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we first model *p. vivax* transmission among individual towns using the simplest deterministic model by assuming that the mosquito population density is independent of location. with this model, the local infection risk at node is given by: (2) where ρ is the local mosquito density, β is the biting rate of mosquitoes on human, and ϕ is the probability of a human being infected by an infectious mosquito per bite, given that the biting rate is β and the average duration of the infectious period of *p. vivax* is ϕ . based on the study of lai et al. [18], we assume that the biting rate of mosquitoes is proportional to the density of human beings. in addition, it has been shown that the proportion of infected mosquitoes is positively correlated with the temperature [19]. therefore, we consider the biting rate to be proportional to the density of human beings, given that it is positively correlated with temperature. note that the density of human beings and the density of mosquitoes may vary from one town to another. to better accommodate the fact that the transmission potential of *p. vivax* is always not larger than its potential to cause severe malaria, we assume that the average incubation period of *p. vivax* is proportional to the density of human beings. for the first step (i), we assume that the underlying transmission networks of *p. vivax* are not known. this is reasonable because in the most cases, the underlying transmission networks of *p. vivax* are hard to be identified from the surveillance data. to demonstrate the potentiality of the proposed method, we perform a simulation study on a synthetic dataset. the results show that the proposed method can effectively reconstruct the underlying transmission networks, which can further serve as a reasonable alternative for surveillance and control of *p. vivax*.

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p. vivax can be transmitted from town to town directly through the air or indirectly through the mosquito vectors. the former is the main route for the transmission of *p. vivax* and has also been used in our work. the latter is more likely to transmit *p. vivax* indirectly. we have calculated the weight for the entire province of yunnan, which is 0.16, and it is much lower than the thresholds of 0.8 and 0.5. therefore, the province can be categorized as a diffusive town. based on the estimation of the weights of the link between a town and the province, it can be found that the largest contribution comes from the link between the town and the province. therefore, we can conclude that the province of yunnan plays a significant role in the transmission of *p. vivax* in the province, as reported by recent studies in china [15], while the town has a less important role. in the current study, we employ the two-step mcmc algorithm to infer the transmission networks of *p. vivax* transmission among 62 towns in yunnan, which is referred to as network inference algorithm (nia) in this paper. in the first step, we infer the transmission networks of *p. vivax* infection among individual towns. the second step is to identify the connections between pairs of individual towns in yunnan. this paper will describe the network inference algorithm (nia) with respect to the transmission dynamics of *p. vivax* in yunnan based on the malaria data reported in the 62 towns in yunnan. nia is motivated by the two assumptions of (i) transmission can only occur between nearest-neighbor nodes and (ii) a node tends to connect to its nearest neighbors. the nia approach can be described as follows. first, a one-step mcmc algorithm is employed to infer the transmission networks among individual towns. second, the recovered networks are refined by applying a two-step mcmc algorithm to identify the connections between pairs of individual towns. 5ec8ef588b

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