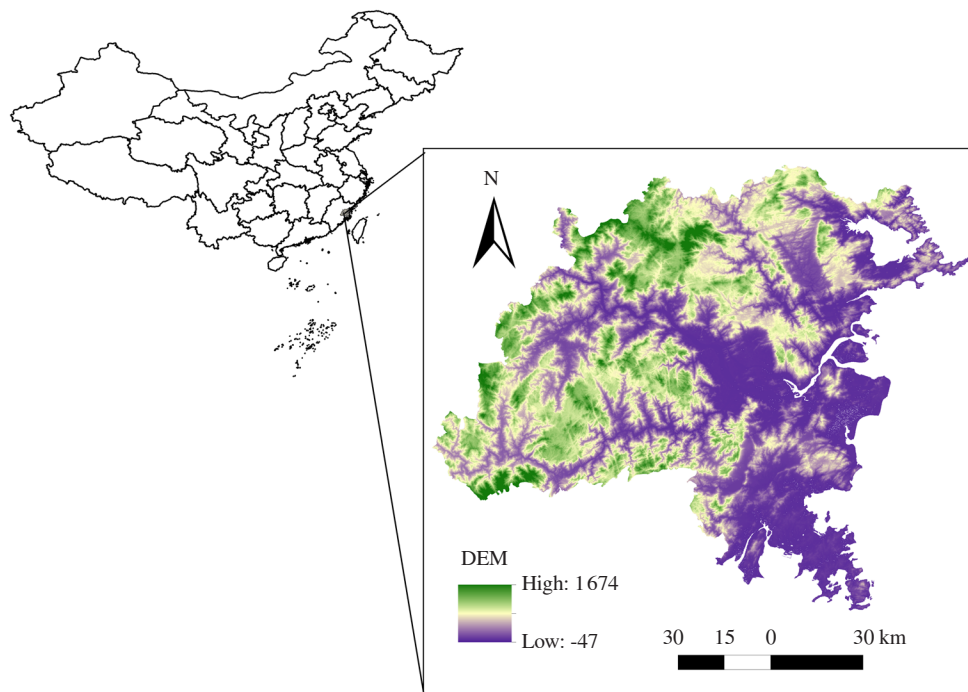


Figure 1. Location and digital elevation model (DEM) of Fuzhou, Fujian Province, China.

defined as March–June, July–September, October–November, and December–February, respectively.

Subsequent analyses were conducted at the township level, including towns, townships, and ethnic minority townships, each comprising several administrative villages. Population data were obtained from the 2020 Fuzhou Population Census Yearbook, published by the Fuzhou Municipal Bureau of Statistics based on the Seventh National Population Census. Township boundaries were aligned with the census statistical units to calculate population-standardized incidence rates. A total of 141 township-level units were included in the spatial analyses.

2.1.2. Ethics statement

This study was approved by the institutional ethics committee of the Affiliated People's Hospital of Fujian University of Traditional Chinese Medicine (approval No. 2024-036-02; approval date: 9 July 2024), which waived written informed consent for the retrospective record review and approved verbal consent for the telephone confirmation. All data were anonymised prior to analysis.

2.1.3. Case data

Between 1 January 2021 and 31 December 2025, 893 patients with confirmed venomous snakebite envenomation were treated at a provincial tertiary referral centre in Fuzhou (Figure 2). Of these, 152 were excluded because the registered residential address fell outside the Fuzhou study area, leaving 741 Fuzhou-resident cases, which were retained in full for the descriptive analyses of demographic, temporal, and taxonomic characteristics reported below.

Of the 741 eligible cases, 399 had both residential township and township-level bite location recorded in the admission record, and the two locations coincided; these were retained directly for spatial analysis. For the remaining 342 cases, in which the recorded locations were discordant or the bite location was not recorded,

two trained investigators conducted telephone confirmation using a standardised, low-burden protocol. Patients were first asked to confirm the township of residence registered at admission and, then whether the bite had occurred in the same township. Cases were excluded when residence and bite location could not both be confirmed as the same township, or when the patient was unwilling to respond. No further attempt was made to trace the actual bite location in cases of mismatch.

To ensure that the numerator (the number of cases assigned to each township) and denominator (the resident population of that township) used to calculate township-level incidence were defined on a consistent geographic basis, the spatial analysis was restricted to cases in which the registered township of residence and the township of bite exposure were concordant. This represented a more conservative criterion than assigning cases by bite location alone and therefore excluded within-Fuzhou cross-township exposures, such as residents of one township who were bitten while working in a neighbouring township. This trade-off is addressed in the discussion. Following this process, 560 cases with concordant residence and bite township were included in the BYM2 model, hotspot analysis, and landscape regression.

2.1.4. Case definition and snake identification

Snakebite cases were identified from hospital medical records and confirmed according to the diagnostic criteria for snakebite envenomation specified in the Chinese guideline for management of snakebites (Supplementary Figure 1)[6]. Throughout the manuscript, a "snakebite case" refers to a clinically confirmed envenomating bite by a venomous snake. Dry bites, non-venomous snakebites, and bites without confirmed envenomation were excluded from all analyses.

Taxonomic classification of the causative snake followed a hierarchical approach based on the same guideline. When the snake was photographed, retained as a specimen, or observed with

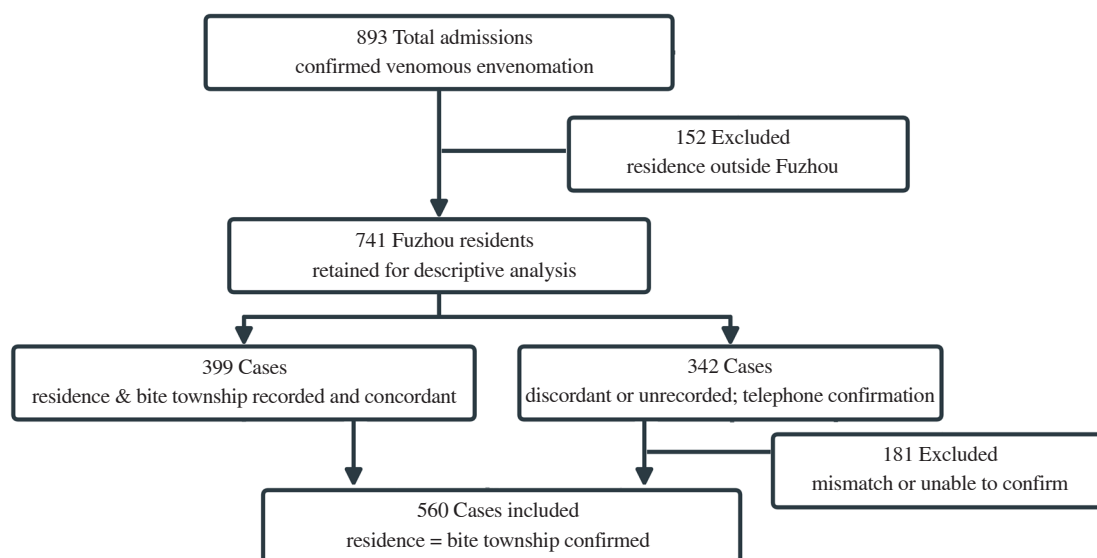


Figure 2. Flowchart of case selection for subsequent spatial analysis.

sufficient descriptive information, morphological characteristics were used to assign the case to the finest taxonomic level supported by the available evidence. When direct morphological identification was not possible, clinical manifestations, wound characteristics, and laboratory findings were used as supporting evidence, and the case was retained at the highest taxonomic level that could be assigned reliably. Cases that could be assigned to a family but not to a genus or species were retained as family-level unidentified cases. Cases in which envenomation was confirmed but the causative snake could not be reliably assigned even at the family level were classified as taxonomically unidentified. Detailed operational definitions are provided in Supplementary Figure 1.

2.1.5. Land-cover data

Land-cover data were obtained from the GLC-FCS10 dataset[27] and processed in ArcGIS 10.8.1. To reduce confusion among vegetation-related classes, the original classes were reclassified into eight ecologically relevant categories: cropland, forest, shrubland, grassland, wetland, impervious surfaces, bare areas, and water. Cropland classification was further refined using the high-resolution CropLayer China dataset[28], which was rasterized and resampled to 10 m to match GLC-FCS10. Pixels classified as cropland in GLC-FCS10 but as non-cropland in CropLayer were conservatively reassigned to grassland because of their similar vegetation characteristics. All spatial data were projected to the Albers Equal Area Conic coordinate system.

2.1.6. Landscape metrics data

Land-use patterns reflect human activity and may influence snake habitat selection and snakebite risk[17,29]. Based on evidence that landscape composition and human-modified land cover contribute to spatial variation in snakebite risk[15], forest, cropland, and impervious surfaces were selected to represent potential snake habitat, areas associated with human-snake encounters, and anthropogenic disturbance, respectively.

Landscape metrics describing fragmentation, connectivity, shape complexity, and edge effects were calculated (Supplementary Table 1). Mean patch area (AREA_MN) and mean Euclidean nearest-neighbour distance (ENN_MN) represented patch size and spatial isolation, respectively, while the patch cohesion index (COHESION) quantified connectivity among patches of the same class. The landscape shape index (LSI) was used to measure boundary complexity. Because cropland-forest interfaces may increase opportunities for human-snake encounters, contrast-weighted edge density (CWED) was calculated to quantify the intensity of these edges and their potential contribution to exposure risk.

All landscape metrics were calculated using FRAGSTATS 4.2, with connectivity defined according to an eight-neighbour rule[30].

2.2. Data processing

2.2.1. Spatial Bayesian smoothing of incidence and estimation of risk areas

The crude incidence measure used in this study represents five-year cumulative incidence per 100 000 population, calculated using the total number of eligible cases recorded during 2021–2025 as the numerator and the township resident population as the denominator. It should not be interpreted as an annual incidence rate.

First, the crude incidence rate (CIR) for each township was calculated as follows:

$$CIR_i = \frac{C_i}{P_i} \times 100\,000 \quad (1)$$

Where CIR_i denotes the crude incidence rate in township i (cases per 100 000 population), C_i is the number of snakebite cases in township i during the study period, and P_i is the total population of the township.

Because snakebite is a low-frequency, sporadic event at the township level, small populations can produce unstable incidence estimates from random fluctuation. To reduce this variability, a Besag–York–Mollié 2 (BYM2) spatial hierarchical model was fitted in R using the R-INLA package[13,14] to obtain posterior estimates of township-level relative risks and smoothed incidence rates.

The number of observed snakebites was assumed to follow a Poisson distribution:

$$C_i \sim \text{Poisson}(E_i \theta_i)$$

Where E_i is the expected number of cases based on the incidence rate and population, and θ_i represents the relative risk. Using the integrated nested Laplace approximation (INLA) framework, the BYM2 model decomposes spatial risk variation into structured and unstructured random components:

$$\log(\theta_i) = \alpha + \frac{1}{\sqrt{\tau}} (\sqrt{\phi} u_i^* + \sqrt{1-\phi} v_i) \quad (2)$$

Where α is the intercept, u_i^* is the standardized spatially structured random effect, v_i is the unstructured random effect, τ is the precision parameter, and ϕ is the mixing parameter. Default penalized complexity priors were used for BYM2 hyperparameters. Posterior mean relative risks and corresponding 95% Bayesian credible intervals (CrIs) were extracted for smoothed rates.

The mixing parameter ϕ , representing the proportion of variance attributable to spatially structured variation, was extracted with its 95% credible interval. To evaluate if accounting for spatial dependence improved fit, the deviance information criterion (DIC) and Watanabe–Akaike information criterion (WAIC) of the BYM2 model were compared against a model incorporating only

unstructured (IID) effects.

Global Moran's I was calculated for both crude and smoothed rates to assess spatial autocorrelation, using a Queen contiguity spatial weights matrix with significance assessed *via* 999 Monte Carlo permutations; positive Moran's I with $P < 0.05$ indicated significant clustering. Getis–Ord G_i^* analysis, based on the same weights matrix, identified local spatial clusters, with Z -scores defining significant hotspots ($Z > 1.96$) and coldspots ($Z < -1.96$).

2.2.2. Variable selection and model development

Variable selection followed a multistage procedure: highly correlated variables ($|r| > 0.7$) were excluded *via* Spearman correlation analysis, followed by variance inflation factor screening ($VIF < 3$), and final explanatory variables were retained using bidirectional stepwise regression based on Akaike's information criterion (AIC).

Because preliminary Poisson regression indicated substantial overdispersion in township-level case counts, a negative binomial regression model was used instead to examine the associations between landscape metrics and township-level snakebite incidence, with model adequacy confirmed by the estimated dispersion parameter θ . The natural logarithm of township population was included as an offset to account for differences in population size, and all explanatory variables were standardised using Z -score transformation before model fitting. So that estimated IRRs reflect the change in risk associated with a one-standard-deviation increase in each landscape metric. The model was specified as follows:

$$\ln(E[C_i]) = \ln(pop_i) + \beta_0 + \sum_{j=1}^k \beta_j X_{ij} \quad (3)$$

Where $E[C_i]$ denotes the expected number of snakebite cases in township i ; β_0 is the intercept; $\ln(pop_i)$ is included as an offset to account for differences in population size; X_{ij} represents the j th standardised landscape metric in township i ; and β_j is the corresponding regression coefficient.

To evaluate whether selected landscape covariates captured the spatial structure identified by the BYM2 analysis, spatial autocorrelation in Pearson residuals was assessed using Global Moran's I .

3. Results

3.1. Descriptive analysis of snakebite cases

Among the 741 confirmed snakebite envenomation cases treated at the participating provincial tertiary referral centre between 2021 and 2025, 659 cases (88.93%) could be assigned to a snake family.

Of these, 493 cases (66.53% of all cases) were further assigned to the genus or species level, whereas 166 cases (22.40%) could be assigned only to Viperidae (Table 1).

Table 1. Taxonomic classification of the causative snakes among 741 confirmed snakebite envenomation cases.

Taxonomic classification	<i>n</i> (%)
Viperidae	589 (79.49)
<i>Trimeresurus</i> spp.	245 (33.06)
<i>Protobothrops mucrosquamatus</i>	158 (21.32)
<i>Deinagkistrodon acutus</i>	20 (2.70)
Unidentified Viperidae	166 (22.40)
Elapidae	70 (9.45)
<i>Naja atra</i>	55 (7.42)
<i>Bungarus multicinctus</i>	9 (1.21)
<i>Ophiophagus hannah</i>	6 (0.81)
Unidentifiable species	82 (11.07)
Total	741 (100.00)

Overall, Viperidae was the predominant identified family, accounting for 589 cases (79.49%), followed by Elapidae with 70 cases (9.45%). In the remaining 82 cases (11.07%), snakebite envenomation was clinically confirmed, but the available photographs, patient descriptions, clinical manifestations, wound characteristics, and laboratory findings were insufficient to support a reliable family-level taxonomic assignment. These cases were therefore classified as taxonomically unidentified (Table 1).

Snakebite cases showed distinct seasonal distributions across taxonomic groups (Figure 3). Viperidae cases increased from February, rose during summer, and peaked in September–October; cases occurring during these two months accounted for 209 cases (35.5%) of all Viperidae cases recorded over the study period, followed by a decline after November. Elapidae cases increased from February and peaked in midsummer (July), followed by a gradual decrease. The unidentified group showed a similar seasonal increase from February, with a minor peak in July and a major peak in October.

With respect to sex distribution, snakebite cases were more common in males than in females overall (416 *vs.* 325), with a male-to-female ratio of 1.28:1 (Figure 4). A slight male predominance was observed in the Viperidae group (315 *vs.* 274; 1.15:1) and the unidentified group (46 *vs.* 36; 1.28:1), whereas a more pronounced male predominance was observed in the Elapidae group (55 *vs.* 15; 3.67:1).

Cases were predominantly concentrated in individuals aged 40–79 years, who accounted for 630 cases (85.02%) of the total. The highest proportion was observed in the 60–69 years of age group 242 cases (32.66%), followed by the 50–59 years 188 cases (25.37%), 70–79 years 122 cases (16.46%), and 40–49 years 78 cases (10.53%) of age groups.

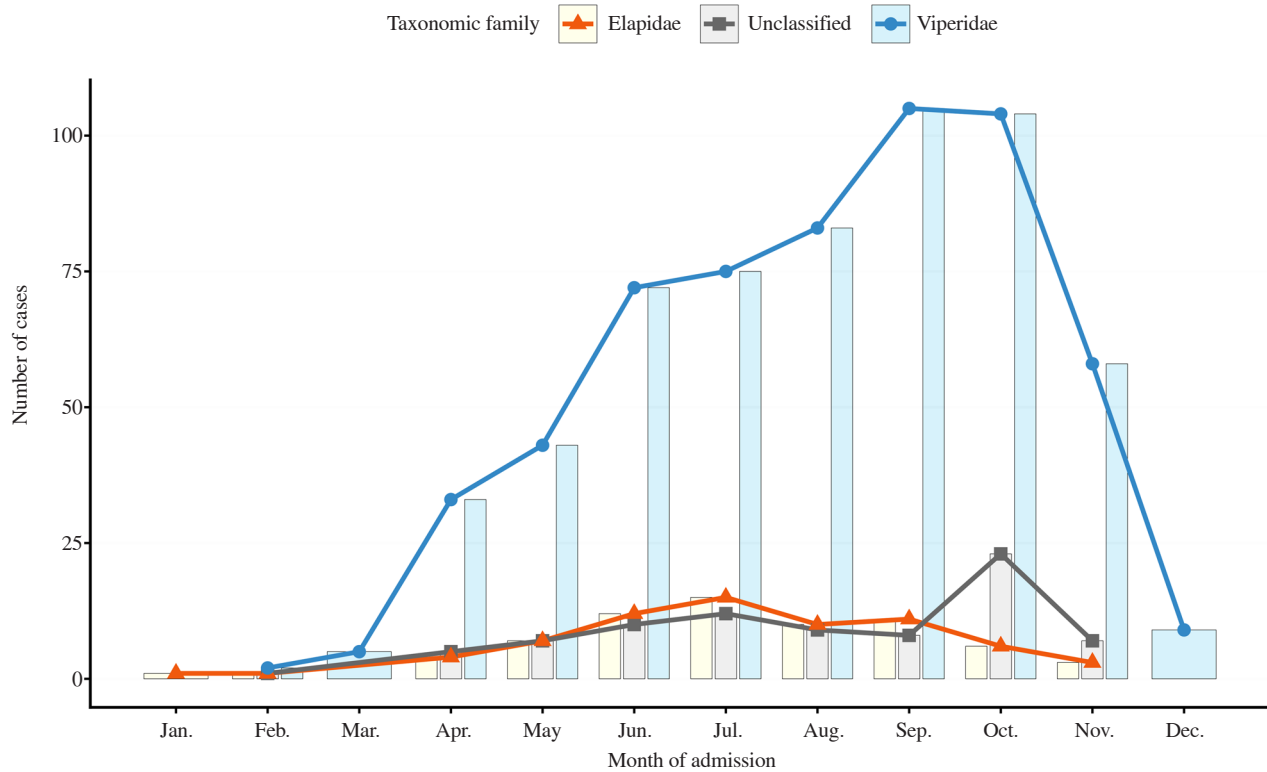


Figure 3. Seasonal patterns of snakebite cases in Fuzhou, 2021-2025.

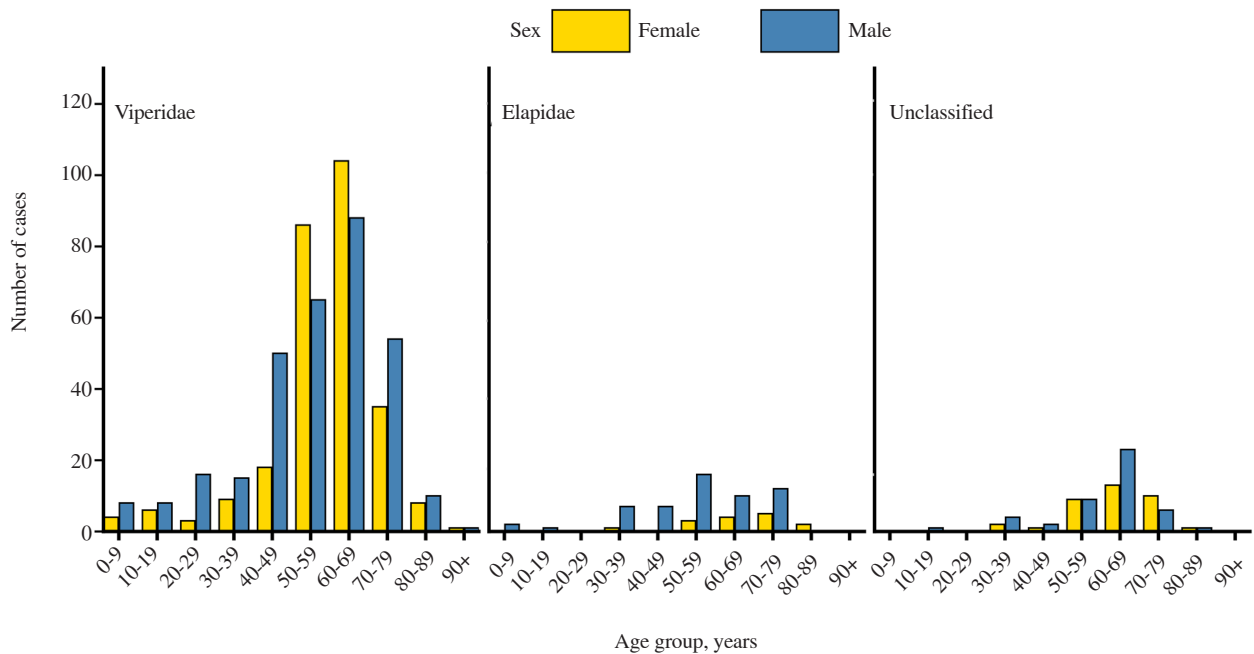


Figure 4. Snakebite cases stratified by snake species and age groups in Fuzhou, China, 2021-2025.

3.2. High-risk area

Spatial autocorrelation analysis indicated significant positive clustering of Bayesian-smoothed snakebite incidence across Fuzhou (Global Moran's $I=0.322$, $Z=6.08$, $P=0.001$), suggesting a non-random spatial distribution of snakebite risk among townships. Getis-Ord G_i^* analysis identified 13 significant hotspot townships (Figure 5, Table 2). Posterior mean relative risks (RRs) for these

hotspot townships ranged from 3.40 to 22.16 (Supplementary Table 2).

The posterior mean of the spatial mixing parameter ϕ was 0.637 (95% CrI 0.342-0.875), indicating that spatially structured variation accounted for approximately 64% of the total random-effect variance. Model comparison supported the inclusion of spatial structure; the BYM2 model fit better than a model with only unstructured effects (DIC: 624.65 *vs.* 641.69; WAIC: 630.95

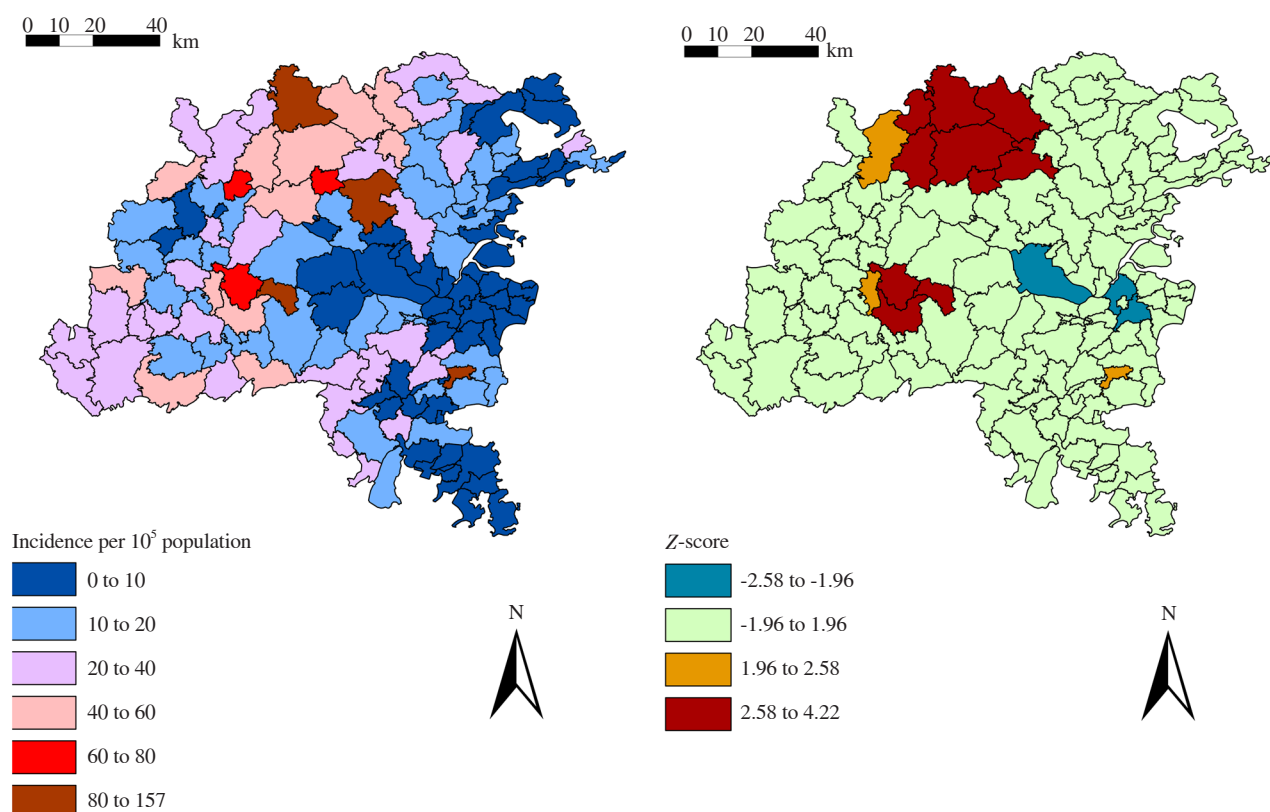


Figure 5. Spatial distribution of Bayesian-smoothed snakebite incidence and Getis-Ord Gi* hotspot analysis.

Table 2. High-risk townships identified by Bayesian spatial modelling and hotspot analysis.

No.	Township	Gi* Z-score	Smoothed RR	95% credible interval for RR	Smoothed incidence (per 10 ⁵)
1	Da Hu	4.221	7.779	(3.928, 13.884)	55.175
2	Huo Kou	3.787	5.771	(1.902, 13.576)	40.929
3	Yang Li	3.715	6.945	(3.223, 13.162)	49.26
4	Ting Ping	3.463	13.037	(7.099, 22.024)	92.465
5	Ri Xi	3.396	4.823	(0.975, 14.640)	34.208
6	Jiang Yang	3.392	9.599	(1.996, 29.030)	68.082
7	Bai Yun	3.232	11.189	(4.868, 22.147)	79.359
8	Dan Yun	3.001	11.627	(2.121, 37.457)	82.467
9	Qing Liang	2.759	7.089	(2.750, 15.145)	50.281
10	Xia Zhu	2.675	4.601	(1.529, 10.791)	32.635
11	Dong Qiao	2.419	3.402	(1.202, 7.676)	24.126
12	Nan Ling	2.077	22.156	(9.103, 45.312)	157.143
13	Hong Xing	2.041	7.759	(2.202, 19.994)	55.031

vs. 655.84). Global Moran's I for the crude incidence rates was also significant ($I=0.189$, $P=0.002$), confirming observed clustering reflects genuine spatial structure rather than an artefact of BYM2 smoothing. The higher Moran's I after smoothing ($I=0.322$) suggests BYM2 reduces small-area noise, clarifying the underlying spatial signal.

3.3. Negative binomial regression

After Spearman correlation analysis ($|r|>0.7$) and variance inflation factor screening ($VIF<3$), six landscape metrics were retained as candidate explanatory variables. Bidirectional stepwise regression based on AIC retained all six variables in the final negative binomial regression model. Impervious-surface metrics were highly negatively

correlated with forest-cover metrics ($|r|>0.7$). Forest metrics were retained as more ecologically relevant to venomous snake habitat. Cropland contrast-weighted edge density (CWED) was highly correlated with cropland landscape shape index (LSI) ($|r|>0.7$); LSI was retained as it more comprehensively represents patch geometric complexity and edge configuration.

The final negative binomial regression model showed that all six selected landscape metrics were significantly associated with township-level snakebite incidence (Table 3). Reported IRRs reflect the risk change per one-standard-deviation increase in each Z-score-standardised metric. Forest COHESION exhibited the strongest positive association ($IRR=3.37$, 95% CI 1.72–6.59, $P<0.001$), while Forest ENN_MN showed the strongest negative association ($IRR=0.59$, 95% CI 0.49–0.72, $P<0.001$). Among cropland metrics,

Table 3. Results of the negative binomial regression model.

Variable	β (Estimate)	SE	IRR	95% CI	P value
Forest LSI	-0.401	0.099	0.67	0.55–0.82	<0.001
Forest COHESION	1.216	0.343	3.37	1.72–6.59	<0.001
Forest ENN_MN	-0.527	0.099	0.59	0.49–0.72	<0.001
Cropland COHESION	0.229	0.104	1.26	1.03–1.54	0.027
Cropland ENN_MN	-0.336	0.128	0.71	0.55–0.91	0.009
Cropland LSI	0.393	0.1	1.48	1.22–1.80	<0.001

LSI was positively associated with incidence ($IRR=1.48$, 95% CI 1.22–1.80, $P<0.001$), while ENN_MN was negatively associated ($IRR=0.71$, 95% CI 0.55–0.91, $P=0.009$). All retained variables remained statistically significant.

A negative binomial model was used given evident overdispersion in the count data ($\theta=3.86$, $SE=1.02$). To evaluate whether selected landscape covariates accounted for the spatial structure identified in the BYM2 analysis, spatial autocorrelation in the Pearson residuals was assessed. No significant residual spatial autocorrelation was detected (Global Moran's $I=-0.110$, $P=0.968$), indicating the landscape covariates included in the final model adequately captured the underlying spatial structure in township-level snakebite risk.

4. Discussion

Effective snakebite prevention requires fine-scale risk assessment to identify high-risk communities and guide targeted interventions[5,12]. However, locating where risk concentrates is not sufficient; understanding what accounts for that spatial variation is equally essential for explaining why risk differs among locations[12,15–18]. This study operationalises an integrated framework linking spatial risk estimation, landscape ecology, and species-specific interpretation, using Fuzhou, Fujian Province, as a case study to examine where risk concentrates, how landscape configuration is statistically associated with this pattern, and how species ecology and human exposure may further shape observed bite patterns.

The first step addresses where risk concentrates. Global Moran's I on the crude, unsmoothed incidence rates was already significant ($I=0.189$, $P=0.002$), confirming genuine spatial structure rather than random distribution, a precondition for spatial modelling to be meaningful. Because snakebite is rare and sporadic, crude township-level rates are prone to unstable estimation from small case counts; Bayesian spatial smoothing (BYM2) addressed this while preserving local resolution[13,14], a choice itself statistically supported: the posterior mixing parameter ϕ was 0.637 (95% CrI 0.342–0.875), indicating that structured spatial variation accounted for the majority of random-effect variance, and BYM2 outperformed an equivalent non-spatial (IID) model on both DIC (624.65 *vs.* 641.69) and WAIC (630.95 *vs.* 655.84). Applied to Fuzhou's 141 townships, this identified 13 significant hotspot townships (Getis-Ord G_i^*) in the northwest, southwest, and southeast, a step that is diagnostic rather than explanatory, motivating the second step.

Snakebite risk emerges from the spatial overlap between snake

habitats and human activities[12,15–18]. Landscape ecology addresses this by quantifying how habitat configuration shapes snake occurrence and its potential overlap with human activity[12,15,17,23].

Applied to Fuzhou, this lens identified two forest metrics pointing in a convergent direction: COHESION was the strongest positive correlate of incidence ($IRR=3.37$, 95% CI 1.72–6.59, $P<0.001$), and ENN_MN the strongest negative correlate ($IRR=0.59$, 95% CI 0.49–0.72, $P<0.001$), both indexing the same underlying property, greater forest connectivity and shorter inter-patch distances, and so reinforcing rather than merely supplementing one another. This extends prior evidence linking forest extent to snake population density[19,23,31,32]: where earlier work emphasised how much forest exists, our results suggest that, in Fuzhou, how it is spatially arranged carries additional explanatory value. Connectivity is considered essential for maintaining snake population structure, as fragmented habitats often cannot sustain stable populations[21,23,31–34]; the region's dominant venomous species favour forest or forest-edge habitat[22,35–39], so well-connected patches could buffer core populations against isolation-driven decline[21,23,32–34]. Stable core populations have elsewhere been shown to spill over into peripheral, human-modified habitats, an effect reportedly amplified by connectivity[22,33,40], one plausible pathway linking forest connectivity to elevated encounter risk on adjacent agricultural land.

Cropland LSI was likewise positively associated with incidence ($IRR=1.48$, 95% CI 1.22–1.80, $P<0.001$): townships with more irregular, complex cropland edges carried higher risk, pointing to the forest-cropland interface itself as ecologically relevant. Such edges are reported to offer prey resources and thermoregulation opportunities that draw snakes toward them[23–25,33], and snakes are thought to use vegetated linear corridors during dispersal to reduce predation risk[22,33]; seasonal crop growth generates comparable continuous cover that could extend this corridor effect into cropland, increasing spatiotemporal overlap between snakes and human activity: highly connected forest patches provide stable core habitats for snake populations and support the maintenance of venomous snake abundance; forests with high connectivity and short inter-patch distances facilitate snake dispersal into surrounding agricultural areas, where irregular field edges and vegetated corridors act as movement pathways and suitable habitats; snake dispersal into human-dominated landscapes increases human-snake contact frequency, ultimately elevating the risk of snakebite incidence. Population density, movement, and spillover were not directly measured, so both pathways remain hypotheses rather than confirmed mechanisms.

What Fuzhou does demonstrate, with stronger evidential support, is that this landscape-ecological lens is statistically sufficient to account for the spatial structure identified in the first step. A negative binomial model was used given clear overdispersion ($\theta=3.86$, $SE=1.02$), and residuals from this model showed no significant residual spatial autocorrelation (Global Moran's $I=-0.110$, $P=0.968$): the spatial structure that justified BYM2 smoothing was fully accounted for once landscape configuration was included, without a spatial term in the second-step model. This closes the analytical loop and is the framework's central contribution: not a claim about Fuzhou's snakes specifically, but formal statistical evidence that landscape configuration, rather than habitat extent or macro-environmental variables alone, statistically accounts for the spatial clustering identified in the first step. Progression from this landscape-level pattern to individual bite events is further shaped by species behaviour and human activity, as reflected in the taxonomic and demographic patterns observed in Fuzhou.

Viperidae species (*Trimeresurus albolabris*, *Trimeresurus stejnegeri*, *Protobothrops mucrosquamatus*, *Deinagkistrodon acutus*) accounted for most bites, peaking in September–October, coinciding with their reproductive and pre-hibernation feeding period[35–38,41–45]; cryptic coloration and ambush behaviour likely reduce their detectability during agricultural activity[39,46]. Cases were concentrated among adults aged 40–79 with a modest male predominance (1.28:1), consistent with regional agricultural sex ratios, though females exceeded males in the 50–69 years group. This reversal may be worth interpreting through labour-task type rather than agricultural exposure in general: clinicians involved in this study have anecdotally observed hand bites attributed to *Trimeresurus stejnegeri* among women of this age engaged in tea-picking, though bite site and occupation were not systematically recorded in this dataset, and this observation is offered only as a direction for future task-specific data collection rather than an explanation supported by the present study.

Elapidae bites clustered in summer with a pronounced male predominance (3.67:1), possibly reflecting greater male involvement in direct encounters with these larger, more conspicuous species; intent was not recorded in this dataset, so this explanation remains speculative. Conspicuous defensive displays may partly explain their lower bite frequency relative to crotalines[47].

Taken together, Fuzhou's high-risk townships show how spatial risk estimation and landscape-ecological interpretation, each independently supported by formal statistical evidence, can jointly generate an actionable, mechanistically grounded risk profile. To our knowledge, this is among the first studies in China to combine Bayesian spatial modelling with landscape ecology for snakebite risk assessment, and to formally evaluate, rather than assume, how much landscape configuration accounts for spatially structured risk. Fuzhou serves here as a proof-of-concept case study; the framework itself is not tied to this location and is intended to be transferable to other regions and, potentially, other landscape-shaped human-

wildlife conflict systems.

This study has several limitations. First, the data were obtained from a single provincial tertiary referral centre and should therefore be interpreted as a hospital-treated case series rather than complete population-based surveillance. Severe cases or patients requiring antivenom may have been overrepresented, whereas mild cases treated elsewhere or not seeking formal care may have been missed, potentially affecting both cumulative incidence estimates and spatial patterns. Second, township-level bite locations were not uniformly available in historical records. For cases requiring telephone follow-up, a low-burden confirmation approach was used, which may have introduced recall or confirmation bias, and exclusion of patients unable or unwilling to provide a clear location may have resulted in selection bias. Restricting spatial analysis to cases with concordant residence and bite township (560/741) ensured internal consistency between numerator and denominator but excluded within-Fuzhou cross-township exposures, for example, residents bitten while working in a neighbouring township. This may understate the true spatial risk faced by mobile agricultural populations and represents a scope limitation distinct from, though related to, the residence–bite-location conflation. Third, the analysis was conducted using township-level aggregate data and is therefore subject to ecological fallacy and the modifiable areal unit problem; individual-level factors such as activity at the time of bite, specific occupational tasks, protective behaviour, and movement between residential and working locations were not systematically recorded. The 2020 census population was used as a fixed denominator for the 2021–2025 study period and did not capture migration or population change. In addition, the environmental analysis focused mainly on forest, cropland, and impervious-surface landscape metrics and did not include other potentially relevant factors such as climate, elevation, healthcare accessibility, socioeconomic conditions, snake abundance, or agricultural seasonality. The observed associations should therefore be interpreted as ecological correlates rather than causal drivers. Variable selection based on correlation screening, VIF, and stepwise AIC may also be sensitive to sampling variation and model instability. Finally, taxonomic classification relied on available photographs, patient descriptions, clinical findings, wound characteristics, and laboratory results rather than systematic specimen verification, so some misclassification cannot be excluded.

In conclusion, this study demonstrates that combining Bayesian spatial modelling with landscape ecology provides a coherent, statistically grounded framework for fine-scale snakebite risk assessment. In Fuzhou, Getis-Ord G_i^* analysis of Bayesian-smoothed incidence identified 13 hotspot townships with posterior relative risks ranging from 3.40 to 22.16, confirming genuine, non-random spatial clustering rather than an artefact of small-area noise. Landscape configuration, particularly forest connectivity (COHESION, ENN_MN) and cropland edge complexity (LSI), was statistically sufficient to account for this spatial structure, with no significant residual autocorrelation remaining after adjustment. This

closes the analytical loop between where risk concentrates and why it varies, moving beyond hotspot mapping toward an explanatory, ecologically grounded account of local risk patterns.

Fuzhou serves here as a proof-of-concept case study rather than an endpoint: the framework itself is not tied to this location and is intended to be transferable to other regions, and potentially to other landscape-shaped human-wildlife conflict systems. As the associations reported remain correlational, future work incorporating direct measures of snake population density, movement, and human exposure behaviour will be needed to test the proposed ecological pathways and establish their generalisability. In the meantime, this framework offers local health authorities a practical, replicable approach for prioritising prevention resources at the township level.

Conflict of interest statement

The authors declare no conflict of interest.

Acknowledgements

The authors gratefully acknowledge Miao Song for sharing long-term field observation records relevant to this study, and Hangdong Jiang for his valuable comments and constructive suggestions, and the staff of the Affiliated People's Hospital of Fujian University of Traditional Chinese Medicine for their assistance with data collection and management.

Funding

This work was supported by the Fujian Research and Training Grants for Young and Middle-aged Leaders in Healthcare and the Hospital-funded Research Project of the Affiliated People's Hospital of Fujian University of Traditional Chinese Medicine (No. 2023-03).

Declaration of generative AI use

During the preparation and revision of this manuscript, the authors used GPT-5.6 Sol (OpenAI) to assist with English-language editing and to improve clarity and readability. All AI-assisted content was reviewed and revised by the authors, who take full responsibility for the final manuscript.

Authors' contributions

G.G. developed the study design, performed the data analysis and drafted the manuscript. Q.Z. and Y.Z. contributed to data collection and interpretation. Y.C. and S.W. contributed to the final version of the manuscript. S.W. supervised the project.

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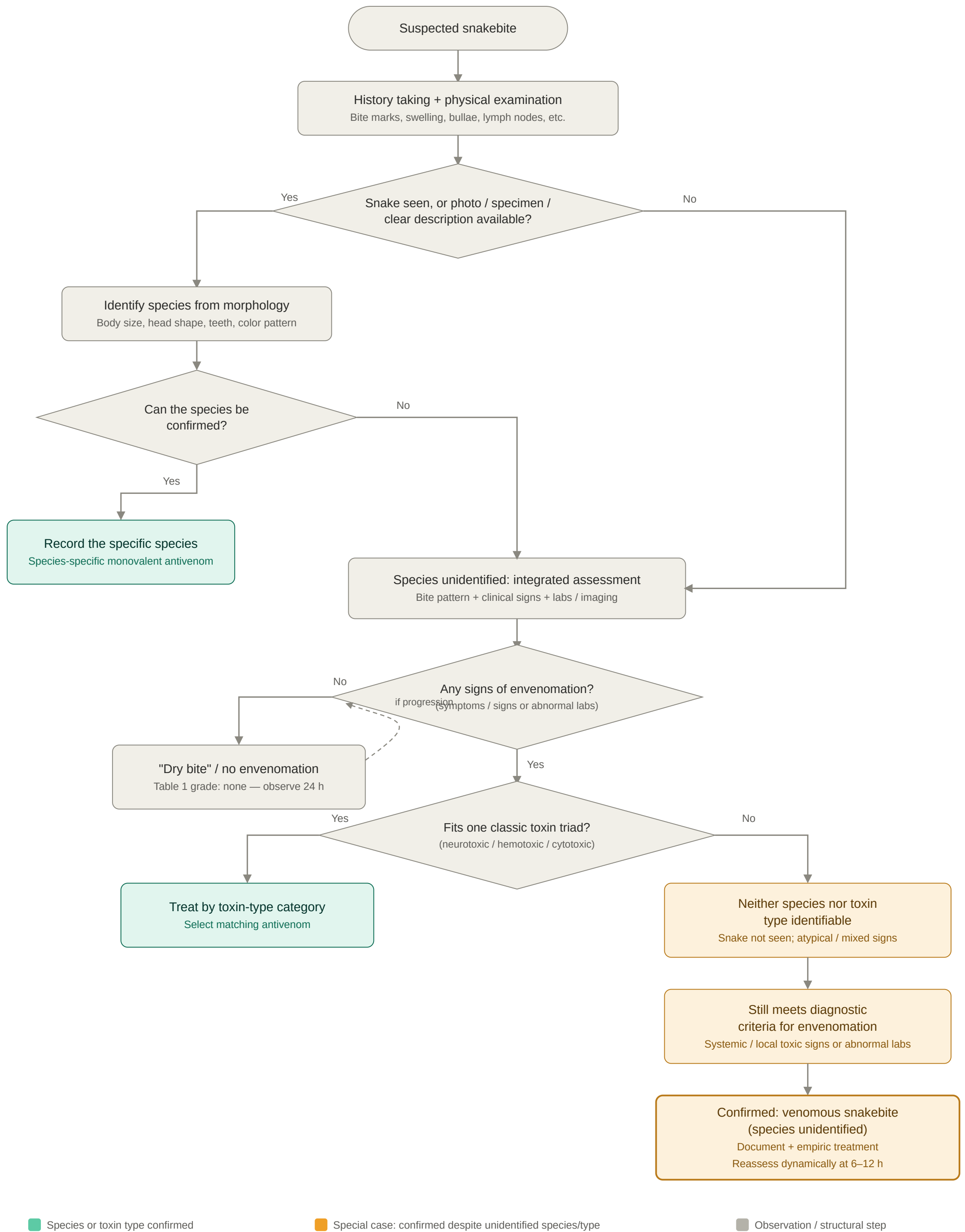
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Edited by Zhang Q, Lei Y, Pan Y



Supplementary Figure 1. Flowchart for snake species identification and case classification of venomous snakebite envenomation.
Diagnostic classification followed the criteria specified in the Chinese guideline for the management of snakebites. Green boxes: species and/or toxin type confirmed; orange boxes: envenomation confirmed despite unidentified species or toxin type; grey boxes: observation or structural decision step.

Supplementary Table 1. Classification and definition of selected landscape metrics.

Metrics	Description
	$AREA_MN = \frac{n}{\sum_{j=1}^n a_{ij}} \cdot \left(\frac{1}{10000} \right).$
AREA_MN (mean patch area)	Average area of all patches of the corresponding type (a_{ij}, m²), converted to hectares (ha). It reflects patch size characteristics and provides an indication of habitat fragmentation, with smaller values generally suggesting greater fragmentation.
	$ENN_MN = \frac{\sum_{j=1}^n h_{ij}}{n}.$
ENN_MN (mean Euclidean nearest-neighbor distance)	Average shortest edge-to-edge distance from each patch to its nearest patch of the same type. h_{ij} represents the shortest edge-to-edge distance (m) between patch j and its nearest neighboring patch of the same type. It quantifies the spatial isolation of habitat patches.
	$COHESION = \left[1 - \frac{\sum_{j=1}^{n_i} p_{ij}^*}{\sum_{j=1}^{n_i} \left(\frac{p_{ij}^*}{\sqrt{a_{ij}^*}} \right)} \right] \cdot \left[1 - \frac{1}{\sqrt{Z}} \right]^{-1} \times 100.$
COHESION (patch cohesion index)	Measurement of the physical connectivity of patches. Higher COHESION values indicate greater patch aggregation and connectivity, while lower values indicate increased fragmentation. p_{ij}^* and a_{ij}^* represent patch perimeter and area in numbers of cells, respectively; Z is the total number of cells in the landscape.
	$LSI = \frac{0.25 \sum_{j=1}^n p_{ij}^*}{\sqrt{Z}}.$
LSI (landscape shape index)	Measurement of the geometric complexity of patches. Higher LSI values indicate more complex and irregular patch shapes, whereas lower values indicate more compact shapes.
	$CWED = \frac{\sum_{k=1}^m e_{ik} \cdot d_{ik}}{A} \cdot (10000).$
CWED (contrast-weighted edge density)	Measurement of the density of contrast-weighted edges within a landscape. It is calculated as the sum of edge lengths (e_{ik}, m) between focal class i and neighbor-

Metrics	Description
	ing class k , weighted by the edge contrast weight (d_{ik}), divided by the total landscape area (A). Higher CWED values indicate stronger edge contrast and greater potential edge effects (e.g., forest-cropland interfaces).

Supplementary Table 2. Posterior mean relative risks and smoothed incidence for all 141 townships in Fuzhou.

Estimates were derived from the Besag-York-Mollié 2 (BYM2) spatial model. RR_Lower95 and RR_Upper95 denote the 95% credible interval of the posterior relative risk; Smoothed_Incidence is the BYM2-smoothed five-year cumulative incidence per 100 000 population. Townships are ranked in descending order of posterior relative risk.

Township	Cases	Population	Posterior_RR	RR_Lower95	RR_Upper95	Smoothed_Incidence
nan_ling	8	3245	22.15599916	9.103212951	45.31214449	157.1431045
ting_ping	12	12313	13.03688415	7.099191085	22.02444342	92.46508965
shou_shan	7	5873	11.78765326	4.852948449	24.15993401	83.60482477
dan_yun	2	1335	11.62718607	2.121309541	37.4574862	82.46669907
bai_yun	7	7013	11.18898424	4.867909406	22.1465823	79.35871937
xiao_ruo	4	4585	10.55746848	3.482442268	24.89745475	74.87964591
jiang_yang	2	1896	9.599044276	1.995689375	29.03002683	68.08194958
fei_zhu	4	5940	8.075691117	2.752872719	18.67948749	57.27745176
wu_tong	12	20462	7.850416876	4.276969784	13.2592939	55.67967712
da_hu	9	16019	7.779278079	3.927874713	13.8844572	55.17511981
hong_xing	3	4079	7.758995657	2.202113926	19.99426553	55.03126519
qing_liang	5	8620	7.089225819	2.750065146	15.14464614	50.28087181
yang_li	7	13893	6.94534219	3.222542583	13.16155542	49.26036626
xiong_jiang	2	2378	6.527003637	1.305912846	20.13720906	46.29326834
bai_sha	14	30651	6.184685242	3.565261079	10.01234168	43.86534916
xiao_cang	1	1693	6.118982778	0.976028004	20.89411685	43.39934946
shang_lian	3	5948	6.115801552	1.783824448	15.49918132	43.37678637
huo_kou	3	7844	5.770629171	1.90177333	13.57613934	40.92862508
ling_lu	2	4050	5.696245575	1.294762697	16.49991321	40.40105378
dong_zhang	10	23208	5.63811028	2.886191103	9.967292395	39.98872479
zhong_fang	4	9133	5.274370452	1.831543352	12.05773436	37.40887247
ju_lin	1	2464	5.232742903	0.735736209	18.80657837	37.11362592
jing_yang	14	36008	5.152975422	2.942960066	8.400411636	36.54786901
ri_xi	1	3411	4.823070818	0.975455574	14.64042374	34.20799559
dan_yang	9	23756	4.771005861	2.334126067	8.710708042	33.83872093
yi_du	3	7577	4.68817286	1.404737822	11.70564697	33.25122159
song_kou	6	17950	4.660239716	2.046740441	9.172603248	33.05310365
xia_zhu	3	10712	4.601289368	1.528591264	10.79073941	32.63499383
chi_xi	3	9536	4.473734013	1.4110191	10.8335141	31.73029781
chang_qing	4	12955	4.429645181	1.637428439	9.747909264	31.41759442
qi_bu	6	17067	4.210798957	1.772428615	8.525403666	29.86541098
yang_xia	20	65386	4.107273649	2.585504329	6.207910527	29.13114988
huan_xi	5	11944	4.068003185	1.410663488	9.286277795	28.85262114
dong_yang	1	4352	4.063228304	0.734657876	13.09159595	28.81875493
hong_wei	8	27887	4.041202745	1.978812047	7.375782421	28.66253698

gai_yang	1	4682	3.875520576	0.697977076	12.5057267	27.48742363
xia_ba	2	8469	3.643089649	1.037006713	9.347441002	25.83888965
yun_long	3	10126	3.588837213	1.082461148	8.917551704	25.45410013
qing_kou	26	99571	3.587736946	2.400508243	5.16185377	25.4462964
fu_kou	1	5430	3.566432048	0.60389425	11.82160541	25.2951898
xin_cuo	7	27011	3.562259447	1.611086341	6.869771545	25.26559531
ta_zhuang	4	16058	3.464366583	1.281514085	7.623247071	24.57128275
xi_lan	1	4666	3.447280001	0.692612994	10.55377681	24.45009487
dong_qiao	3	14997	3.401637187	1.20236772	7.676001654	24.12636975
xia_guan	3	11124	3.356357375	0.913212871	8.830720069	23.80521925
luo_lian	2	7190	3.074188231	0.683226916	9.004604928	21.80391319
shang_jing	7	28053	3.069122954	1.34920913	6.034179506	21.76798734
da_yang	4	20246	3.009287422	1.173717247	6.398770414	21.34359928
sheng_huang	2	11956	2.78321215	0.807684997	7.058638572	19.74014327
xian_qian	13	61593	2.76459858	1.542027342	4.587279926	19.60812512
liao_yan	3	17482	2.707026788	0.937653875	6.187240616	19.19979281
ge_ling	4	20224	2.681525986	1.026817008	5.76736335	19.01892644
dong_dai	4	18330	2.63736197	0.886790062	6.149505932	18.70568981
tong_an	2	14580	2.574380001	0.775398668	6.380393607	18.25898542
bai_ta	1	5949	2.526605689	0.496228741	7.809015485	17.92014248
fu QUAN	0	3756	2.505952126	0.37360651	8.687373423	17.77365552
jin_xi	16	89974	2.482471955	1.49390851	3.887583753	17.60712063
mei_xi	5	33013	2.396824531	1.040464906	4.747333479	16.99965978
zhu_qi	4	26557	2.38628872	0.945116854	5.018642859	16.92493374
chi_yuan	3	19331	2.367467921	0.801044376	5.497900757	16.79144579
yu_xi	9	53806	2.307461905	1.168395849	4.112648161	16.36584858
cheng_tou	7	47876	2.136354453	1.003365317	4.012524196	15.152256
hong_yang	0	4696	2.115563874	0.26273055	7.899908613	15.00479723
san_xi	0	4765	2.101317006	0.34497619	6.916008155	14.90375024
shang_gan	3	22078	2.075959827	0.643799406	5.07320328	14.72390252
jing_sha	1	9007	2.056676667	0.405986764	6.341832291	14.58713525
an_kai	2	12455	2.040840978	0.480729651	5.800250826	14.47481943
pan_gu	0	5694	2.011710148	0.30579679	6.914856165	14.2682068
dong_hu	2	16572	1.969289083	0.558387607	5.060201438	13.96733219
jiang_nan	4	28027	1.868994493	0.682871003	4.149007579	13.2559852
cheng_feng	8	68145	1.85164694	0.941540905	3.28625748	13.13294636
tou_bao	2	15759	1.808241567	0.442968871	5.029362421	12.82509046
chang_long	1	7944	1.796573537	0.369197007	5.473937969	12.74233408

tang_qian	0	3418	1.788167609	0.210391284	6.835485145	12.68271439
ban_dong	4	36122	1.75666753	0.686771124	3.727283236	12.4592977
huang_qi	3	19349	1.752531772	0.477435012	4.606437038	12.42996452
ma_bi	4	33479	1.728781223	0.625415101	3.854108193	12.26151195
song_xia	3	28439	1.687913867	0.536890129	4.064082633	11.97165712
long_tian	15	119389	1.673230549	0.97549618	2.684349399	11.86751458
jiang_tian	6	54705	1.640100703	0.73993479	3.164986434	11.63253863
pan_du	5	47129	1.632981774	0.710152948	3.222380554	11.58204709
ting_jiang	5	43743	1.519168769	0.600592889	3.204087504	10.77481972
zhang_cheng	3	36220	1.515979104	0.519026592	3.488879956	10.75219678
long_shan	7	71924	1.477845279	0.706991452	2.739494152	10.48172973
ao_jiang	6	59371	1.47586506	0.662089316	2.862817559	10.46768487
jiang_ying	8	80653	1.453810672	0.708853271	2.660930367	10.31126246
nan_tong	5	52646	1.445879227	0.61366598	2.909653347	10.25500808
hou_yu	1	4765	1.387711451	0.140649242	5.66905983	9.842448722
nan_yu	11	112618	1.387665382	0.751703666	2.35279155	9.842121974
hai_kou	5	59620	1.326842307	0.569538464	2.645101077	9.4107297
shou_zhan	5	50639	1.313989194	0.521280814	2.765216344	9.319568018
dong_ge_huaqiao	0	3477	1.308927093	0.086599191	6.034548913	9.283664683
gu_huai	4	47591	1.217526876	0.453734892	2.665463011	8.635401713
bi_li	1	11499	1.186316293	0.146519469	4.435152533	8.414038288
hong_lu	5	66606	1.179707523	0.500319241	2.374252686	8.367165085
gan_zhe	8	109567	1.170252326	0.589854923	2.090660786	8.300103384
ying_xi	9	119132	1.151590148	0.60222433	2.003372079	8.167740465
keng_yuan	1	18137	1.106015667	0.23650833	3.286401504	7.844500003
bai_zhang	0	15204	1.090508342	0.217762478	3.30653433	7.734513124
shi_zhu	4	64911	1.089795615	0.440610743	2.258133945	7.729458056
yu_tian	2	33889	1.054452437	0.323969355	2.579369126	7.478783885
guan_tou	4	63755	0.973062291	0.362619085	2.128790175	6.901518104
pu_kou	1	23627	0.947010959	0.224103175	2.671395586	6.716747056
bai_zhong	0	16107	0.939864078	0.160806815	3.054826911	6.666057256
guan_ban	1	22766	0.88288834	0.193796345	2.581365695	6.261952517
feng_shan	4	89811	0.826395758	0.33885337	1.697221805	5.861274593
jian_jiang	0	7947	0.818407857	0.025309031	4.450010177	5.804619802
long_jiang	3	68777	0.806757475	0.298723672	1.766873225	5.721988581
ying_qian	2	38923	0.792031865	0.221224688	2.052084216	5.617546074
jin_feng	5	79932	0.78924471	0.303691214	1.691529883	5.597777969
tan_tou	3	46664	0.748291686	0.227855774	1.84842847	5.307315539

song_shan	3	80955	0.738641402	0.280761915	1.590160523	5.238870165
xiao_cheng	0	20015	0.640138296	0.090375677	2.261992302	4.540229416
xiao_ao	0	23806	0.611778356	0.094609658	2.084727113	4.339084391
jiang_jing_huaqiao	0	4615	0.573351577	0.02400497	2.89572396	4.066539547
xin_dian	8	240970	0.537117092	0.27402458	0.951049992	3.809543715
feng_cheng	4	132366	0.53461443	0.208379229	1.135223181	3.791793393
lang_qi	2	67389	0.523417491	0.125942816	1.467739581	3.712378252
tai_lu	0	22556	0.507423639	0.035951609	2.26745097	3.598940647
wen_wu	0	24737	0.481173198	0.074147148	1.641707651	3.412757399
yu_ping	1	77173	0.469000879	0.133449298	1.190882298	3.326424303
mei_cheng	0	47993	0.465007135	0.084337745	1.456489587	3.298098375
ma_wei	3	115427	0.460730229	0.163986208	1.034783681	3.267764095
he_shang	1	52694	0.453655245	0.117273818	1.220665647	3.21758423
shang_jie	8	306352	0.444168508	0.230144406	0.777174805	3.150298828
luo_xing	1	63995	0.395239304	0.096144675	1.094326527	2.803264743
mei_hua	0	11665	0.377809822	0.007805368	2.175271553	2.67964482
zhang_gang	1	57874	0.372898092	0.079570314	1.103986647	2.644807998
gu_shan	5	222752	0.370048104	0.157933967	0.740048331	2.624594242
sha_pu	1	36943	0.363993029	0.044842155	1.364603989	2.581648162
jiang_jing	0	76021	0.301753027	0.068545743	0.852895006	2.140206234
wu_hang	1	81255	0.29190701	0.058366819	0.885825603	2.070372609
hang_cheng	1	103172	0.274402234	0.0764842	0.704602901	1.946218658
wen_ling	0	31409	0.273904732	0.032036123	1.039400938	1.942690088
hu_nan	0	34719	0.265777605	0.030309523	1.015306917	1.885047824
yue_feng	1	132717	0.253691543	0.068902978	0.659648072	1.799326513
gang_tou	0	62594	0.233753496	0.037223302	0.777458496	1.657914399
gao_shan	1	64946	0.208282857	0.030901313	0.722192287	1.477261961
dong_han	0	29444	0.194975267	0.005510996	1.071174001	1.382876872
san_shan	0	92092	0.165165778	0.027615522	0.541214621	1.17145081