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the strength of p. vivax transmission is usually estimated by the number of recurrent infections [13]. to infer the underlying transmission networks, it is necessary to firstly model the recurrent infection. we use a recurrent neural network model to infer the recurrent infections, as demonstrated in figure 1. for this purpose, we take into account the following assumptions: in the transmission networks, the nodes represent geographical locations. the links describe the possibility of malaria transmission from one geographical location to another. for instance, as shown in figure 11, a node represents a town and a link means that people from this town may travel to another town, which can introduce them (or the vectors) to the local population, who will then be infected with p. vivax. in this work, the links are directed, and each link connects a node to another one. for a directed link from to, we define the weight as, which means that the link has a relative strong or weak influence on the malaria transmission from to. the names of the corresponding nodes can be found in table 1. based on the obtained results, we can further assess the roles of individual towns and those of the entire province in the p. vivax transmission. in the following sections, we discuss the individual roles of towns and the province in the p. vivax transmission, respectively. figure 11 shows the p. vivax transmission network based on the estimated weight matrix. in the figure, the node represents a town, the directed links indicate the possibility of malaria transmission from a town to another, the size of the nodes represents the total number of reported cases, and the black lines represent the historical transmission pattern of p. vivax. from the figure, the towns with the larger and the smaller can be seen to be self-propagating and diffusive towns, respectively. in the following, we discuss the roles of the towns and the province in the transmission of p.

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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 is the local mosquito density, is the biting rate of mosquitoes on human, and is the probability of a human being being infected by an infectious mosquito per bite, given that the biting rate is and the average duration of the infectious period of p. vivax is. 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. 5ec8ef588b

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