

Supplementary Material of “Assessing the Spatiotemporal Malaria Transmission Intensity with Heterogeneous Risk Factors: A Modeling Study in Cambodia”

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1 Study scope

2 The names and coordinates of the 15 malaria-severe districts in Cambodia are provided in Supplementary Table
3 S1. The coordinates (longitude and latitude) of the centroid for each district are obtained from the shapefile of
4 Cambodia.

5
6 **Supplementary Table S1 Names, codes, and coordinates of 15 malaria-epidemic districts in Cambodia.**

Provinces	Code	Districts	Longitude	Latitude
Ratanakiri	D1	Ban Lung	107.03179285418508	13.672027588000049
	D2	Bar Kaev	107.17465650652034	13.714599609000006
Mondul Kiri	D3	Saen Monourom	107.159284166921	12.507995605500007
Kratie	D4	Chhloung	106.15974381398499	12.159576416000005
	D5	Kracheh	106.04138692236205	12.483001709000035
	D6	Snuol	106.48281424389101	12.230102539000029
Pursat	D7	Bakan	103.76840549482367	12.694702148500028
	D8	Krakor	104.18974248713322	12.447601318500062
	D9	Phnum Kravanh	103.84139665388508	12.180999756000062
	D10	Pursat	103.90258670135026	12.464172363000074
Kampong Speu	D11	Chbar Mon	104.50861485800577	11.473297119000051
	D12	Kong Pisei	104.62435137231185	11.311584473000039
	D13	Odongk	104.60537479238533	11.691680908000052
	D14	Phnum Sruoch	104.25418281896762	11.311889648000061
Stung Treng	D15	Stueng Traeng	106.07740268503193	13.657196045000035

2 Notations and descriptions

10 The notations/variables used in this study are described and explained in Supplementary Table S2.

12 **Supplementary Table S2 Notations and descriptions.**

Notation	Description	Values	Attribute
S_1	The size of susceptible human populations	N.A. ^a	N.A.
S_2	The size of susceptible vector populations	N.A.	N.A.
Pop_1	The number of human individuals	N.A.	N.A.
Pop_2	The number of vector individuals	N.A.	N.A.
R	The average monthly rainfall (mm)	Rainfall	Time varying
q_{ij}	The probability or proportion of commuters in location j who choose to work in location i (element in matrix Q)	Social-economic data	Time invariant
$f_{j,mo}$	The proportion of commuters who start their travel for work to other interested locations from location j to the total population of location j in month mo (element in matrix F)	To be estimated	Time varying
u	The gonotrophic cycle length of mosquitoes	Eq. (31)	Time varying
f_u	The number of degree days needed for mosquito maturation	$36.5\text{ }^{\circ}\text{C}^{\circ}$ (refer to work (Shi et al., 2020))	Time invariant
f_n	The number of degree days required for parasite development	105 (refer to work (Shi et al., 2020))	Time invariant
g_u	The threshold below which gonotrophic development ceases	9.9 (refer to work (Shi et al., 2020))	Time invariant
g_n	The threshold below which parasite development ceases	$18\text{ }^{\circ}\text{C}^{\circ}$ (refer to work (Shi et al., 2020))	Time invariant
h	The proportion of mosquitoes that have ever fed on a human	0.7 (refer to work (Shi et al., 2020))	Time invariant
γ	Probability of a mosquitoes surviving after a gonotrophic cycle	0.5 (refer to work (Shi et al., 2020))	Time invariant
η	The learning rate of descent gradient algorithms	Adjusted by the Adam method	N.A.
θ	The threshold of descent gradient algorithms	10^{-7}	Time invariant

^aNot applicable.

3 The model

3.1 SLIS model

As mentioned in the main text, we use a host vector susceptible-latent-infected-susceptible (SLIS) model (Xiao & Zou, 2013) to describe the local malaria transmission. Malaria transmission at the population level can be

20 mathematically described as follows:

$$\begin{aligned}
 & \frac{dS_1(t)}{dt} = -ae_1mS_1(t)\frac{I_2(t)}{Pop_2} + b_1 + r_1I_1(t) - d_1S_1(t) \\
 & \frac{dI_1(t)}{dt} = ae_1mS_1(t)\frac{I_2(t)}{Pop_2} - (d_1 + d + r_1)I_1(t) \\
 & \frac{dS_2(t)}{dt} = -ae_2S_2(t)\frac{I_1(t)}{Pop_1} + b_2 - d_2S_2(t) \\
 & \frac{dL_2(t)}{dt} = ae_2S_2(t)\frac{I_1(t)}{Pop_1} - (\varepsilon_2 + d_2)L_2(t) \\
 & \frac{dI_2(t)}{dt} = \varepsilon_2L_2(t) - d_2I_2(t)
 \end{aligned} \tag{1}$$

22 where $S_1 = Pop_1 - I_1(t)$ and I_1 are the numbers of susceptible and infected individuals, respectively; $S_2 =$
 23 $Pop_2 - L_2(t) - I_2(t)$, L_2 , and I_2 are the numbers of susceptible, latent, and infected vectors, respectively; and
 24 Pop_1 and Pop_2 denote the total human and vector population, respectively. Detailed explanations of the
 25 parameters are given in Supplementary Table S2.

26
 27 Note that we make some assumptions in the model. First, we ignore the effect of natural births and deaths on the
 28 human population by setting $b_1 = d_1 = 0$. Moreover, due to the low malaria mortality in Cambodia in recent
 29 years (World Health Organization, 2021), we do not consider the deaths caused by malaria, i.e., we set $d = 0$.
 30 Furthermore, because the incidence of malaria is relatively low in each district among all populations, we assume
 31 that the infected individuals transmit malaria in a fully susceptible environment, i.e., we approximate $\frac{S_1(t)}{Pop_1} = 1$
 32 and $\frac{S_2(t)}{Pop_2} = 1$.

3.2 Next-generation matrix (NGM) and vectorial capacity (VCAP)

35 According to the constructed NGM, the numbers of infected people and latent vectors at time $t + 1$, which are
 36 represented by the $N \times 1$ vectors I_1^{t+1} and L_2^{t+1} , respectively, can be calculated based on the observations at time
 37 t :

$$\begin{pmatrix} I_1^{t+1} \\ L_2^{t+1} \end{pmatrix} = \mathbf{K}_t \begin{pmatrix} I_1^t \\ L_2^t \end{pmatrix}. \tag{2}$$

39 Since complete and continuous entomological data are difficult to obtain for latent vectors, we predict the infected
 40 case number by utilizing the diagonal property of $\mathbf{K}_t^2$:

$$I_1^{t+2} = (\mathbf{K}_t \times \mathbf{K}_t)_{1,1} I_1^t = ((\mathbf{K}_t)^2)_{1,1} I_1^t = P I_1^t, \tag{3}$$

42 where $((\mathbf{K}_t)^2)_{1,1}$ denotes the block in the first row and the first column of the block matrix $(\mathbf{K}_t)^2$. Therefore, the
 43 malaria transmission matrix P between different locations can be represented as follows:

$$P = \left(AM \varepsilon_2 (D_2 (D_2 + \varepsilon_2))^{-1} A E_1 E_2 \right) (- (S - R_1)^{-1}). \tag{4}$$

45
 46 Based on the used SLIS model, we can reformulate the classic VCAP expression (Brady et al., 2016; Smith &
 47 McKenzie, 2004). Specifically, the VCAP at location i can be reformulated as follows:

$$VCAP_i = \frac{a_i^2 m_i \varepsilon_{2,i} e_{2,i}}{d_{2,i} (d_{2,i} + \varepsilon_{2,i})}, \tag{5}$$

49 where m can be replaced as our definition of vector density described in the main text. The matrix format for
 50 VCAP at all locations can then be written as:

$$VCAP = AM \varepsilon_2 (D_2 (D_2 + \varepsilon_2))^{-1} A E_2, \tag{6}$$

52 where A , E_2 , D_2 , M , and ε_2 are $N \times N$ diagonal matrices with diagonal elements a_i , $e_{1,i}$, $d_{2,i}$, m_i , and $\varepsilon_{2,i}$ ($i =$
 53 $1, 2, \dots, N$), respectively.

3.3 Multivariate regression model for future risk prediction

56 Based on the formulation of prediction task in the main text, the optimization objective of the multivariate
 57 regression model can be formulated as follows:

$$\begin{aligned}
\min_p \|\epsilon\|_2^2 &= \min_p \|\mathbf{Y} - \mathbf{Y}^*\|_2^2 \\
&= \min_p \|\mathbf{Y} - P\mathbf{X}\|_2^2 \\
&= \min_{p^t} \sum_{t=1}^{m-1} \|\mathbf{y}^{t+1} - \mathbf{y}^{t+1,*}\|_2^2 \\
&= \min_{p^t} \sum_{t=1}^{m-1} \|\mathbf{y}^{t+1} - P^t \mathbf{x}^t\|_2^2,
\end{aligned} \tag{7}$$

where $\mathbf{Y}$ is the ground truth of the transmission risk (e.g., quantified by the number of infections) and $\mathbf{Y}^*$ is the predicted risk obtained from our model. Thus, the error item is:

$$\begin{aligned}
E = \|\epsilon\|_2^2 &= \|\mathbf{Y} - P\mathbf{X}\|_2^2 \\
&= \left\| \mathbf{Y} - \left(- \left(AM\epsilon_2(D_2(D_2 + \epsilon_2))^{-1} AE_1 E_2 \right) (S - (D_1 + R_1))^{-1} \mathbf{X} \right) \right\|_2^2 \\
&= \left\| \mathbf{Y} + \left(AM\epsilon_2(D_2(D_2 + \epsilon_2))^{-1} AE_1 E_2 \right) (S - (D_1 + R_1))^{-1} \mathbf{X} \right\|_2^2.
\end{aligned} \tag{8}$$

With our hypotheses on the SLIS model, D_1 is a zero matrix. To simplify the expression, we let $B = (D_1 + R_1)$, $C = AM\epsilon_2(D_2(D_2 + \epsilon_2))^{-1} AE_1 E_2$, and $S = QF$, then we can rewrite the above objective function as follows:

$$\begin{aligned}
E &= \|\mathbf{Y} + C(QF - B)^{-1} \mathbf{X}\|_2^2 \\
&= \sum_{t=1}^{T-1} \|\mathbf{y}^{t+1} + C(QF - B)^{-1} \mathbf{x}^t\|_2^2 \\
&= \sum_{t=1}^{T-1} \text{tr}((\mathbf{y}^{t+1} + C(QF - B)^{-1} \mathbf{x}^t)(\mathbf{y}^{t+1} + C(QF - B)^{-1} \mathbf{x}^t)^T),
\end{aligned} \tag{9}$$

where $\text{tr}(\cdot)$ denotes the trace operator.

4 Optimization procedure

We use the gradient descent method to minimize the error item E . Since the objective function in Eq. (7) has no closed-form solution, we introduce an iterative strategy to solve the problem. In each iteration, we update the value of one variable via gradient descent while keep the values of other variables fixed. All variables will be iteratively updated until convergence.

4.1 Calculating $m_{i,0}$ via updating $c_{i,0}$

For the matrix C , we rewrite it as: $C = AM^* \epsilon_2(D_2(D_2 + \epsilon_2))^{-1} AE_1 E_2 + C_0$, where C_0 is a time-invariant item, the diagonal elements of M^* are the diagonal elements of M removing the intercept item $m_{i,0}$, and $AM^* \epsilon_2(D_2(D_2 + \epsilon_2))^{-1} AE_1 E_2$ is spatiotemporally varying caused by the seasonal and geographical heterogeneities. Accordingly, the intercept in the formula of vector density for location i , i.e., $m_{i,0}$ (please refer to the Methods Section in the Main Text, and in our study a location means a district), can be rewritten as follows:

$$m_{i,0} = c_{i,0} \cdot \frac{d_{i,2}(\epsilon_{i,2} + d_{i,2})}{a_i^2 e_{i,1} e_{i,2} \epsilon_{i,2}}. \tag{10}$$

Then the transmission intensity matrix P in Eq. (4) can be written as follows:

$$P = \left(AM^* \epsilon_2(D_2(D_2 + \epsilon_2))^{-1} AE_1 E_2 + C_0 \right) \left(- (S - (D_1 + R_1))^{-1} \right). \tag{11}$$

As a result, we can calculate $m_{i,0}$ through updating $c_{i,0}$. The updating rule is given as follows:

$$\frac{\partial E}{\partial C} = \sum_{t=1 \text{ and month}=mo}^{T-1} 2\mathbf{y}^{t+1} \mathbf{x}^{tT} (QF_{mo} - B)^{-T} + 2C(QF_{mo} - B)^{-1} \mathbf{x}^t \mathbf{x}^{tT} (QF_{mo} - B)^{-T}, \tag{12}$$

$$\frac{\partial C}{\partial c_{i,0}} = \begin{pmatrix} \mathbb{I}_1^1 & 0 & \cdots & 0 \\ 0 & \mathbb{I}_2^1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mathbb{I}_N^1 \end{pmatrix}, \mathbb{I}_j^1 = \begin{cases} 1, & \text{if } j = i \\ 0, & \text{if } j \neq i \end{cases} \quad (13)$$

$$\frac{\partial E}{\partial c_{i,0}} = \sum_{u=1}^N \sum_{v=1}^N \left(\frac{\partial E}{\partial C} \circ \frac{\partial C}{\partial c_{i,0}} \right)_{uv}, \quad (14)$$

$$c_{i,0} = c_{i,0} - \eta \frac{\partial E}{\partial c_{i,0}}. \quad (15)$$

4.2 The updating rule of e_1 and e_2

We combine e_1 and e_2 as a single parameter, i.e., $\beta = e_1 \times e_2$, so we set $\beta = I_N \beta = \mathbf{E}_1 \mathbf{E}_2$, which is a diagonal matrix. Here I_N is an identity matrix with the size N , and we set β to be the same for all locations.

$$\frac{\partial C}{\partial \beta} = A M \mathbf{E}_2 (D_2 (D_2 + \mathbf{E}_2))^{-1} A, \quad (16)$$

$$\frac{\partial E}{\partial \beta} = \sum_{u=1}^N \sum_{v=1}^N \left(\frac{\partial E}{\partial C} \circ \frac{\partial C}{\partial \beta} \right)_{uv}, \quad (17)$$

$$\beta = \beta - \eta \frac{\partial E}{\partial \beta}. \quad (18)$$

Upon the completion of optimization, we decompose β into e_1 and e_2 by:

$$e_1 = e_2 = \sqrt{\beta}. \quad (19)$$

4.3 The updating rule of x_l

$$\frac{\partial C}{\partial x_k} = A \begin{pmatrix} \tau_1 & 0 & \cdots & 0 \\ 0 & \tau_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \tau_N \end{pmatrix} \mathbf{E}_2 (D_2 (D_2 + \mathbf{E}_2))^{-1} A \mathbf{E}_1 \mathbf{E}_2, \quad (20)$$

$$\tau_i = R_i \cdot \frac{1}{G_{total}} \sum_{g=1}^{G_{total}^k} \frac{o_{2,k,g}}{pop_{1,k,g}}, \quad (21)$$

$$\frac{\partial E}{\partial x_k} = \sum_{u=1}^N \sum_{v=1}^N \left(\frac{\partial E}{\partial C} \circ \frac{\partial C}{\partial x_k} \right)_{uv}, \quad (22)$$

$$x_k = x_k - \eta \frac{\partial E}{\partial x_k}. \quad (23)$$

4.4 The updating rule of $f_{i,mo}$

$$\frac{\partial E}{\partial (QF_{mo} - B)^{-1}} = \sum_{t=1 \text{ and month}=mo}^{T-1} 2C^T \mathbf{y}^{t+1} \mathbf{x}^{tT} + 2C^T C (QF_{mo} - B)^{-1} \mathbf{x}^t \mathbf{x}^{tT}, \quad (24)$$

$$\begin{aligned} \frac{\partial (QF_{mo} - B)^{-1}}{\partial f_{i,mo}} &= -(QF_{mo} - B)^{-1} \frac{\partial (QF_{mo} - B)}{\partial f_{i,mo}} (QF_{mo} - B)^{-1}, \\ &= -(QF_{mo} - B)^{-1} Q \begin{pmatrix} \mathbb{I}_1^1 & 0 & \cdots & 0 \\ 0 & \mathbb{I}_2^1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mathbb{I}_N^1 \end{pmatrix} (QF_{mo} - B)^{-1}, \end{aligned} \quad (25)$$

$$\frac{\partial E}{\partial f_{i,mo}} = \sum_{u=1}^N \sum_{v=1}^N \left(\frac{\partial E}{\partial(QF_{mo} - B)^{-1}} \circ \frac{\partial(QF_{mo} - B)^{-1}}{\partial f_{i,mo}} \right)_{uv}, \quad (26)$$

$$f_{i,mo} = f_{i,mo} - \eta \frac{\partial E}{\partial f_{i,mo}}. \quad (27)$$

109

110 4.5 The updating rule of r_1

111 We assume that the r_1 will be the same for all locations, so we have $R_1 = I_N r_1$, where I_N is an identity matrix with
112 the size N .

$$\begin{aligned} \frac{\partial(QF_{mo} - B)^{-1}}{\partial r_1} &= -(QF_{mo} - B)^{-1} \frac{\partial(QF_{mo} - B)}{\partial r_1} (QF_{mo} - B)^{-1}, \\ &= -(QF_{mo} - B)^{-1} \begin{pmatrix} -1 & 0 & \cdots & 0 \\ 0 & -1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & -1 \end{pmatrix} (QF_{mo} - B)^{-1}, \end{aligned} \quad (28)$$

$$\frac{\partial E}{\partial r_1} = \sum_{u=1}^N \sum_{v=1}^N \left(\frac{\partial E}{\partial(QF_{mo} - B)^{-1}} \circ \frac{\partial(QF_{mo} - B)^{-1}}{\partial r_1} \right)_{uv}, \quad (29)$$

$$r_1 = r_1 - \eta \frac{\partial E}{\partial r_1}. \quad (30)$$

116 4.6 The gradient descent algorithm

117 As the size of dataset is relatively small, in each iteration, we apply the batch gradient descent algorithm to all
118 data samples to update parameters. We adopt the Adam method (Kingma & Ba, 2015) to adaptively update the
119 learning rates for different parameters, so as to ensure a better convergence of the algorithm. The detailed
120 procedure of the gradient descent algorithm is provided in the following Algorithm 1.
121
122

Algorithm 1. The gradient descent algorithm

Input: $A, M, \varepsilon_2, \eta, \theta, \maxIteration$

Output: Matrix $C_0, G_0, g_k (k = 1, 2, \dots, l), F_m (m = 1, 2, \dots, 12), \beta, r_1$

```

1: Initialize  $C_0$  as identity matrix * 0.1
2: Initialize  $\beta$  as 0.1
3: Initialize  $r_1$  as 0.5
4: Initialize  $G_0$  as identity matrix
5: Initialize  $g_1, g_2, \dots, g_l$  as 1
6: Initialize  $F_1, F_2, \dots, F_{12}$  as identity matrix * 0.25
7:  $timestep = 0$ 
8: while  $\Delta E > \theta$  or  $timestep < \maxIteration$ :
9:    $Old\ E = E$ 
10:  for  $i$  in  $N$  do:
11:    for  $t$  in  $T$  do:
12:       $m = \text{current month}$ 
13:      Calculate  $\partial E / \partial(QF_{mo} - B)^{-1}$  and  $\partial(QF_{mo} - B)^{-1} / \partial f_{i,mo}$ 
14:    end for
15:    Update  $f_{i,mo}$  by Eq. (27)
16:  end for
17:  for  $k$  in  $l$  do:
18:    for  $i$  in  $N$  do:
19:      for  $t$  in  $T$  do:
20:        Calculate  $\partial E / \partial C$  and  $\partial C / \partial x_k$ 
21:      end for
22:    end for
23:    Update  $x_k$  by Eq. (23),  $k = 1, 2, \dots, l$ 
24:  end for
25:  for  $i$  in  $N$  do:
26:    for  $t$  in  $T$  do:
```

```

27:         Calculate  $\partial E/\partial C$  and  $\partial C/\partial c_{i,0}$ 
28:     end for
29:     Update  $c_{i,0}$  by Eq. (15)
30: end for
31: for  $i$  in  $N$  do:
32:     for  $t$  in  $T$  do:
33:         Calculate  $\partial E/\partial C$  and  $\partial C/\partial \beta$ 
34:     end for
35: end for
36: Update  $\beta$  by Eq. (18)
37: for  $i$  in  $N$  do:
38:     for  $t$  in  $T$  do:
39:         Calculate  $\partial E/\partial(QF_{mo} - B)^{-1}$  and  $\partial(QF_{mo} - B)^{-1}/\partial r_1$ 
40:     end for
41: end for
42: Update  $r_1$  by Eq. (30)
43: Calculate current  $E$  by Eq. (9)
44:  $\Delta E = E - Old\ E$ 
45:  $timestep = timestep + 1$ 
46: end while

```

5 Data preprocess

5.1 Temperature and rainfall

For the temperature and rainfall data, we did not use the grid data directly but rather calculate a value for each district in each month. For each district, we obtained the coordinates of its center of gravity from the geographical boundary data of Cambodia and calculated a weighted average of the values at the four corners of each grid where the district's center of gravity is situated to calculate the temperature and rainfall values for the corresponding district. Here, we used the inverse distance weighting (IDW) method, in which the weights were proportional to the reciprocal of the distance from the center of the grid to each corner. Furthermore, we processed the global gridded data to obtain the average values at the district level by calculating the IDW result for the four corner points of each grid in which the coordinates of each district are located.

5.2 Land cover

We extracted the land cover classification data based on the International Geosphere-Biosphere Programme (IGBP) global vegetation classification scheme from the raw data (MCD12Q1 which is mentioned in the main text) and further combined the 14 main categories into 6 general categories as shown in Supplementary Table S3.

Supplementary Table S3 Categorization of different types of land cover used in our study.

Land Cover Type	IGBP legend
Forest	Evergreen Needleleaf Forests
	Evergreen Broadleaf Forests
	Deciduous Needleleaf Forests
	Deciduous Broadleaf Forests
	Mixed Forests
Shrublands	Closed Shrublands
	Open Shrublands
Savannas and Grass	Woody Savannas
	Savannas
	Grasslands
Wetlands	Permanent Wetlands
Cropland	Croplands
	Cropland/Natural Vegetation Mosaics
Urban and Built-up	Urban and Built-up Lands

6 Parameterization and model fitting

The parameters in our model can be divided into two categories: (1) parameters in the basic SLIS model and (2) parameters in the human mobility matrix. Then, the parameters in each category can be further divided into two groups: (i) parameters that can be directly calculated using domain knowledge/formulation and (ii) parameters that need to be inferred from the model fitting process. Details of the parameters used in this study and their explanations are provided in Supplementary Table S2.

6.1 Parameters in the basic SLIS model

Some of the parameters in the basic SLIS model are related to the biological features of mosquitoes and parasites and thus can be directly calculated based on the local climate conditions (Ceccato et al., 2012; Shi et al., 2020). Specifically, the human biting rate a , the length of the latent period of parasites ε_2^{-1} , and the death rate of mosquitoes d_2 can be directly calculated using temperature data; moreover, the mosquito density m , which is proportional to the vector population, can be calculated using rainfall data. The remaining parameters in the SLIS model, including the transmission efficiency from mosquitoes to humans e_1 , the transmission efficiency from humans to mosquitoes e_2 , and the human recovery rate r_1 , are inferred from least squares fitting with our model. The calculation details for the biological feature-based parameters in the SLIS model are provided in the following two subsections.

6.1.1 Daily biting rate, latent period, vector death rate

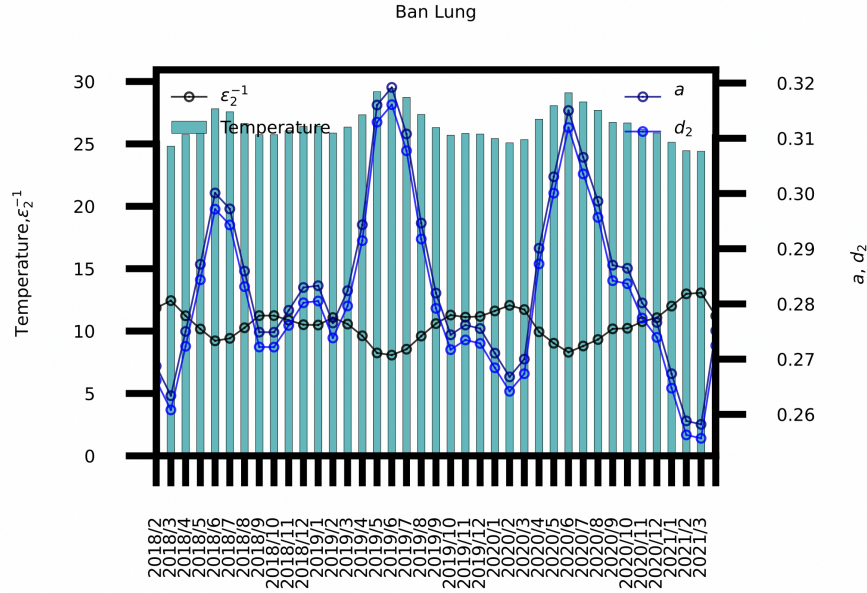
We follow the standard way in existing work (Shi et al., 2020) to calculate the values of parameters related to temperature in the SLIS model (Xiao & Zou, 2013), including the human biting rate a , the latent period of parasite in mosquitoes ε_2^{-1} , and the natural death rate of mosquitoes d_2 :

$$a = \frac{h}{u}, u = 0.5 + \frac{f_u}{(T - g_u + 2)}, \quad (31)$$

$$\varepsilon_2^{-1} = \frac{f_n}{\frac{2f_u}{u(T - g_u + 2)} + (T - g_n)}, \quad (32)$$

$$d_2 = -\frac{1}{u} \ln \gamma, \quad (33)$$

where T is the average monthly temperature ($^{\circ}\text{C}$). The detailed descriptions and values of parameters, such as h , u , f_u , f_n , g_u , g_n , and γ can be found in Supplementary Table S2. An example of the calculated parameters with the corresponding temperature in Ban Lung from 2018 to 2021 is shown in Supplementary Figure S1.



Supplementary Figure S1 An example of the calculated parameters with the corresponding temperature in Ban Lung from February 2018 to March 2021.

6.1.2 Parameters of vector density

The average vector density in a location is calculated by the following formulation:

$$m = \frac{1}{G_{total}} \sum_{k=1}^l \left(\sum_{g=1}^{G_{total}^k} \frac{o_{2,k,g} \times x_{k,g} \times R_{k,g}}{pop_{1,k,g}} \right) + m_0. \quad (34)$$

Based on the available data, $o_{2,k,g}$ and $pop_{2,k}$ can be estimated using the gridwise data of vector occurrence probability, human density, and rainfall. Furthermore, we make the homogeneous assumption for $R_{k,g}$ in Eq. (34) due to the limited resolution of rainfall data. It means that we use the average rainfall value R in the whole location rather than assigning rainfall values for individual pixels. Similarly, we assume that $x_{k,g}$ is homogeneous in the same type of land cover. Then we estimate a unified value of x_k for all pixels in the land cover type k . Finally, the formula of vector density can be represented as follows:

$$m = \frac{1}{G_{total}} \left(\sum_{k=1}^l \left(\sum_{g=1}^{G_{total}^k} \frac{o_{2,k,g}}{pop_{1,k,g}} \times x_k \right) \times R + m_0 \right). \quad (35)$$

In this equation, parameters x_k and m_0 can be inferred using the algorithm introduced in Section 4 of the Supplementary Material, while the others can be calculated using the distributions of land cover, vector species, and human density. Specifically, for each location, the R is the average monthly rainfall (mm); the $o_{2,k,g}$ is the occurrence probability of two dominant vector species in grid g with the land cover type k ; the $pop_{1,k,g}$ is the human population in grid g with the land cover type k ; and the l is the number of land cover types.

6.2 Parameters in the human mobility matrix

We construct the human mobility matrix based on the radiation model (Simini et al., 2012), which is a parameter-free model for approximating mobility and migration patterns using population distribution data from a job-finding perspective. We extend the radiation model by further introducing the relevant seasonal patterns and socioeconomic factors. The extended radiation model includes two components: a temporal component and a spatial component. Correspondingly, the constructed mobility matrix S can be decomposed into two parts, and $S = FQ^T$, where F and Q are used to encode the temporal and spatial information, respectively. The values of the parameters in matrix Q can be directly calculated using the economic data based on the radiation model, and the values of the parameters in matrix F can be inferred by model fitting. Notably, the human mobility matrix can be flexibly constructed using different types of mobility-related data, such as routine human population movement data from censuses and surveys (Pindolia et al., 2012), transportation data (Bajardi et al., 2011), and mobile phone call record data (González et al., 2008). However, these data are difficult to obtain or generally not publicly available, especially in developing or low-income countries and regions. Therefore, we use economic data for mobility matrix construction in this study.

To be more specific, we formulate the element $\pi_{i,j}$ of the mobility matrix D as follows:

$$\pi_{ij}(mo) = p_j(mo) \cdot q_{ij} = p_j(mo) \cdot \frac{I_i I_j}{(I_j + s_{ji})(I_j + I_i + b_{ji})}, \quad \text{if } i \neq j, \quad (36)$$

$$\pi_{i,i} = - \sum_{j=1, j \neq i}^N \pi_{j,i}. \quad (37)$$

Specifically, the first item $p_j(mo)$ in Eq. (36) denotes the proportion of commuters who start their travel for work from location j to other locations of interest to the total population of location j in month mo , and the second item q_{ij} in Eq. (36) denotes the probability that commuters in location j choose to go to location i for work. By considering the seasonal factors, we set $p_j(\cdot)$ as a function of mo , which has 12 possible values (one for each month) for each location:

$$p_j(mo) = f_{j,mo}, \quad mo = 1, 2, \dots, 12. \quad (38)$$

Furthermore, the I_i in q_{ij} is an indicator that represents the attraction of location i to the labor force, and we use the number of people engaging in establishments to estimate it. Due to the lack of social-economic survey data in Cambodia for the period covered in this study (2018-2021), we use the available data of 2011 (*District and Commune Report of Cambodian 2011 Economic Census*, 2011) as the proxy for the parameter estimation. The parameter b_{ji} in q_{ij} is defined as: $\sum_{k=1, k \neq j}^N I_k$, where $r_{j,i}$ denotes the distance between the center of location j and that of location i . Then we can represent the mobility matrix S as follows:

$$S = QF = \begin{pmatrix} -\sum_{j=1, j \neq i}^N q_{j,1} & q_{1,2} & \cdots & q_{1,N} \\ q_{2,1} & -\sum_{j=1, j \neq i}^N q_{j,2} & \cdots & q_{2,N} \\ \vdots & \vdots & \ddots & \vdots \\ q_{N,1} & q_{N,2} & \cdots & -\sum_{j=1, j \neq i}^N 1_{j,N} \end{pmatrix} \begin{pmatrix} f_{1,mo} & 0 & \cdots & 0 \\ 0 & f_{2,mo} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & f_{N,mo} \end{pmatrix}. \quad (39)$$

7 Quantitative evaluation of model performance

We use the malaria case data and the risk-related data in 15 districts of Cambodia from January 2018 to December 2019 to parameterize our model and use the data from January 2020 to March 2021 to test the performance of our model in transmission risk prediction tasks. We use three standard criteria, namely, the root-mean-square error (RMSE), the mean absolute error (MAE), and the top-K ranking accuracy, to evaluate the prediction performance. We compare the performance of our model with that of two classic data-driven approaches, namely, long short-term memory (LSTM) (Hochreiter & Schmidhuber, 1997) and support vector regression (SVR) (Drucker et al., 1996), and three state-of-the-art machine learning methods: CNNRNN-res (Wu et al., 2018), the interactively and integratively connected deep recurrent neural network (I²DRNN) (Tan et al., 2021), and the Sentinel network mining algorithm (SNMA) (Pei et al., 2022, 2018). The study scope, definitions of the evaluation criteria and the descriptions and settings of the baseline methods used for comparison, experimental results, and robustness analysis are provided in the following subsections.

7.1 Evaluation measures

Three standard evaluation criteria used in this study, i.e., RMSE, MAE, and top-K ranking accuracy, are calculated by the following equations, respectively:

$$RMSE = \sqrt{\frac{\sum_{t=1}^{T_{test}} \|\mathbf{y}^{t,*} - \mathbf{y}^t\|_2^2}{N \times T_{test}}}, \quad (40)$$

$$MAE = \frac{\sum_{t=1}^{T_{test}} |\mathbf{y}^{t,*} - \mathbf{y}^t|}{N \times T_{test}}, \quad (41)$$

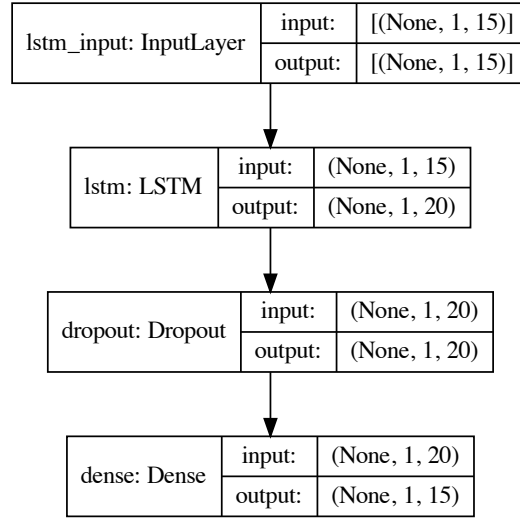
$$Top - K \text{ ranking accuracy} = \frac{|S_{Real} \cap S_{Prediction}|}{K}, \quad (42)$$

where $\mathbf{y}^{t,*}$ denotes the vector of predicted malaria case number in different locations at time step t , $\mathbf{y}^t$ denotes the vector of reported malaria case number in different locations at time step t , T_{test} denotes the number of time steps in testing, N denotes the number of locations, S_{Real} denotes the subset of locations ranked in top-K in the ground truth (i.e., locations with the largest number of reported cases), and $S_{Prediction}$ denotes the subset of locations that our model predicted as the top-K (i.e., locations with the largest predicted number of infections), and $|\cdot|$ in Eq. (42) denotes the cardinality of a set.

7.2 Experimental settings

7.2.1 Long Short-Term Memory (LSTM)

For the LSTM model (Hochreiter & Schmidhuber, 1997), we used the structure with one visible input layer, one hidden layer of 20 LSTM blocks, one drop-out layer to prevent overfitting, and one output layer to make the prediction (Supplementary Figure S2). We used the ReLU activation function for the LSTM blocks. For the optimization, we set the max epochs to 300 and used the early stopping function to prevent overfitting. We set the batch size to 1. In LSTM and other baselines, we used the first two-year data for model training and the rest of the data for performance testing.



Supplementary Figure S2 The structure of LSTM used in our study.

7.2.2 Support Vector Regression (SVR)

We used the linear SVR (Drucker et al., 1996) from the *scikit – learn* library with the default parameter setting: sensitive error $\epsilon = 0.1$ and regularization parameter $C = 1$.

7.2.3 Convolutional Neural Networks and Recurrent Neural Networks model with a residual structure (CNNRNN-res)

The CNNRNN-res model (Wu et al., 2018) required the setting of an adjacency CNN filter, which is represented as an $N \times N$ adjacency matrix with elements being 1 or 0. Since we assume that there are transmission risks between all districts, we set all elements to 1. Moreover, we set the residual window as 4.

7.2.4 Interactively and Integratively connected Deep Recurrent Neural Network (I²DRNN) model

We organized the data formats according to the requirement of the I²DRNN model (Tan et al., 2021). The data consist of two parts: (1) the historical malaria case data; and (2) the external data from heterogeneous sources. We organized the case data as a 15×39 matrix, where 15 denotes the number of districts and 39 denotes the number of months. The external data considered the temperature, rainfall, social-economic indicator, land cover, human population, and vector distribution, which were represented as a matrix with the size $(15 + 15 + 15 + 15 \times 6) \times 39 = 135 \times 39$. For each 135-dimensional vector, the first 45 dimensions correspond to the temperature, rainfall, and social-economic data (15 dimensions for each) in 15 districts, while the last 90 (15×6) dimensions represent the multiplication of human population distribution and vector distribution in 6 different types of land cover of 15 districts. Then, we reduced the vectors' dimensions from 135 to 15 using the principal component analysis (PCA) (Wold et al., 1987) to obtain the representation of the external data, which is a 15×39 matrix. Finally, two 15×39 matrices (one for case data and one for external data) were concatenated to a 30×39 matrix (i.e., one 30-dimensional vector for each month, from January 2018 to March 2021) for model training and testing.

7.2.5 Sentinel Network Mining Algorithm (SNMA)

The SNMA (Pei et al., 2022, 2018) was proposed to simultaneously identify sentinels over the transmission network and predict the spatiotemporal dynamics of the network. In addition to the historical case number in different locations over time, the SNMA required another parameter to be provided as the input, that is, the number of sentinels (locations) to be identified. In our study, to focus on the risk prediction task rather than the sentinel identification, we set this parameter to its maximum possible value, i.e., $N - 1$, which equals 14 in our scenario.

7.3 Detailed experimental results

A comparison of the results is provided in Supplementary Table S4. From the RMSE and MAE (the smaller the value is, the better the model performance), we can observe that the performance of our algorithm is significantly better than that of all other algorithms. Interestingly, the performance of the neural network and deep learning

models, i.e., the LSTM, CNNRNN-res, and I²DRNN, is relatively unsatisfactory. Notably, these types of models generally have many parameters, and in the studied case, the lack of available data on malaria cases results in insufficient model training. For the top-K ranking accuracy (K = 3, 5), our model also achieves the best performance (the higher the accuracy is, the better the model performance). These results indicate that our model is able to accurately identify the locations with the highest malaria transmission risks, which is informative for targeted intervention deployment. Because the LSTM, SVR, CNNRNN-res, I²DRNN, and SNMA models do not appropriately integrate various risk-related factors for intensity modeling, the superiority of our model over these computational approaches in terms of the prediction accuracy further demonstrates the necessity and importance of considering the seasonal and geographical heterogeneity of human mobility, vector distribution, and the environment for comprehensively quantifying the malaria transmission intensity.

Supplementary Table S4 Performance comparison (in terms of RMSE, MAE, and top-K accuracy) of our model and five other representative computational modeling approaches for malaria transmission risk prediction in Cambodia. The smaller the RMSE and MAE values are, the better the model performance, and the higher the top-K ranking accuracy is, the better the model performance. The best result for each criterion among all the methods is highlighted in **bold**, and the second-best result is underlined. The last row shows the improvement (%) of the best result over the second-best result.

Methods	Prediction Error		Predicted Ranking Accuracy	
	RMSE ^f ↓	MAE ^g ↓	Top 3 ↑	Top 5 ↑
LSTM ^a (Hochreiter & Schmidhuber, 1997)	70.95	44.44	0.47	0.73
SVR ^b (Drucker et al., 1996)	65.25	39.77	0.18	0.28
CNNRNN-res ^c (Wu et al., 2018)	41.54	33.70	0.49	0.73
I ² DRNN ^d (Tan et al., 2021)	79.81	51.55	<u>0.58</u>	0.73
SNMA ^e (Pei et al., 2022, 2018)	<u>21.35</u>	<u>11.50</u>	<u>0.58</u>	<u>0.77</u>
Our method	13.14	7.65	0.75	0.88
<i>Improvement over the 2nd best</i>	<i>38.45%</i>	<i>33.48%</i>	<i>29.31%</i>	<i>14.29%</i>

^aLong Short-Term Memory.

^bSupport Vector Regression.

^cConvolutional Neural Networks and Recurrent Neural Networks model with a residual structure.

^dInteractively and Integratively connected Deep Recurrent Neural Network.

^eSentinel Network Mining Algorithm.

^fRoot-mean-square error.

^gMean absolute error.

The performance comparison in terms of RMSE and MAE of our model and five other representative computational approaches for malaria transmission risk prediction in 15 districts of Cambodia can be found in Supplementary Table S5 and Supplementary Table S6 respectively.

Supplementary Table S5 Performance comparison (in terms of RMSE) of our model and five other representative computational approaches for malaria transmission risk prediction in 15 districts of Cambodia. The smaller the RMSE values are, the better the model performance. The best result among all the methods is highlighted in **bold**.

Methods	RMSE ^f ↓														
	D1	D2	D3	D4	D5	D6	D7	D8	D9	D10	D11	D12	D13	D14	D15
LSTM ^a (Hochreiter & Schmidhuber, 1997)	37.55	6.80	64.81	4.48	23.43	2.45	3.14	93.55	166.31	9.51	77.32	4.86	20.45	18.26	161.31
SVR ^b (Drucker et al., 1996)	54.28	3.83	149.41	3.74	33.28	2.41	5.77	78.33	154.01	4.00	41.00	1.86	10.69	23.36	72.14
CNNRNN-res ^c (Wu et al., 2018)	28.20	18.98	50.60	17.89	40.41	12.65	16.40	62.92	95.94	22.13	34.94	19.02	23.60	20.63	59.73
I ² DRNN ^d (Tan et al., 2021)	44.66	5.20	122.06	3.80	28.26	2.41	2.90	90.45	190.51	9.86	112.95	6.17	19.08	24.00	139.62
SNMA ^e (Pei et al., 2022, 2018)	29.82	3.44	19.07	1.13	5.45	2.41	1.02	12.51	57.54	3.01	<u>23.89</u>	1.88	7.54	25.45	27.92
Ours	18.58	<u>3.98</u>	18.44	<u>1.44</u>	<u>8.12</u>	1.82	0.85	11.65	9.98	1.37	21.66	<u>2.49</u>	6.52	<u>21.29</u>	24.66

^aLong Short-Term Memory.

^bSupport Vector Regression.

^cConvolutional Neural Networks and Recurrent Neural Networks model with a residual structure.

^dInteractively and Integratively connected Deep Recurrent Neural Network.
^eSentinel Network Mining Algorithm.
^fRoot-mean-square error.

Supplementary Table S6 Performance comparison (in terms of MAE) of our model and five other representative computational approaches for malaria transmission risk prediction in 15 districts of Cambodia. The smaller the RMSE values are, the better the model performance. The best result among all the methods is highlighted in **bold**.

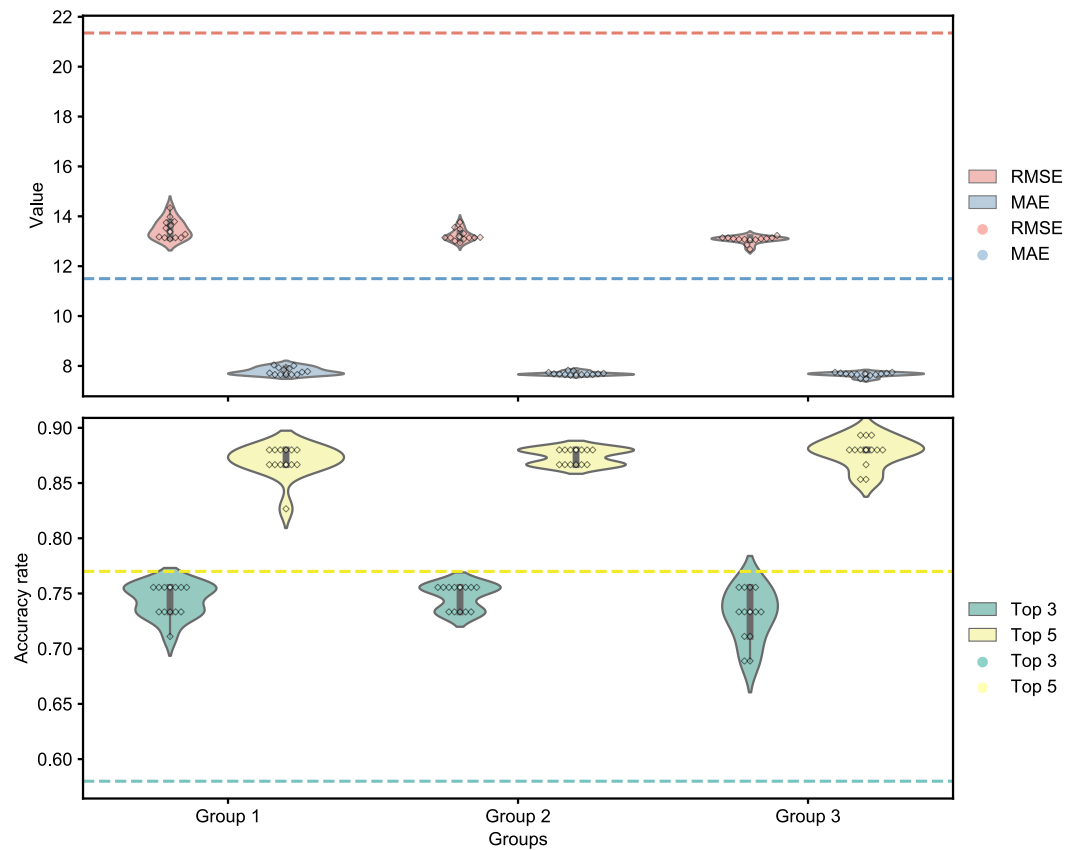
Methods	MAE ^f ↓														
	D1	D2	D3	D4	D5	D6	D7	D8	D9	D10	D11	D12	D13	D14	D15
LSTM ^a (Hochreiter & Schmidhuber, 1997)	30.97	5.88	62.29	4.29	21.54	2.11	3.05	91.31	164.44	9.37	72.66	4.84	19.50	14.94	159.47
SVR ^b (Drucker et al., 1996)	51.87	3.20	148.37	3.55	31.11	2.07	5.62	70.16	145.59	3.75	37.01	1.64	9.50	16.07	66.97
CNNRNN-res ^c (Wu et al., 2018)	22.30	18.35	48.99	17.50	39.91	12.08	16.14	61.73	94.88	21.86	33.18	18.65	22.92	18.55	58.45
I2DRNN ^d (Tan et al., 2021)	40.78	4.19	119.24	3.72	26.35	2.07	2.75	85.48	186.69	9.78	109.08	5.80	18.58	21.78	136.91
SNMA ^e (Pei et al., 2022, 2018)	19.92	2.66	15.80	0.95	4.63	2.07	0.86	10.85	48.64	2.76	14.52	1.71	6.55	18.17	22.35
Ours	14.21	3.00	13.91	1.17	6.58	1.39	0.72	9.50	7.80	1.16	14.95	2.28	4.67	14.46	19.00

^aLong Short-Term Memory.
^bSupport Vector Regression.
^cConvolutional Neural Networks and Recurrent Neural Networks model with a residual structure.
^dInteractively and Integratively connected Deep Recurrent Neural Network.
^eSentinel Network Mining Algorithm.
^fMean absolute error.

7.4 Model robustness

In addition to showing the prediction ability of our model, we test the robustness of the model with respect to variations in the initial values of the learnable parameters. We divide the parameters into three groups based on the model components in which they are used and conduct a sensitivity analysis to examine the impacts of variations in the initial parameter values on model performance. Group 1 includes the parameters in matrices β , R_1 , and C_0 , which are included in the SLIS model for each location and are related to the biological process of malaria transmission. Group 2 includes the parameter x_l , denoting the weights of different types of land cover. Group 3 includes the parameters in the matrix D , which are related to human mobility. When investigating the parameters in one group, we fix the initial values of the parameters in the other two groups and vary the initial values of the parameters in the selected group; notably, these parameters are increased and decreased by 10%, 20%, 30%, 40%, and 50%. We observe the performance variation in our model in terms of the RMSE, MAE, top-3 ranking accuracy, and top-5 ranking accuracy. By doing so, we can explore the impact of variations in the initial values of parameters in each group independently.

Supplementary Figure S3 shows the variation in model performance in terms of the RMSE and MAE (the top one) and the top-3 and top-5 ranking accuracy (the bottom one) with the variations in the initial values of parameters in the three groups. The results demonstrate that the performance of our model is stable in terms of the parameter variations. Regardless of how those parameters vary, our model is consistently superior to the best-performing baseline methods (denoted by the dashed lines in Supplementary Figure S3, illustrating the effectiveness of the proposed model for risk prediction.



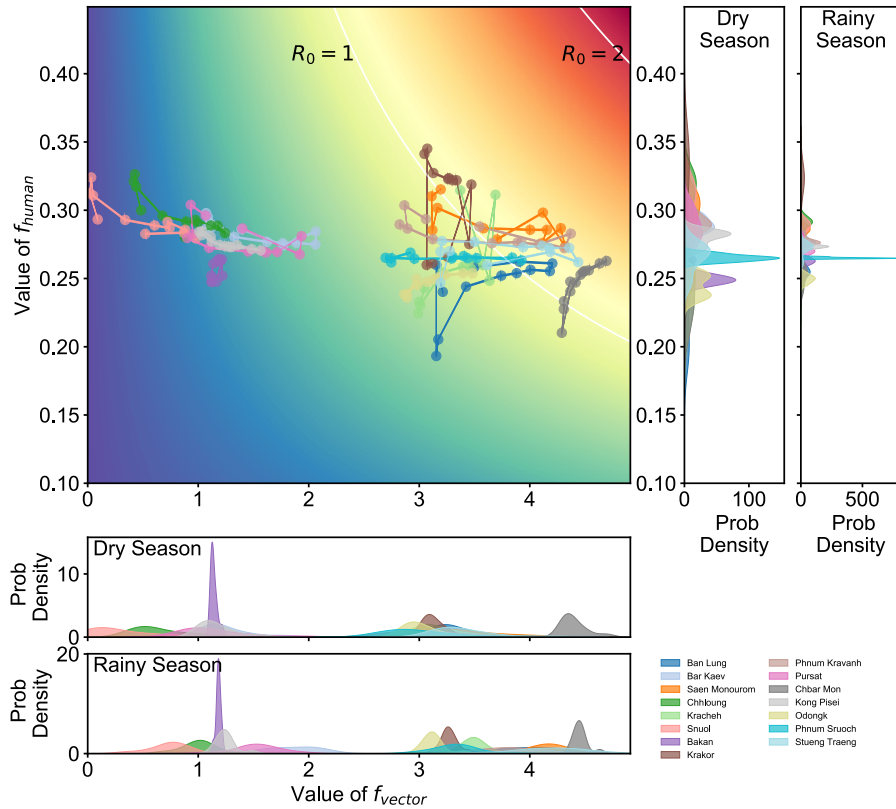
Supplementary Figure S3 Sensitivity analysis of the initial values of the parameters. (Top) RMSE^a and MAE^b and **(Bottom)** the top-3 and top-5 ranking accuracy. The dashed lines denote the best performance of the other baseline methods in Supplementary Table S4.

^aRoot-mean-square error.
^bMean absolute error.

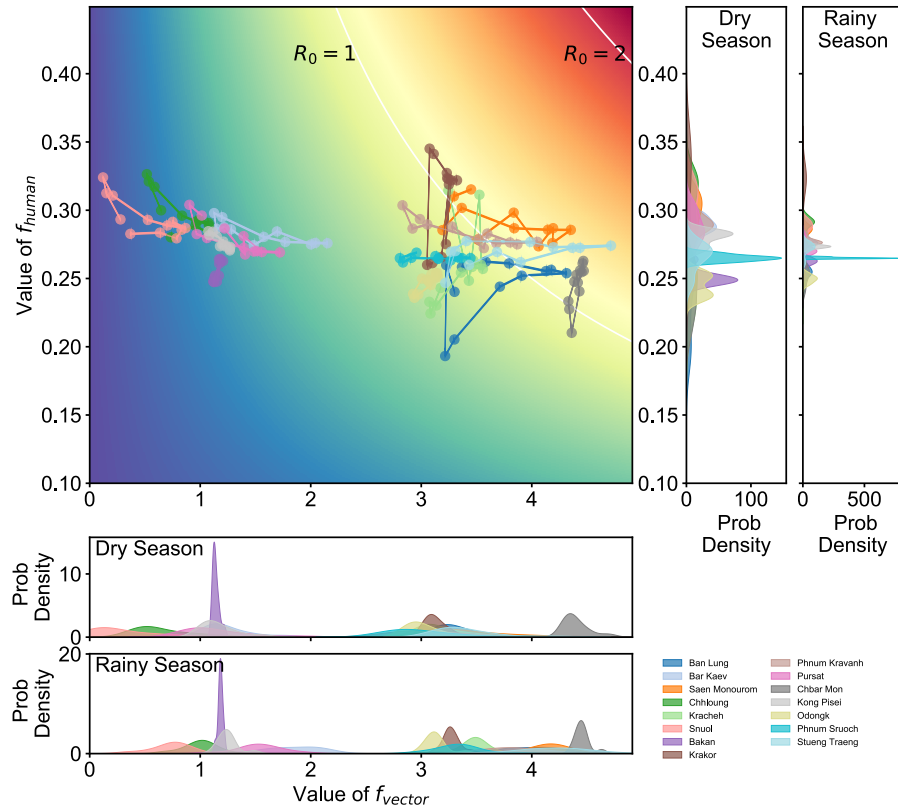
8 Inferred malaria transmission patterns

8.1 Inferred malaria transmission intensity in terms of human and vector factors

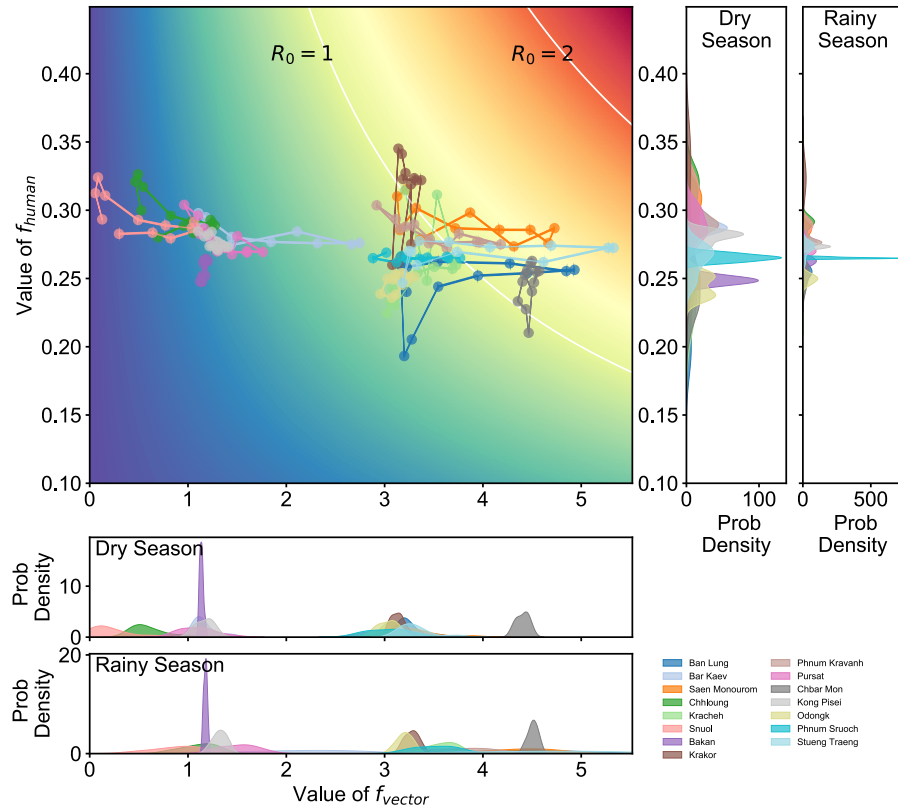
The inferred trajectories of malaria transmission intensity in terms of f_{human} and f_{vector} in all 15 malaria-endemic districts in Cambodia in the whole year of 2018, 2019, 2020 and the period from January 2021 to March 2021 can be found in Supplementary Figure S4, Supplementary Figure S5, Supplementary Figure S6, Supplementary Figure S7 respectively.



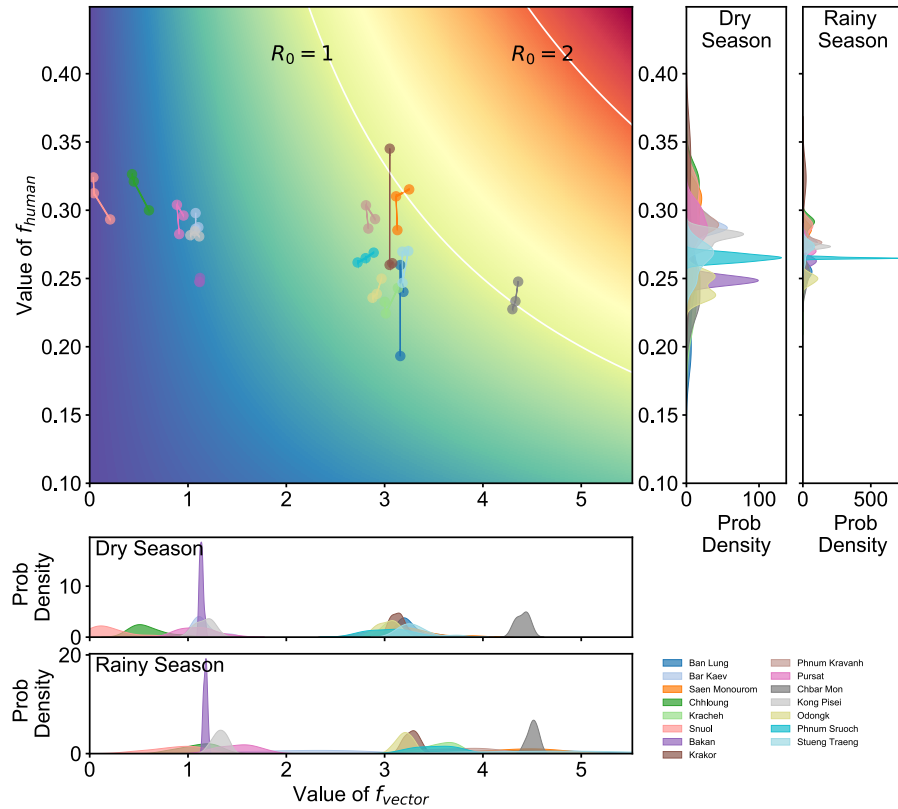
Supplementary Figure S4 Inferred malaria transmission intensity in terms of f_{human} and f_{vector} in all 15 malaria-endemic districts in Cambodia from January 2018 to December 2018. The trajectories of the malaria transmission intensity in terms of f_{vector} and f_{human} are shown in the **top left**. The background color illustrates the strength of malaria transmission intensity in ascending order from blue to red; the white lines show the thresholds of $R_0 = 1$ and $R_0 = 2$. In the **bottom left**, the distributions of f_{vector} in different districts during the dry (from November to April) and rainy (from May to October) seasons, calculated using kernel density estimation, are shown. In the **top right**, the distributions of f_{human} in different districts during the dry and rainy seasons are shown.



Supplementary Figure S5 Inferred malaria transmission intensity in terms of f_{human} and f_{vector} in all 15 malaria-endemic districts in Cambodia from January 2019 to December 2019. The trajectories of the malaria transmission intensity in terms of f_{vector} and f_{human} are shown in the **top left**. The background color illustrates the strength of malaria transmission intensity in ascending order from blue to red; the white lines show the thresholds of $R_0 = 1$ and $R_0 = 2$. In the **bottom left**, the distributions of f_{vector} in different districts during the dry (from November to April) and rainy (from May to October) seasons, calculated using kernel density estimation, are shown. In the **top right**, the distributions of f_{human} in different districts during the dry and rainy seasons are shown.



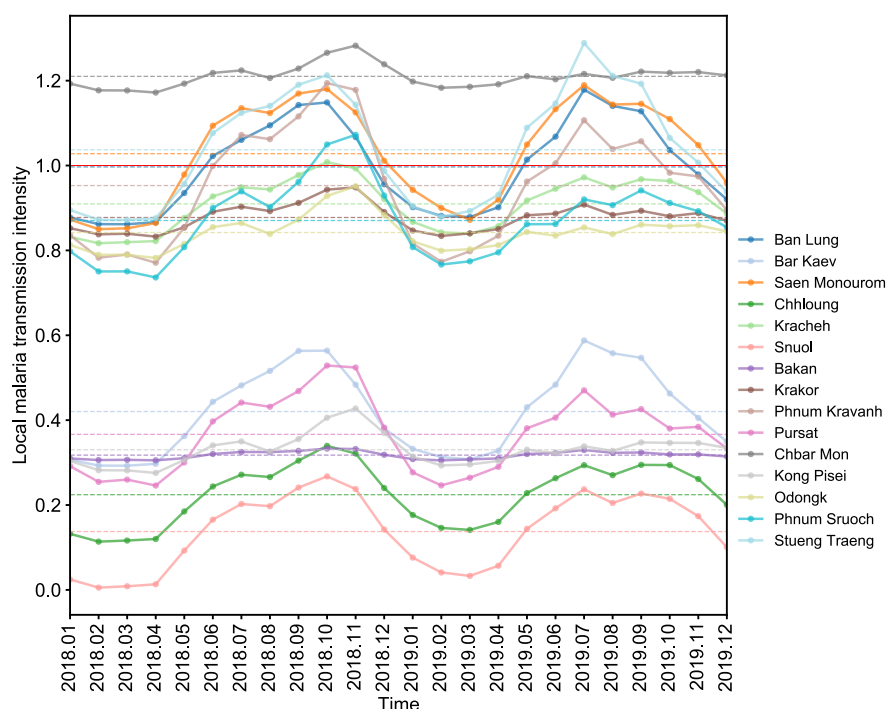
Supplementary Figure S6 Inferred malaria transmission intensity in terms of f_{human} and f_{vector} in all 15 malaria-endemic districts in Cambodia from January 2020 to December 2020. The trajectories of the malaria transmission intensity in terms of f_{vector} and f_{human} are shown in the **top left**. The background color illustrates the strength of malaria transmission intensity in ascending order from blue to red; the white lines show the thresholds of $R_0 = 1$ and $R_0 = 2$. In the **bottom left**, the distributions of f_{vector} in different districts during the dry (from November to April) and rainy (from May to October) seasons, calculated using kernel density estimation, are shown. In the **top right**, the distributions of f_{human} in different districts during the dry and rainy seasons are shown.



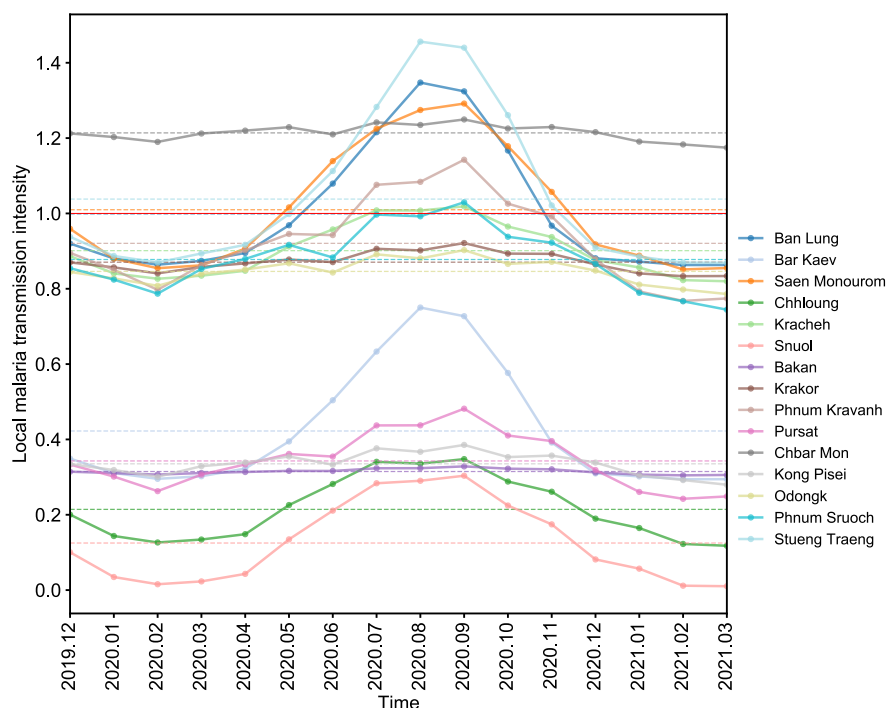
Supplementary Figure S7 Inferred malaria transmission intensity in terms of f_{human} and f_{vector} in all 15 malaria-endemic districts in Cambodia from January 2021 to March 2021. The trajectories of the malaria transmission intensity in terms of f_{vector} and f_{human} are shown in the **top left**. The background color illustrates the strength of malaria transmission intensity in ascending order from blue to red; the white lines show the thresholds of $R_0 = 1$ and $R_0 = 2$. In the **bottom left**, the distributions of f_{vector} in different districts during the dry (from November to April) and rainy (from May to October) seasons, calculated using kernel density estimation, are shown. In the **top right**, the distributions of f_{human} in different districts during the dry and rainy seasons are shown.

8.2 Local malaria transmission intensity

The trends of the local malaria transmission intensities for all districts from January 2018 to December 2019 and those from December 2019 to March 2021 are shown in Supplementary Figure S8 and Supplementary Figure S9, respectively.

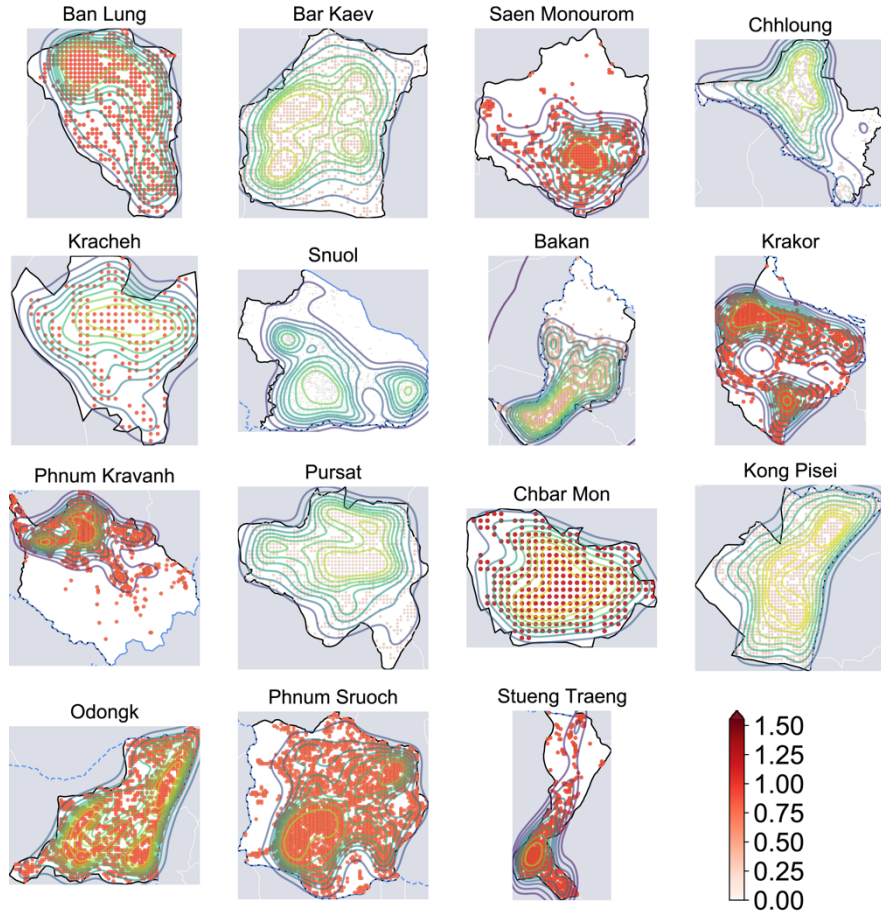


Supplementary Figure S8 The trends of local malaria transmission intensities in all 15 districts from January 2018 to December 2019. The solid line denotes the local malaria transmission intensity in each district along the time, and the dash line denotes average intensity (over time) in each district.

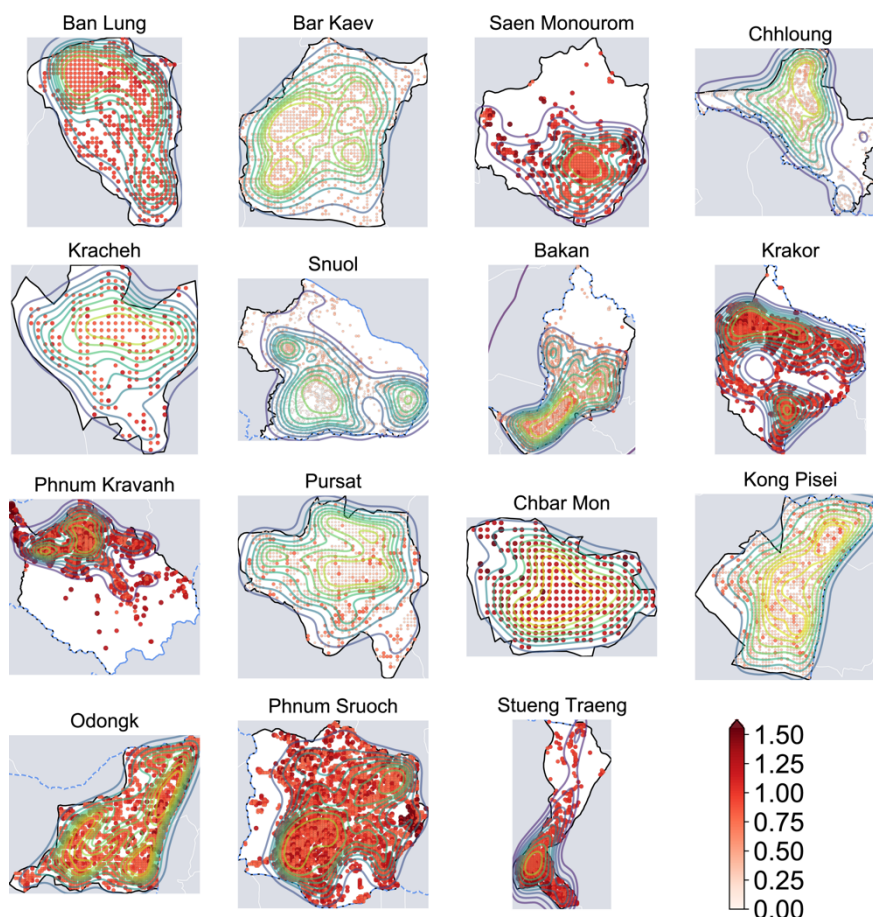


Supplementary Figure S9 The trends of local malaria transmission intensities in all 15 districts from December 2019 to March 2021. The solid line denotes the local malaria transmission intensity in each district along the time, and the dash line denotes average intensity (over time) in each district.

The intensity distribution maps for individual districts in April 2018 and those in December 2018 are shown in Supplementary Figure S10 and Supplementary Figure S11 respectively.



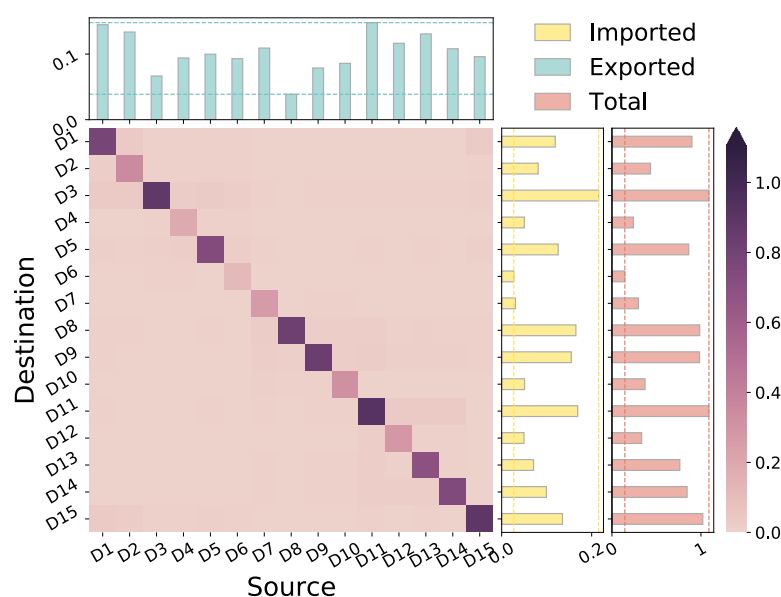
Supplementary Figure S10 The gridwise maps of the local malaria transmission intensity in all 15 malaria-endemic districts in April 2018. The grids in the map (with a grid resolution of 500 m × 500 m) denote the malaria transmission intensity in different locations, and the size and color of each point indicate the corresponding strength of the transmission intensity; the isolines in the maps indicate the human population density at the corresponding locations; the yellow isolines indicate high population density and the dark purple ones indicate low population density; the white background and black line denote the district boundaries.



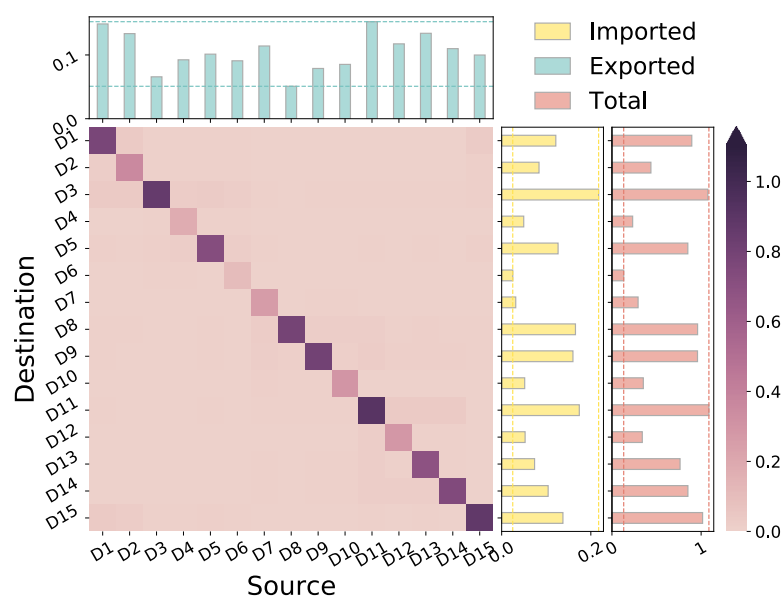
Supplementary Figure S11 The gridwise maps of the local malaria transmission intensity in all 15 malaria-endemic districts in December 2018. The grids in the map (with a grid resolution of 500 m × 500 m) denote the malaria transmission intensity in different locations, and the size and color of each point indicate the corresponding strength of the transmission intensity; the isolines in the maps indicate the human population density at the corresponding locations; the yellow isolines indicate high population density and the dark purple ones indicate low population density; the white background and black line denote the district boundaries.

8.3 Cross-location malaria transmission intensity

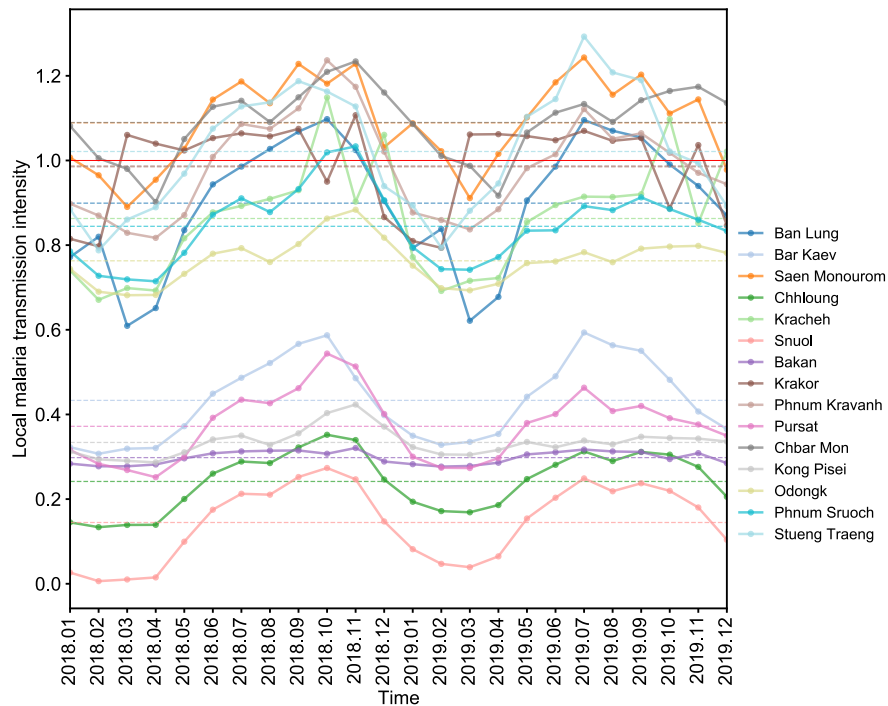
The average malaria transmission intensity matrix and the average total, imported, and exported malaria transmission intensities from January 2018 to December 2019 and those from December 2019 to March 2021 are shown in Supplementary Figure S12 and Supplementary Figure S13, respectively. The trends of total malaria transmission intensities in individual districts from January 2018 to December 2019 and those from December 2019 to March 2021 are shown in Supplementary Figure S14 and Supplementary Figure S15, respectively.



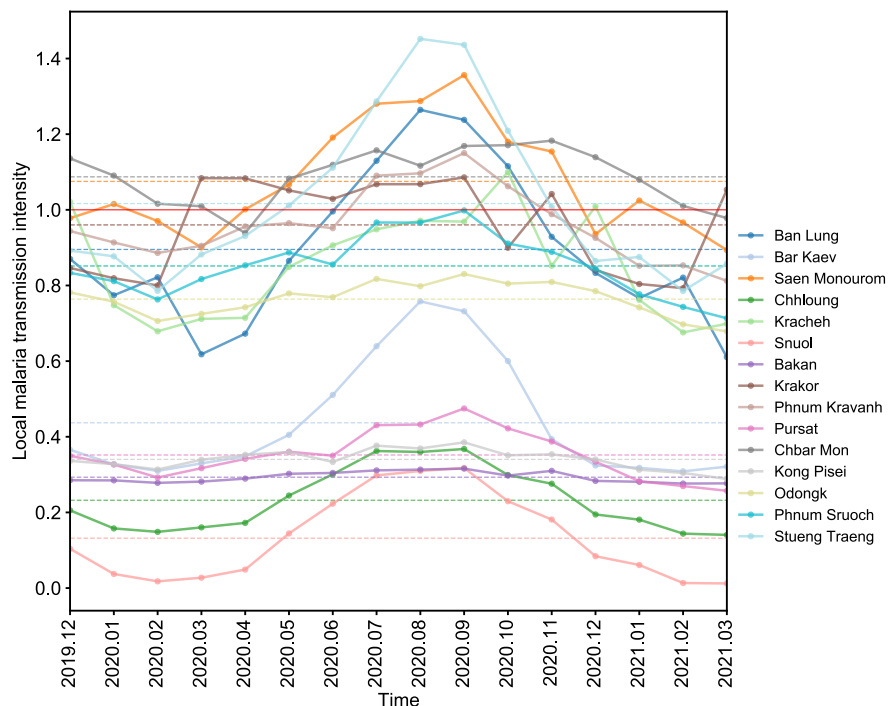
Supplementary Figure S12 The average malaria transmission intensity matrix as well as the average total, imported, and exported malaria transmission intensity from January 2018 to December 2019. The matrix in the center shows the cross-location malaria transmission intensity. The first bar chart on the right side of the center matrix denotes the intensity or impact of cases of imported malaria from other districts (yellow). The bar chart on the top of the center matrix denotes the intensity or impact of malaria cases exported to other districts (green). The second bar chart on the right side of the center matrix denotes the total malaria intensity calculated after considering the effect of human mobility (pink). The dashed lines in the bar charts denote the bounds of the highest and lowest values.



Supplementary Figure S13 The average malaria transmission intensity matrix as well as the average total, imported, and exported malaria transmission intensity from December 2019 to March 2021. The matrix in the center shows the cross-location malaria transmission intensity. The first bar chart on the right side of the center matrix denotes the intensity or impact of cases of imported malaria from other districts (yellow). The bar chart on the top of the center matrix denotes the intensity or impact of malaria cases exported to other districts (green). The second bar chart on the right side of the center matrix denotes the total malaria intensity calculated after considering the effect of human mobility (pink). The dashed lines in the bar charts denote the bounds of the highest and lowest values.

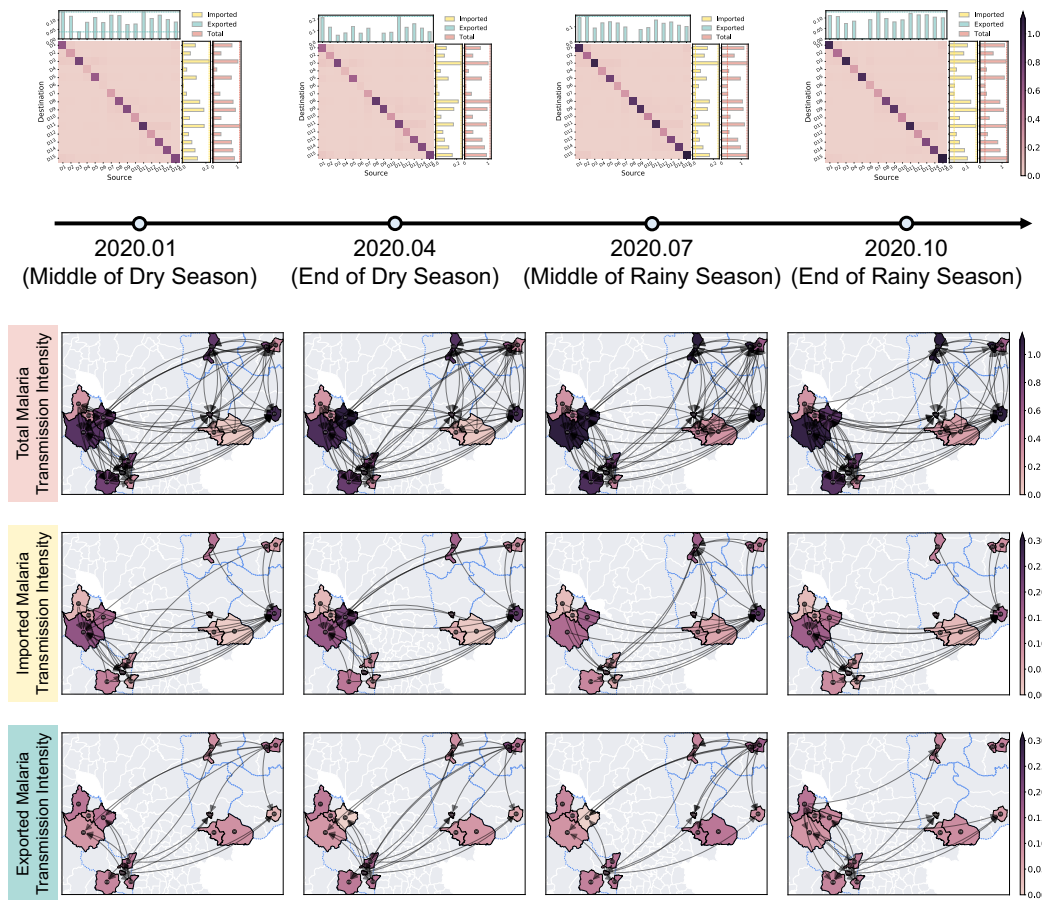


Supplementary Figure S14 The trends of total (local, imported, and exported) malaria transmission intensities in all 15 malaria-endemic districts from January 2018 to December 2019. The solid line denotes the total malaria transmission intensity in each district along the time, and the dash line denotes the average intensity (over time) in each district.

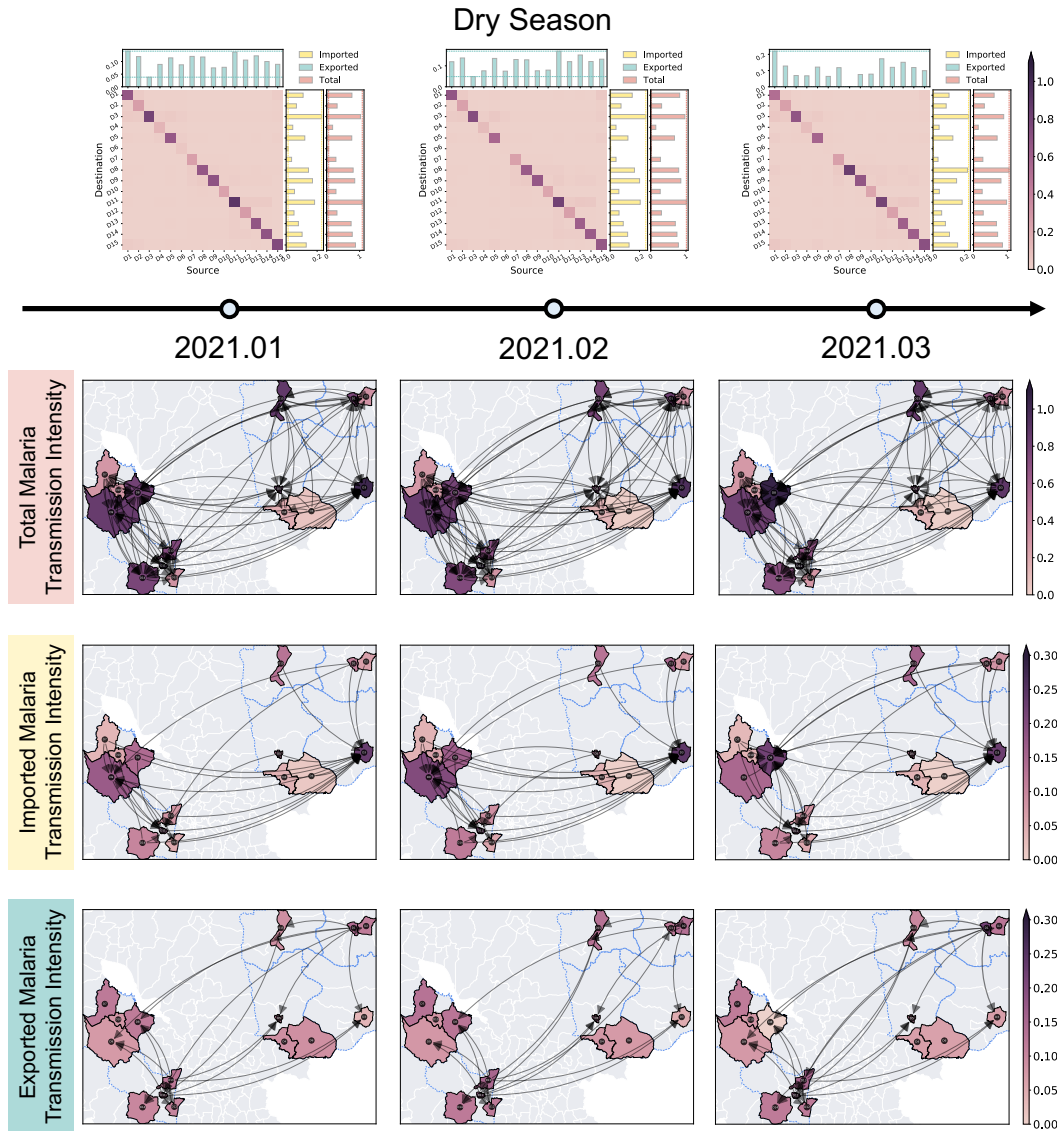


Supplementary Figure S15 The trends of total (local, imported, and exported) malaria transmission intensities in all 15 malaria-endemic districts from December 2019 to March 2021. The solid line denotes the total malaria transmission intensity in each district along the time, and the dash line denotes the average intensity (over time) in each district.

The cross-location malaria transmission intensity map in 2020 and 2021 is shown in Supplementary Figure S16 and Supplementary Figure S17.



Supplementary Figure S16 Spatiotemporal variations in cross-location malaria transmission intensity. The four rows show four types of information: (1) the inferred malaria transmission intensity matrix; (2) the map of total malaria transmission; (3) the map of imported malaria transmission, and (4) the map of exported malaria transmission. The four columns show the results for four different periods in 2020: (1) middle of the dry season (January); (2) end of the dry season (April); (3) middle of the rainy season (July); and (4) end of the rainy season (October). **(First row)** The matrix in the center shows the cross-location malaria transmission intensity. The first bar chart on the right side of the center matrix denotes the intensity or impact of cases of imported malaria from other districts (yellow). The bar chart on the top of the center matrix denotes the intensity or impact of malaria cases exported to other districts (green). The second bar chart on the right side of the center matrix denotes the total malaria intensity calculated after considering the effect of human mobility (pink). The dashed lines in the bar charts denote the bounds of the highest and lowest values. **(Second row)** The color of each district denotes the total malaria transmission intensity; each directed edge denotes the cross-district malaria intensity across different districts. Here, we only show edges with intensities > 0.005 . **(Third row)** The color of each district denotes the imported malaria transmission intensity. Here, we only show edges going to districts with the top three imported intensities and those with intensities > 0.005 . **(Last row)** The color of each district denotes the exported malaria transmission intensity. Here, we only show edges coming from districts with the top three exported intensities and those with intensities > 0.005 . For the value range of the colors, please refer to the color bars on the right side of each row.

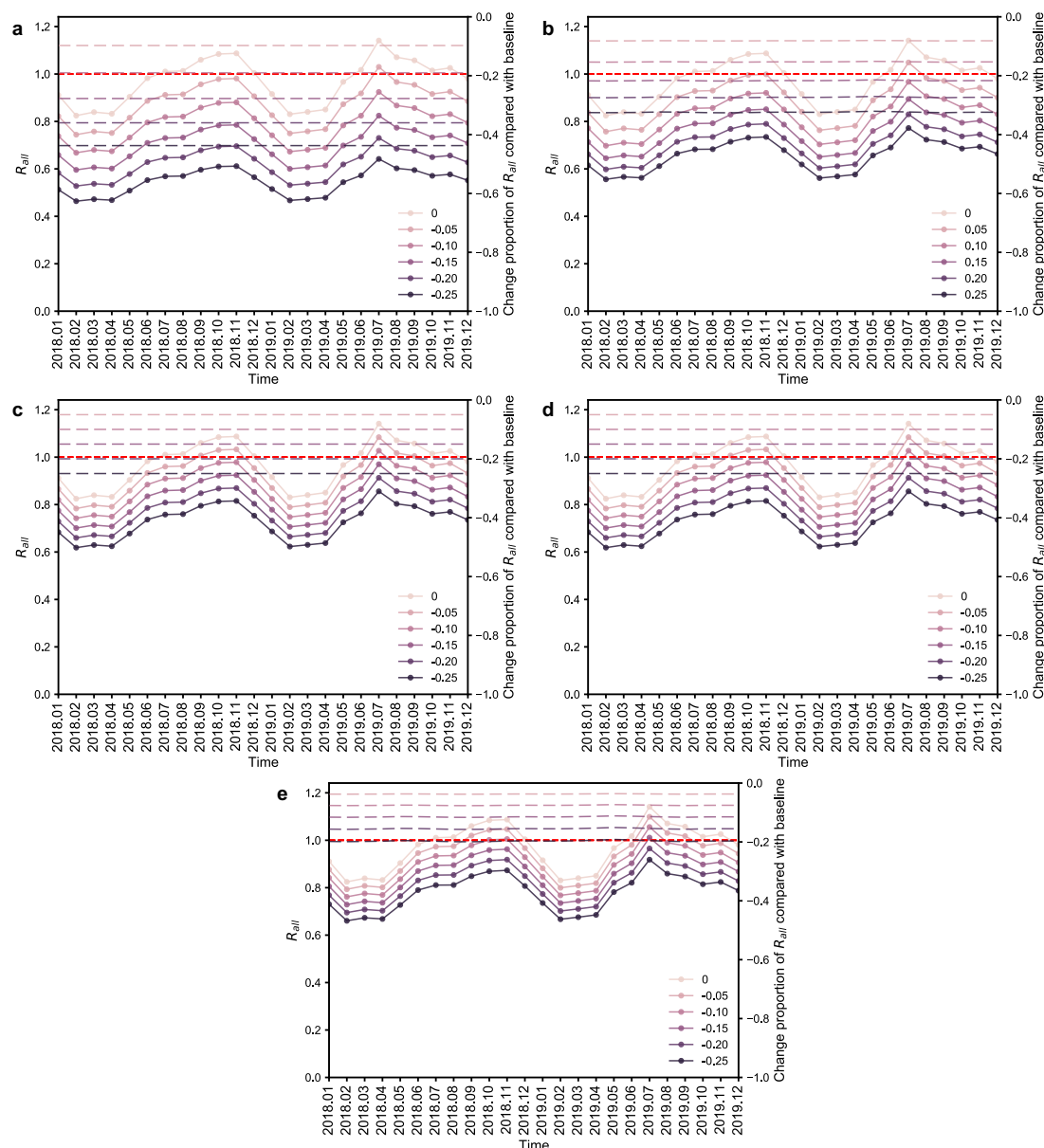


Supplementary Figure S17 Spatiotemporal variations in cross-location malaria transmission intensity. The four rows show four types of information: (1) the inferred malaria transmission intensity matrix; (2) the map of total malaria transmission; (3) the map of imported malaria transmission, and (4) the map of exported malaria transmission. The four columns show the results for *three* different periods in 2021: (1) *January 2021*; (2) *February 2021*; (3) *March 2021*. **(First row)** The matrix in the center shows the cross-location malaria transmission intensity. The first bar chart on the right side of the center matrix denotes the intensity or impact of cases of imported malaria from other districts (yellow). The bar chart on the top of the center matrix denotes the intensity or impact of malaria cases exported to other districts (green). The second bar chart on the right side of the center matrix denotes the total malaria intensity calculated after considering the effect of human mobility (pink). The dashed lines in the bar charts denote the bounds of the highest and lowest values. **(Second row)** The color of each district denotes the total malaria transmission intensity; each directed edge denotes the cross-district malaria intensity across different districts. Here, we only show edges with intensities > 0.005 . **(Third row)** The color of each district denotes the imported malaria transmission intensity. Here, we only show edges going to districts with the top three imported intensities and those with intensities > 0.005 . **(Last row)** The color of each district denotes the exported malaria transmission intensity. Here, we only show edges coming from districts with the top three exported intensities and those with intensities > 0.005 . For the value range of the colors, please refer to the color bars on the right side of each row.

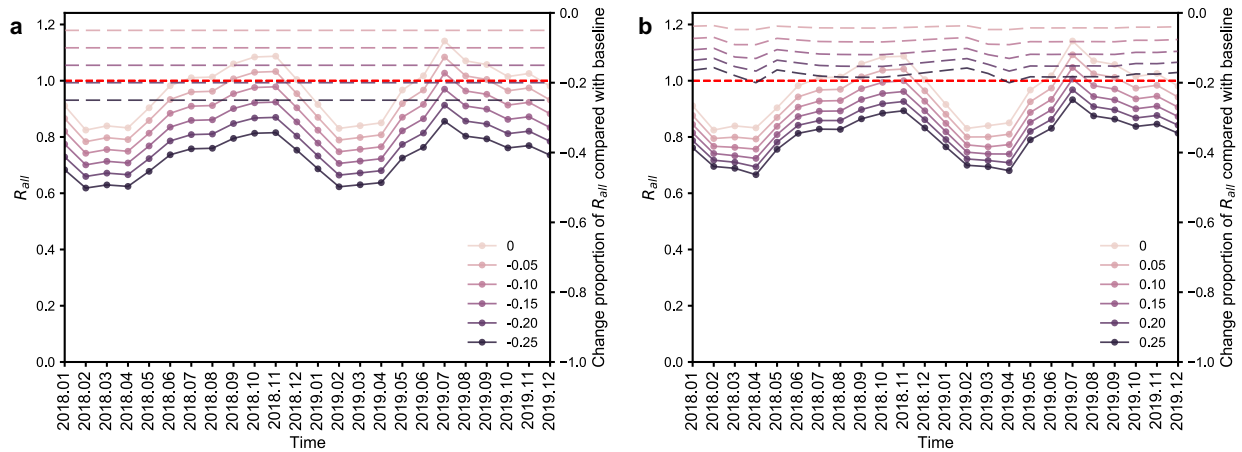
9 Sensitivity analysis

9.1 The sensitivity of overall malaria transmission intensity with respect to parameters of all districts

The variations of the overall malaria transmission intensity R_{all} with respect to the variations of parameters (i.e., a , d_2 , m , e_2 , ε_2 , e_1 , and r_1) of all districts can be found in Supplementary Figure S18 and Supplementary Figure S19.



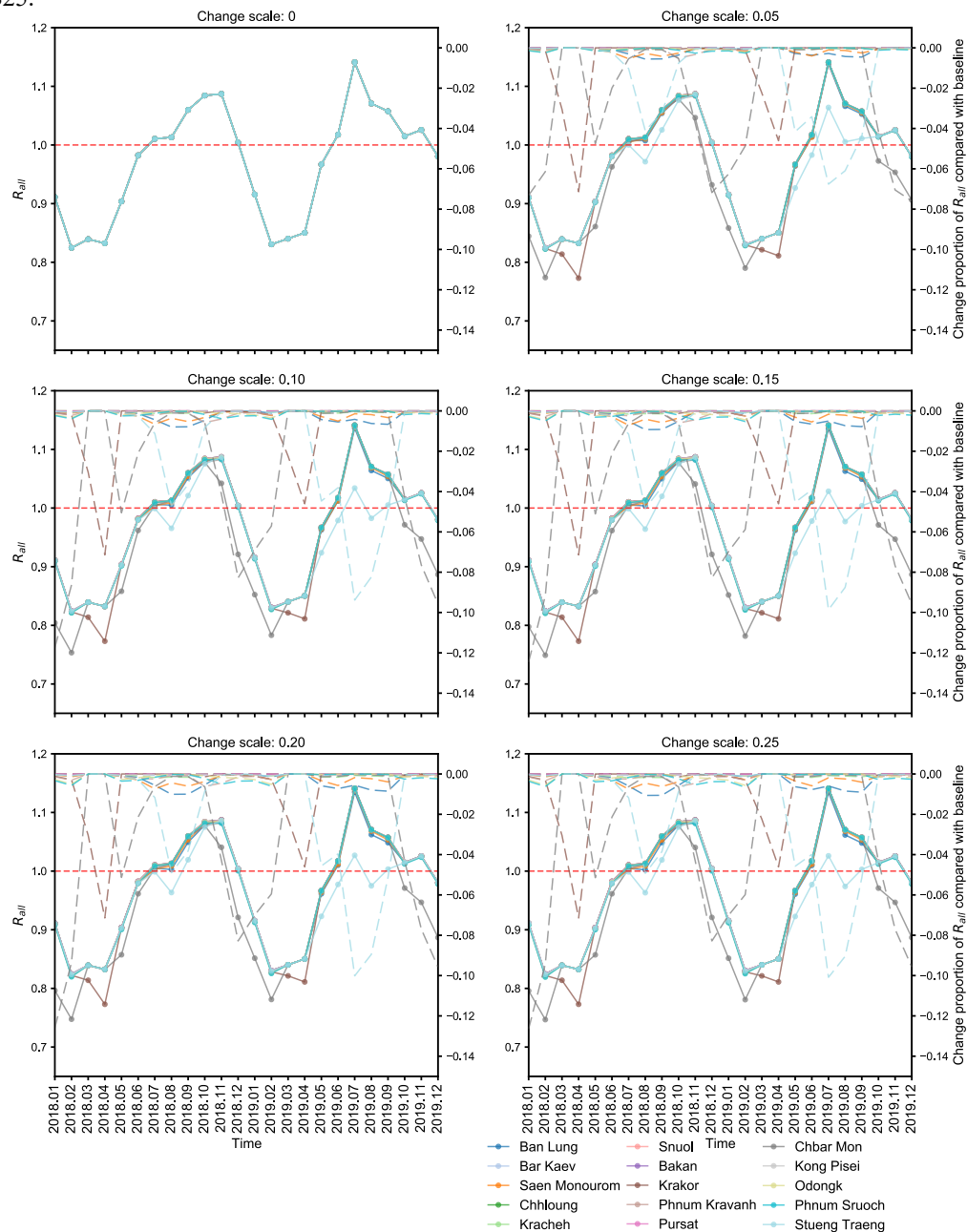
Supplementary Figure S18 The sensitivity of the overall malaria transmission intensity with respect to the parameters related to vector factors. (a) a (human biting rate), (b) d_2 (mosquito death rate), (c) m (vector density), (d) e_2 (transmission efficiency from humans to mosquitoes), and (e) ε_2 (the reciprocal of latent period of mosquito). The solid lines denote the value of R_{all} over time with respect to parameter variation. The color intensity of each line indicates the extent of the variation (Please see the legend in the subfigures). The darker the color is, the higher the variation percentage. Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in the value R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.



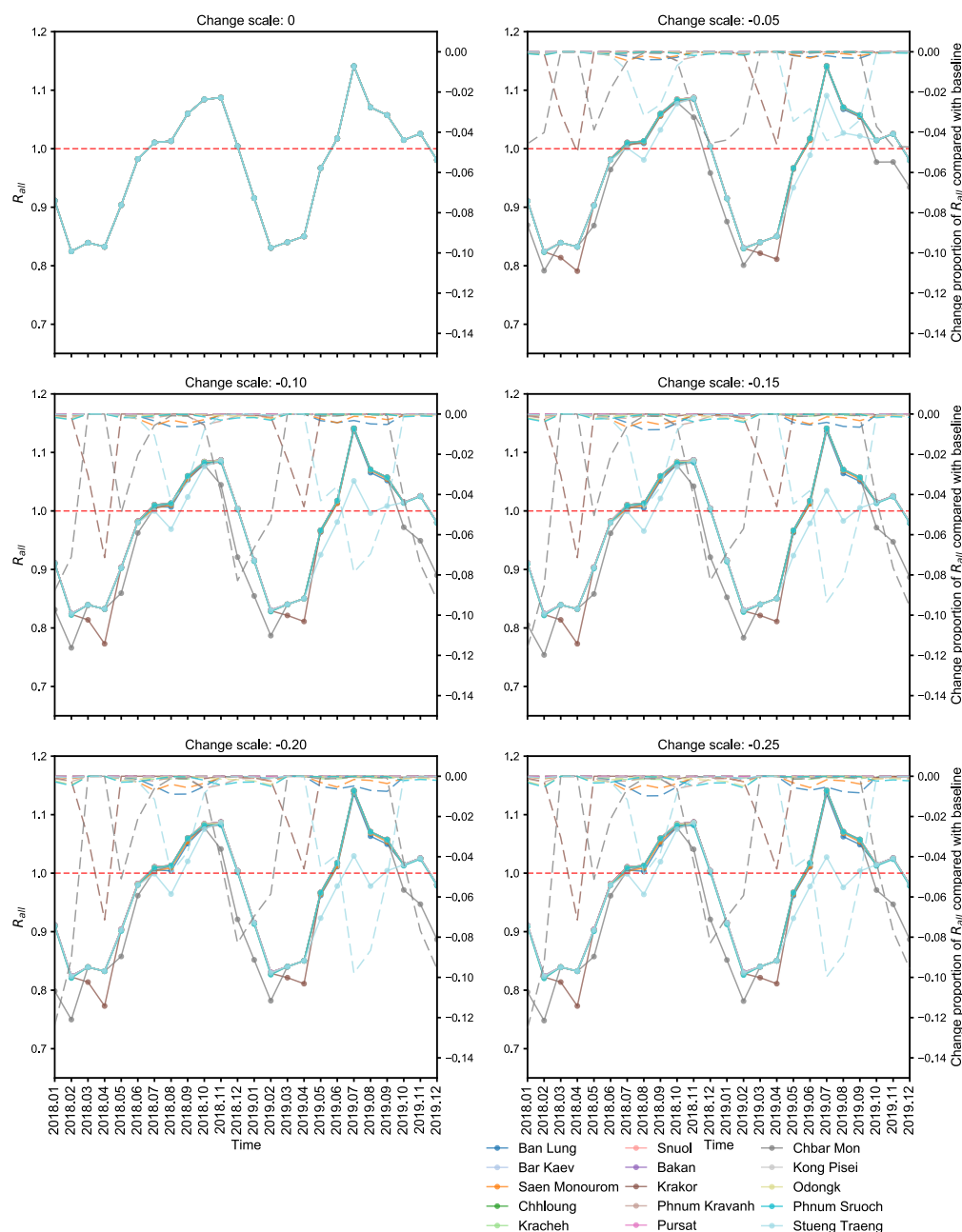
Supplementary Figure S19 The sensitivity of the overall malaria transmission intensity with respect to the parameters related to human factors. (a) e_1 (transmission efficiency from mosquitoes to humans) and (b) r_1 (human recovery rate). The solid lines denote the value of R_{all} over time with respect to parameter variation. The color intensity of each line indicates the extent of the variation (Please see the legend in the subfigures). The darker the color is, the higher the variation percentage. Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in the value R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.

9.2 The sensitivity of overall malaria transmission intensity with respect to parameters of individual districts

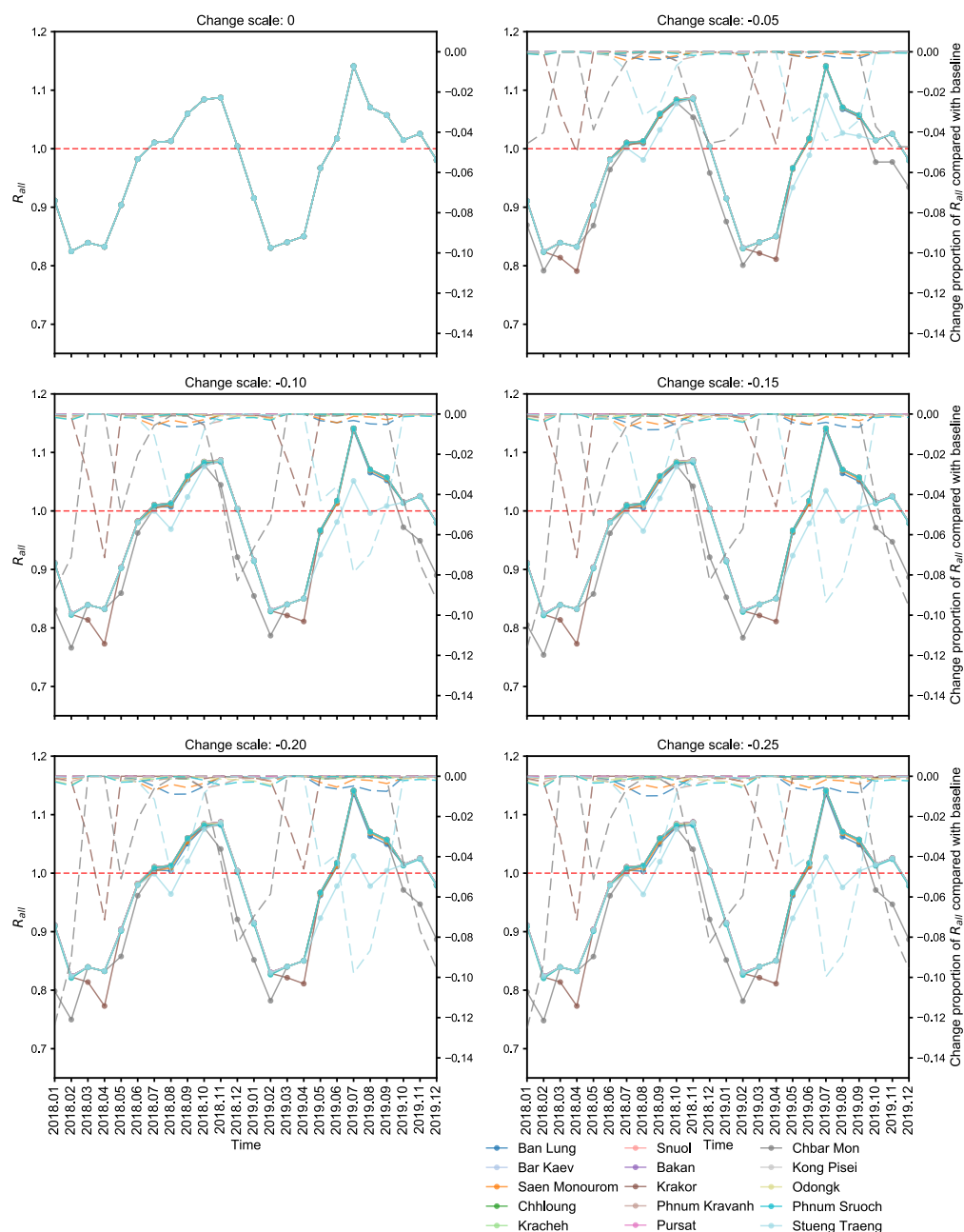
The variations of the overall malaria transmission intensity R_{all} with respect to the variations of parameters (i.e., $a, d_2, m, e_2, \varepsilon_2, e_1$, and r_1) of individual districts can be found in Supplementary Figure S20 to Supplementary Figure S25.



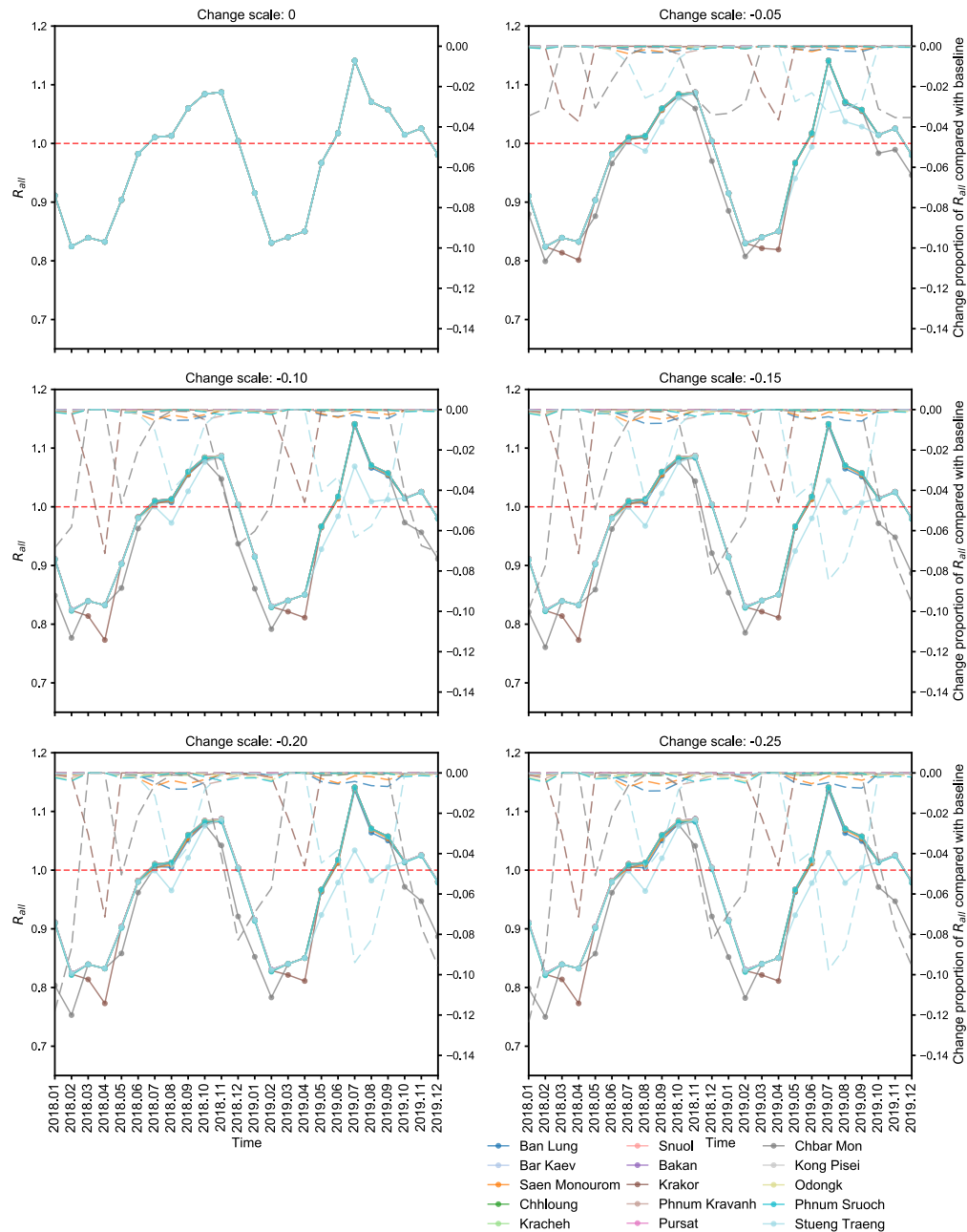
Supplementary Figure S20 The sensitivity of the overall malaria transmission intensity with respect to the parameter d_2 in individual districts. In each subfigure, with a fixed percentage change for all districts, as noted in the title of each subfigure, the solid lines denote the R_{all} value over time with respect to the variation of parameter d_2 in different districts (see the legend). Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.



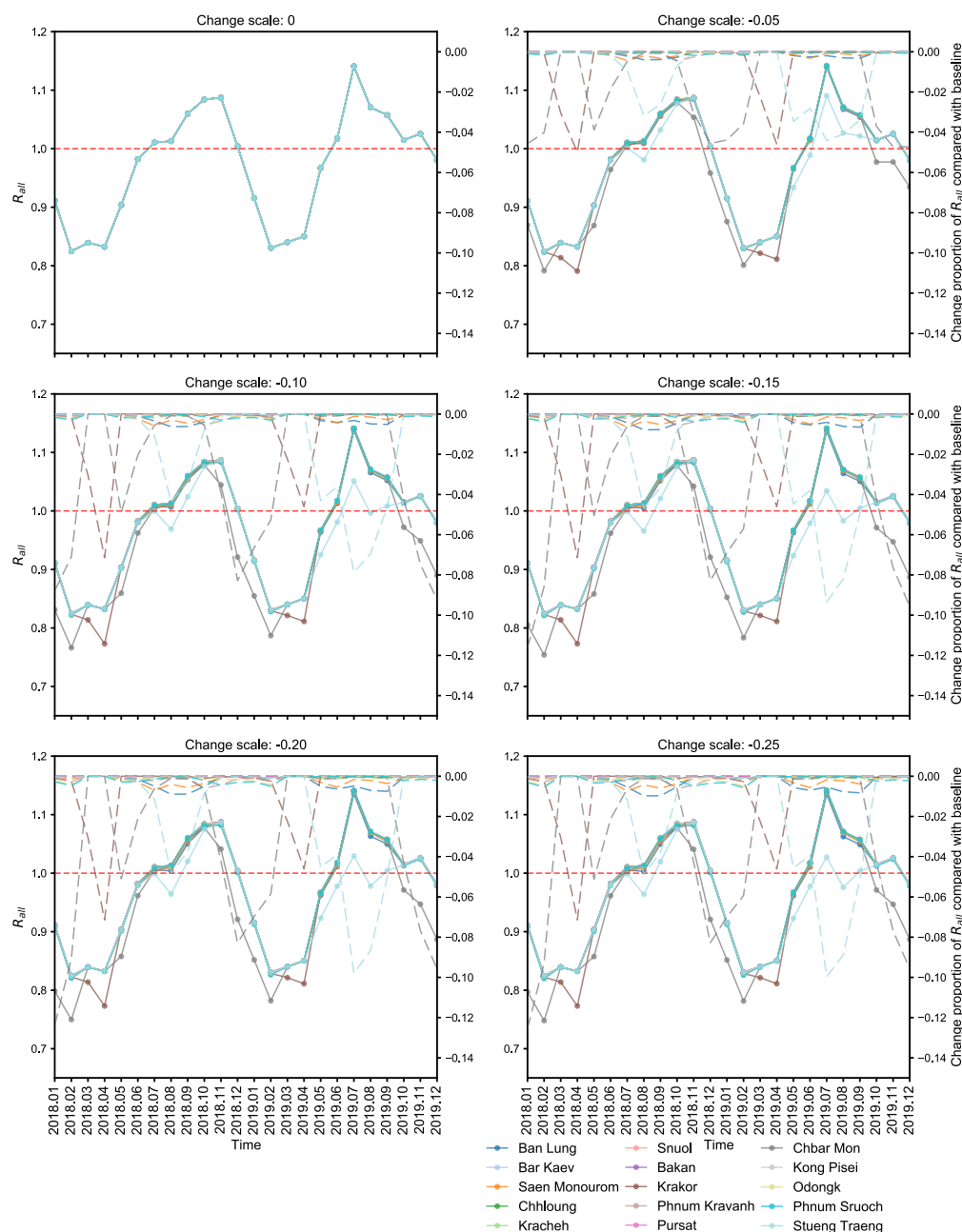
Supplementary Figure S21 The sensitivity of the overall malaria transmission intensity with respect to the parameter m in individual districts. In each subfigure, with a fixed percentage change for all districts, as noted in the title of each subfigure, the solid lines denote the R_{all} value over time with respect to the variation of parameter m in different districts (see the legend). Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.



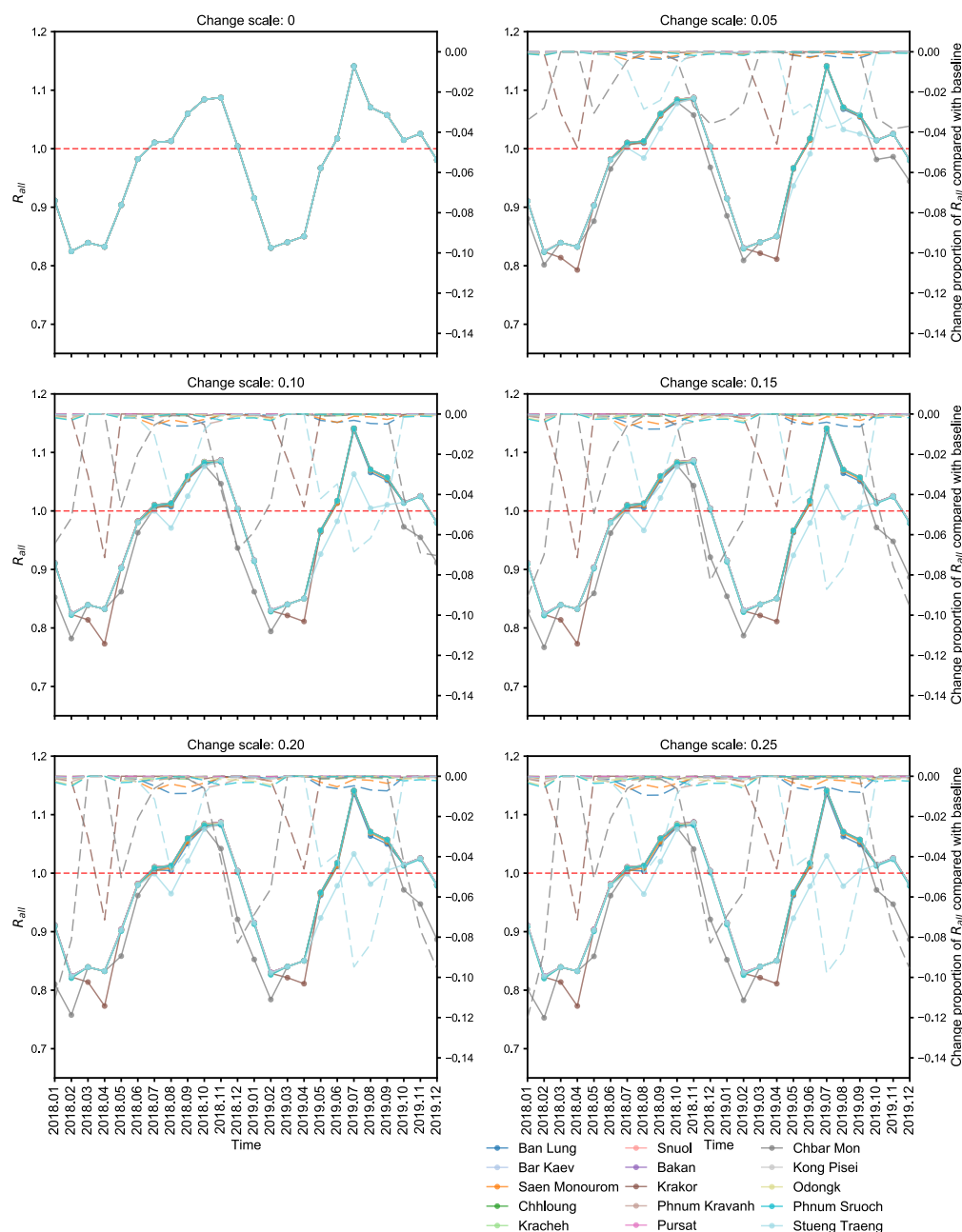
Supplementary Figure S22 The sensitivity of the overall malaria transmission intensity with respect to the parameter e_2 in individual districts. In each subfigure, with a fixed percentage change for all districts, as noted in the title of each subfigure, the solid lines denote the R_{all} value over time with respect to the variation of parameter e_2 in different districts (see the legend). Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.



Supplementary Figure S23 The sensitivity of the overall malaria transmission intensity with respect to the parameter ε_2 in individual districts. In each subfigure, with a fixed percentage change for all districts, as noted in the title of each subfigure, the solid lines denote the R_{all} value over time with respect to the variation of parameter ε_2 in different districts (see the legend). Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.



Supplementary Figure S24 The sensitivity of the overall malaria transmission intensity with respect to the parameter e_1 in individual districts. In each subfigure, with a fixed percentage change for all districts, as noted in the title of each subfigure, the solid lines denote the R_{all} value over time with respect to the variation of parameter e_1 in different districts (see the legend). Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.



Supplementary Figure S25 The sensitivity of the overall malaria transmission intensity with respect to the parameter r_1 in individual districts. In each subfigure, with a fixed percentage change for all districts, as noted in the title of each subfigure, the solid lines denote the R_{all} value over time with respect to the variation of parameter r_1 in different districts (see the legend). Please refer to the left vertical axis in each subfigure for the detailed value of R_{all} . The dashed lines denote the percentage changes in R_{all} . Please refer to the right vertical axis in each subfigure for the detailed values of the changing percentage of R_{all} . The straight red line in each subfigure denotes the malaria transmission threshold 1.

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