1 Modeling the relative role of human mobility, land-use and climate factors on dengue outbreak 2 emergence in Sri Lanka 3 4 5 Ying Zhang<sup>1,2</sup>, Jefferson Riera<sup>3</sup>, Kayla Ostrow<sup>1</sup>, Sauleh Siddiqui<sup>1,4</sup>, Harendra de Silva<sup>5</sup>, Sahotra Sarkar<sup>6</sup>, 6 7 Lakkumar Fernando<sup>7</sup>, Lauren Gardner<sup>8,1\*</sup> 8 9 <sup>1</sup>Department of Civil Engineering, Johns Hopkins University, Baltimore, MD 21218, USA 10 <sup>2</sup>Department of Earth and Planetary Sciences, Johns Hopkins University, Baltimore, MD 21218, USA 11 12 13 <sup>3</sup>Department of Environmental Health and Engineering, Johns Hopkins University, Baltimore, MD 21205, 14 USA 15 <sup>4</sup>Department of Applied Mathematics and Statistics, Johns Hopkins University, Baltimore, MD 21218, 16 17 USA 18 19 <sup>5</sup>Department of Pediatrics, University of Colombo, Colombo, 00900, Sri Lanka 20 <sup>6</sup>Department of Philosophy, Department of Integrative Biology, University of Texas at Austin 21 22 Austin, TX, 78712 23 24 <sup>7</sup>Centre for Clinical Management of Dengue and Dengue Haemorrhagic Fever, Negombo, 11500, Sri Lanka 25 <sup>8</sup>School of Civil and Environmental Engineering, University of New South Wales (UNSW) Sydney, 26 27 Sydney, NSW, 2052 Australia 28 29 \*Corresponding Author: l.gardner@unsw.edu.au, (+61 (02) 9385 5562) 30 31 32 Email of other authors: 33 Ying Zhang: ying.zhang@jhu.edu 34 Jefferson Riera: jriera1@jhu.edu Kayla Ostrow: kostrow5@jhu.edu 35 36 Sauleh Siddiqui: siddiqui@jhu.edu 37 Harendra de Silva: harendra51@gmail.com 38 Sahotra Sarkar: sarkar@austin.utexas.edu

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#### 41 Abstract

42 We present a statistical modeling framework to evaluate the spatial-temporal dynamics of the 2016-2017 dengue outbreak in the Negombo region of Sri Lanka as a function of human mobility, land-use, and 43 44 climate patterns. The analysis was conducted at a 1 km  $\times$  1 km spatial resolution and a weekly temporal 45 resolution. Our results indicate human mobility to be a significantly stronger indicator for local outbreak 46 clusters than land-use or climate variables, thus highlighting the potential value of using travel data to 47 target vector control within a region. The minimum daily temperature was identified as the most 48 influential climate variable on dengue cases in the region; while among the set of land-use patterns considered, urban areas were found to be most prone to dengue outbreak, followed by areas with stagnant 49 50 water and coastal areas. The results are shown to be robust across spatial resolutions. In addition to 51 illustrating the relative relationship between various potential risk factors for dengue outbreaks, the results of our study can be used to predict where and when new cases of dengue are likely to occur within a 52 53 region, and thus help more effectively and innovatively, plan for disease surveillance and vector control.

54

55 Keywords: dengue; outbreaks; risk factors; human mobility; climate; land-use; spatial-temporal dynamics;

- 56 statistical modeling, Sri Lanka
- 57

58

#### 60 1. Introduction

Dengue is a mosquito-borne viral disease that infects approximately 390 million people globally every year, particularly in tropical and subtropical countries (1, 2). The high number of infections combined with the lack, as yet, of an effective vaccine has made dengue a notorious public health problem (2, 3).

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65 Dengue spreads through the bite of infected Ades mosquitoes, especially Aedes aegypti- the primary 66 vector, with an estimated 15 to 17-day delay between the primary and secondary human infections (4). 67 Dengue outbreak control is a challenge for policy makers because Aedes aegypti mosquitoes are well 68 adapted to high density urban environments and actively feed during the day (5-7), thus presenting an 69 elevated risk to humans. Urban settings provide an ideal habitat for Aedes aegypti breeding due to an 70 abundance of discarded trash bags, plastic bottles, tires, and other containers that enable the formation of 71 stagnant shallow water surfaces after precipitation (8). Urban regions in developing countries are 72 particularly vulnerable due to a lack of indoor plumbing infrastructure that, in conjunction with a lack of 73 air-conditioning, results in higher human-mosquito exposure rates during the day. Additionally, because 74 of the daytime feeding behaviors of Aedes aegypti, common vector control measures that work for 75 night-biting mosquitoes, such as bed nets, fail to effectively control dengue transmission. Given these 76 challenges, there is a need to better understand and predict dengue outbreaks and transmission risk within 77 urban regions in developing countries so that vector control and surveillance resources can be optimally 78 allocated.

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80 Previous studies highlighted human mobility as a critical factor for dengue transmission (9-15), which contrasts the more minor role travel plays in the spread of vector-borne diseases transmitted by 81 82 night-biting mosquitoes (15). While Aedes aegypti mosquitoes have a hard time dispersing geographically 83 across large areas because they rarely travel more than 400m from where they emerge as adults (16-19), 84 humans regularly travel much longer distances on a daily basis. As new dengue cases and clusters are 85 regularly reported kilometers apart, it is likely that human mobility play a critical role in the spread of dengue outbreaks, *i.e.*, infected humans introduce dengue into new mosquito populations at their trip ends. 86 87 As an example, Vazquez-Prokopec, Montgomery (12) studied the pattern of dengue transmission using 88 location-based contact tracing on infected dengue patients during a dengue outbreak centered at Cairns, 89 Australia. They collected locations that the patients frequently traveled to during the daytime and 2-4 90 weeks prior to the onset of symptoms through phone interviews. The contact locations with a proximity of 100 meters and a separation of 20 days were spatial-temporally linked into pairs and then chains to 91 92 identify the plausible sites of dengue virus transmission. They showed that the complex pattern of dengue 93 transmission was primarily driven by human mobility, and that targeted residual spaying could potentially 94 reduce the probability of dengue transmission up to 96%. Their study highlights the importance of 95 understanding dengue transmission patterns to optimize the allocation of dengue prevention and 96 vector-control measures.

97

98 In addition to human mobility, recent studies have pointed to a strong association between climate conditions and dengue outbreaks at various locations and across different temporal resolutions (8, 20-24). 99 100 Precipitation, mean temperature and temperature fluctuation were revealed to affect the population 101 dynamics of Aedes aegypti mosquitoes and the dengue virus extrinsic incubation period (25-29). Specifically, a suitable average temperature and moderate temperature fluctuations are often favorable for 102 dengue transmission (25), while an increase in precipitation is strongly associated with the onset of a 103 104 dengue outbreak (22). Humidity, a combined effect of precipitation and temperature, is also a common 105 climate index to evaluate the environmental capacity for dengue emergence (20, 21, 30, 31). Wesolowski, 106 Qureshi (13) accounted for both climate and mobility in a study of dengue virus transmission over a large 107 dengue outbreak period in Pakistan. They developed an epidemiological model that included temperature and relative humidity as input parameters for mosquito dynamics, as well as biting rate to capture the 108 109 interactions between human and mosquito hosts. Human mobility was captured using mobile phone data

110 of ~40 million subscribers to estimate the spatially explicit travel volume, albeit not differentiating 111 infected and non-infected people. They showed that the emergence of dengue epidemics in a new region 112 could be predicted using aggregated travel patterns from endemic areas in combination with the 113 developed epidemiological model. While climatic factors were found to be significant for prediction, this 114 was in part due to the large study region, *i.e.*, country level, which has variable climatic suitability for the 115 mosquito vector. The study region considered in our work is much smaller and has minimal climactic 116 variability, thus alternative methods are required to distinguish site-specific risk.

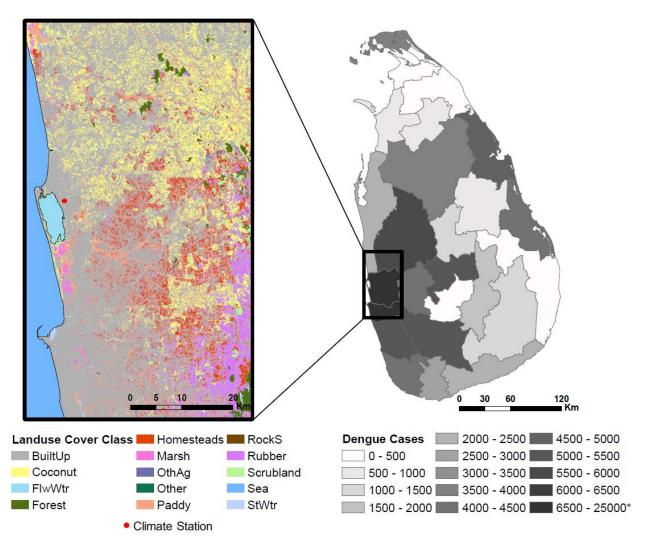
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118 Land-use patterns — indicators of human activities and potential breeding habitats — have also been 119 linked to dengue outbreaks (32-37). Previous studies investigated the effect of land-use patterns on the 120 spread of dengue and found that human settlements, water bodies, and mixed horticulture are the top three 121 associated land-use patterns for dengue emergence in Malaysia (35). In another study (36), areas 122 surrounded by rice paddies and marshes/swamps were associated with a significantly higher population of 123 dengue vectors during the rainy season in Thailand. Orchards (which often contain artificial water containers) and irrigation fields have also been shown to play an important role in dengue infections; 124 125 however, their role varies given different local conditions. Sometimes, land-use type can be a proxy for 126 other features, such as socio-economic factors, which may have a contradictory effect on dengue 127 infections (37).

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129 In this study, we present a statistical modeling framework to evaluate the relative role of human travel 130 patterns, climate conditions, and land-use patterns on dengue outbreak dynamics in Negombo, Sri Lanka 131 (Figure 1). With more than 80,000 dengue cases including 215 deaths reported nationally in less than 132 seven months at the beginning of 2017, the recent dengue outbreak in Sri Lanka increased the number of 133 reported cases by 4.3 times compared to the average number over 2010-2016 (38). The region of Negombo, located in the Western province, experienced the greatest number of dengue cases in the 134 135 country; approximately 45% of the cases nationwide by July 2017 (Figure 1). We applied a mixed-effects 136 model, where the mobility data bridges the time-varying, spatially-invariant climate variables and the 137 rasterized spatially explicit, time-invariant population and land-use variables, to capture the 138 spatial-temporal dynamics of dengue transmission. Our model framework differs from previous studies that simulated the transmission process (12, 13, 39), and instead focuses on estimating the timing and 139 140 location of new case introductions though a non-process based statistical model. Specifically, we focus on 141 modeling the home locations of (newly infected) dengue patients, and assume dengue is introduced in 142 new areas by infected individuals who travel to the area. This assumption is consistent with previous 143 studies that have shown visits to a household by infected people determines the infection risk in that household (11). In addition, the study was conducted at a fine-grained spatial and temporal resolution — 144 145  $1 \text{ km} \times 1 \text{ km}$  spatially and one week temporally — providing an improved understanding of the role of mobility in the spread of dengue. While previous work studied the impact of mobility (12, 13), climate (8, 146 147 20, 22, 25), and land-use (35-37) separately on dengue, the authors are unaware of any existing study that 148 considers these factors within a single integrated framework. Thus, previous studies have been unable to 149 quantify the relative contribution of each factor on the spatial-temporal patterns of dengue transmission as we do. The results from our study indicate that mobility is a much more significant predictor of new 150 151 dengue case clusters compared with land-use and climate data alone. Furthermore, the case study in Sri 152 Lanka provides critical insights into effective application of dengue prevention and vector control

153 measures in developing regions.



#### 154

Fig. 1. Land-use groups and the climate station in the study region of Negombo, Sri Lanka (left), and the
total number of dengue cases at the district level in Sri Lanka (40) during the months from October 2016
to June 2017 that cover our study period (right).

#### 158 2. Data and Methods

A statistical model is applied to investigate the spatial-temporal dynamics of dengue outbreak with respect to a range of potential explanatory variables. The complete set of potential explanatory variables is listed in Table 1. Detailed descriptions of the data followed by a description of the methodology are provided below.

163

## 164 (a) Case and Mobility Data

A patient survey was conducted among dengue patients in the Negombo region of Sri Lanka over an approximately 8-month period during a major outbreak spanning from end of October 2016 to early July

167 2017. Data were collected from all patients admitted to the special High Dependency Unit (HDU) for

168 critically ill dengue patients within the Clinical Centre for Managing Dengue and Dengue Haemorrhagic

169 Fever (CCMDDHF) at the Negombo Hospital in Negombo, Sri Lanka. Specifically, the date of admission,

home address, the complete set of locations visited, and corresponding trips made between all locationsduring the 10-days prior to hospital admission were collected from all HDU CCMDDHF admitted

patients for the entire study period. The case data provide spatial-temporal information on the outbreakpatterns, while the mobility data collected captures daily travel activity of the admitted dengue patients.

174 The data were collected by trained students and supervised by a Senior House Officer on site. For

175 weekday admissions the patients were surveyed upon admittance, for night admissions data were

- 176 collected the following day, and for weekend admissions on the following Monday. The majority of
- admissions were 48 to 72 hours following the onset of fever. Dengue infection was confirmed for the
- 178 patient set using either NS1 antigen or IgM antibody diagnostic test.
- 179

# 180 (b) Climate Data

We used the Global Surface Summary of the Day (GSOD) daily weather data (41) from a station in 181 Negombo (Figure 1) to explore the impact of climate factors on the dengue outbreak. The location of the 182 183 weather station (7.18°N, 79.87°E) is approximately in the center of the study region and it is the only 184 station that falls into our study region with a comprehensive set of climate data available during the study 185 period. There are several global reanalysis products that provide spatial-explicit climate data during the study period; however, upon evaluation against the station observations, these globally gridded data sets 186 187 did not provide accurate representations of the local climate variables, particularly at a daily time-step 188 (Figure S1). Hence, the weather data are assumed to be representative for the region which has relatively 189 homogeneous weather patterns (42). We selected a range of potential climate variables based on previous 190 studies (8, 20-22, 25-31), including daily mean temperature (Tavg), daily maximum temperature (Tmax), 191 daily minimum temperature (Tmin), diurnal temperature range (DTR), precipitation (Pre), the number of 192 raining days (RD), and relative humidity (RH) to analyze climatic influence for the weeks before and 193 during the same period of analysis that the mobility data was collected.

194

# 195 (c) Population and Land-use Data

We used a global population data layer based on Landscan 2016 (43), that is available at an 196 197 approximately 1 km  $\times$  1 km resolution to represent the population distribution spatially. We aggregated 198 the data to 5 km  $\times$  5 km grid for additional analysis with a coarser spatial resolution. Land-use data (44) 199 were obtained from the Sri Lanka Survey Department which performed an initial survey in 2000 and has 200 since continuously updated the maps. The map was extracted for our region of interest and reclassified into several groups (Figure 1): Sea, Standing Water (StWtr), Flowing Water (FlwWtr), Coconut, Marsh, 201 202 Paddy, Built-up (BuiltUp), Scrubland, Homesteads, Forest, Rubber, Rock/Sand (RockS), Other 203 Agriculture (OthAg), and Other. Water bodies were categorized depending on the potential effect on 204 dengue transmission dynamics. Additional details on land-use classification groupings and processing is 205 available in the supplementary material. 206

207 (d) Data Processing and Statistical Model

We divided the study region (Figure 1) into a grid at a  $1 \text{ km} \times 1 \text{ km}$  resolution and aggregated daily data into a 1-weekly resolution. The number of patients who were admitted to the hospital during each week of the recorded time period was used to generate the weekly number of newly admitted dengue patients in each cell based on their home locations.

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213 To incorporate the role of mobility into the model we used the travel itineraries provided by the patients 214 to generate a time-dependent connectivity matrix, which represented the total number of trips made by dengue infected patients between each pair of cells for each week of the study period. The travel data 215 included all destinations visited each day during the 10 days preceding hospital admittance (the time 216 interval that the patient is assumed to be able to spread the disease) for each patient. The number of daily 217 218 trips between each pair of cells was summed over all patients, to provide daily trip volumes between cells, 219 and then aggregated to the weekly level. For each cell the total incoming weekly trips was summed to define our 'trip' variable, which is the total number of trips made by infected dengue patients entering a 220 given cell i in a given week t,  $V_t^i$ , and was used as a spatial-temporal explanatory variable in the model. 221 The same method was used for the 5 km  $\times$  5 km analysis. 222

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Climate variables were averaged or aggregated temporally to a weekly resolution, including weekly average *Tavg*, *Tmin*, *Tmax*, *DTR*, *RH*, weekly total *Pre*, and *RD*. Land-use data were aggregated spatially to match the targeted spatial grid resolution. The population data were in an original resolution that matched the 1 km  $\times$  1 km grid. For land-use, the percentage of occupied land of each type was determined for each 1 km  $\times$  1km grid cell. Both were subsequently aggregated to a 5 km  $\times$  5 km grid.

229 A mixed-effects model combined with backward elimination of insignificant fixed effects was applied to 230 investigate the spatial-temporal dynamics of dengue outbreak with the potential explanatory variables at a 231 weekly time step and 1 km  $\times$  1 km spatial resolution. In building the model we first conducted sensitivity 232 analysis to identify the optimal set of climatic variables to include in the model, and corresponding time lag for each of them. Among the climate variables, significant correlations were observed for weekly 233 234 averaged daily mean temperature (Tavg), daily minimum temperature (Tmin), and diurnal temperature 235 range (DTR) with a lead time ranging from 7 days to 17 days prior to the weekly admitted number of 236 patients  $(N_t)$ , where the lead time  $(d_c)$  is the lag in days between the climate variable and  $N_t$  (Figure S2). 237 Regression models based on different combinations of the climate variables and lead time were developed and compared; the best performance model was select based on F-test and adjusted- $R^2$ . As a result, Tmin 238 239 with an optimal lead time of 10 days was included in the final set of mixed-effects models to account for the partial influence of climate on the dengue outbreak ( $R^2 = 0.248$ ; adj.  $R^2 = 0.226$ ). This is consistent 240 with previous findings (29) that daily minimum temperature were associated with increase in the larval 241 242 abundance. We assumed a relatively homogenous climate over the study region, thus *Tmin* does not vary spatially over the study region. 243

244

Along with the chosen climate variable, Tmin, the remaining set of potential explanatory variables (Table 245 246 1) was taken into the mixed-effects model initially, with population included in the spatial random effects. 247 Population density was incorporated using random effects in the model because population is likely to 248 have spatially heterogeneous effects on dengue outbreaks (39, 45). For example, high population areas 249 may imply access to tap water and better living conditions which could restrict dengue transmission (46), 250 while the higher density of population facilitates disease spread. Furthermore, there could be spatial 251 variance in the distribution of people living in a particular area. In addition to mobility, climate, and 252 land-use variables; the number of new cases in a given cell in the weeks prior were added as explanatory 253 variables to account for autocorrelations in the case data. Subsequently, the variable with the most insignificant fixed-effects coefficient was eliminated each iteration, until only variables with significant 254 coefficients (at 95% significance level) remained in the model. A range of lead time for  $V_t^i$  prior to the 255 admitted week was also tested. A separate analogous process was conducted using a 5 km  $\times$  5 km 256 257 resolution, to test the sensitivity of model results across spatial resolutions, and the robustness of the modeling framework and findings. 258 259

260 Thus, the mathematical representation of the model is given by:

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 $N_t^i = \sum_{l \in \overline{L}} \alpha_l l^i + \sum_{c \in \overline{C}} \beta_c c_{t,d_c} + \sum_u \gamma_u V_{t-u}^i + \sum_w \delta_w N_{t-w}^i + a^i + b^i P^i + \varepsilon_t^i$ 

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262

- 264 Where 265
- 266 *i* is the cell index; i = 1, 2, ...

267 *l* is the land-use variable, which belongs to the land-use group set  $\overline{L}$ , where  $\overline{L}$  includes Sea, StWtr, FlwWtr,

268 Coconut, Marsh, Paddy, BuiltUp, Scrubland, Homesteads, Forest, Rubber, RockS, OthAg, and Other.

269  $l^i$  is the occupation percentage of land-use group l in cell i, time-invariant.

270  $P^i$  is the population in cell *i*, time-invariant

- 271 *t* is the time index at weekly resolution; t = 1, 2, ...
- 272  $N_t^i$  is the number of patients who are admitted to the hospital during week *t*, whose home locations are in 273 cell *i*
- 274  $N_{t-w}^i$  is the number of patients who are admitted to the hospital during week *t-w*, whose home locations 275 are in cell *i*, where *w* is measured in weeks; w = 1, 2, ...
- 276  $V_{t-u}^i$  is the number of total number of trips made into cell *i* during the week *t-u*, where *u* is measured in weeks; u = 1, 2, ...
- 278 *c* is the climate variable which belongs to the climate variable set  $\overline{C}$ .  $\overline{C}$  includes Tavg, Tmax, Tmin, DTR, 279 *Pre*, *RD*, and *RH*.
- 280  $c_{t,d_c}$  is the climate variable during the week that begins  $d_c$  days prior to the start of week t.  $d_c$  ranges
- from 7 to 17 days and can be different for different climate variables. Multiple climate variables can be
- included in the model.
- 283  $\varepsilon_t^i$  is the model residuals associated with cell *i* and week *t*.
- 284  $\alpha_l$  is the estimated fixed-effects coefficient for *l*.
- 285  $\beta_c$  is the estimated fixed-effects coefficient for *c*.
- 286  $\gamma_u$  is the estimated fixed-effects coefficient for  $V_{t-u}^i$ .
- 287  $\delta_w$  is the estimated fixed-effects coefficient for  $N_{t-w}^i$ .
- 288  $a^i$  is the intercept associated with cell *i*.
- 289  $b^i$  is the estimated spatial random-effects coefficient for  $P^i$ .

## 290 **3. Results**

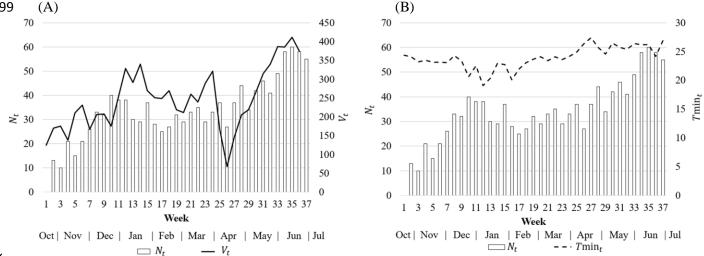
## 291 (a) Data Analysis

The number of admitted dengue patients aggregated over the study region peaks during December and June (Figure 2), aligned with the monsoon months (47). Figure 2A illustrates the relationship between the total number of dengue patients,  $N_t$ , admitted during each week *t* and the total number of recorded patient trips during the same week ( $V_t$ ). Figure 2B illustrates  $N_t$  and the weekly averaged minimum daily

temperature in week t  $(T\min_t)$ . It shows a lagged relationship of  $N_t$  with  $T\min_t$ , mostly in the same

- direction. For the purposes of these graphics, the variables are aggregated over the entire study region.
- 298





36.

**Fig. 2.** The number of admitted dengue patients in week t ( $N_t$ ) and (A) the number of recorded trips in week t ( $V_t$ ) summed over the entire study region, and (B) the weekly averaged minimum daily temperature ( $T\min_t$ ).

The travel destinations recorded in our study include medical facilities, homes, workplaces, schools, and others (Figure S3). Additional analysis performed reveals that a vast majority of trips were longer than the distance a mosquito can travel. Specifically, 96.6% of the trips were longer than 0.4 km (Table S1; Figure S4), outside the range of a mosquito's maximum travel distance (16-19), further supporting the role human mobility is likely to play in the outbreak.

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Figure 3 illustrates both the spatial-temporal distribution of dengue patients' home locations over the course of the outbreak, and the corresponding travel patterns of the patients during 5-week periods. The patient home locations were well distributed over the area of the study region for the first few months of the outbreak, with correspondingly scattered travel patterns. However, as the outbreak progressed, the recorded case locations and the trip ends of newly infected dengue patients became more concentrated near the town center and just above the lake. There were also a large amount of trips (>100) within the cell near the town center.

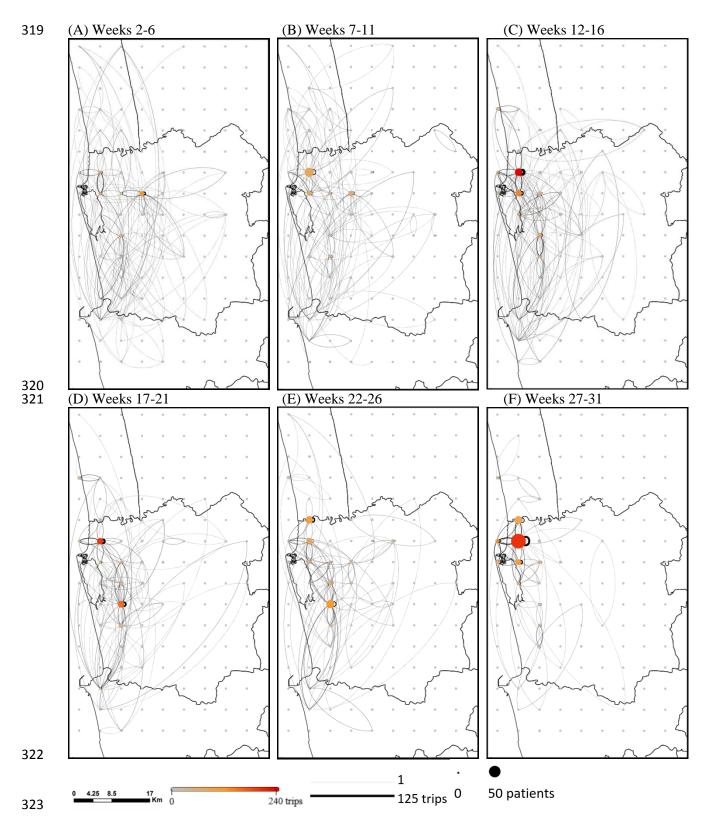


Fig. 3. Weekly number of patients and the number of trips summed over 5-week intervals for a  $5 \text{ km} \times 5$ km resolution. Patient home locations are plotted as the case location. The size of the circle indicates the number of patients admitted during the time period. The color of the circle indicates the number of trips

that end in the grid cell during the time period. The thickness of the line is proportional to the number of

- trips made between two locations. Week 2 begins on October 27, 2016 and week 31 begins on May 18, 2017. For viewel elevity, the 5 km we 5 km accelution was used for the forum, instead of 1 km × 1 km
- 329 2017. For visual clarity, the 5 km  $\times$  5 km resolution was used for the figure, instead of 1 km  $\times$  1 km.
- 330

## 331 (b) Model Results

- A mixed-effects model was developed to estimate the number of new dengue cases in a given cell in a
- 333 given week as a function of the mobility patterns of individuals infected with dengue in the preceding 334 week(s), as well as land-use and climate data from days prior.
- week(s), as well as land-use and climate data from days prior.

## 335 Table 1: Summary of potential explanatory variables

336

Variables	Description	Properties		
$l^i$	occupation percentage of land-use group $l$ in cell $i$ (%)			
BuiltUp	urban area	-		
Coconut	coconut cultivation land			
Homesteads	homesteads and garden	spatially-explicit,		
Paddy	rice cultivation land	time-invariant		
Sea	ocean			
StWtr	standing water			
FlwWtr	flowing water			
$C_{t,d_c}$	weekly value of climate variable in week $t$ with a lag of $d_c$			
Tavg	weekly averaged daily mean temperature	-		
Tmax	weekly averaged maximum daily temperature			
<i>T</i> min	weekly averaged minimum daily temperature	time-varying, spatially -invariant		
DTR	weekly averaged diurnal temperature range			
Pre	weekly total precipitation			
RD	weekly number of raining days			
RH	weekly averaged daily relative humidity			
$P^i$	population in cell <i>i</i>	spatially -explicit, time-invariant		
$V_{t-u}^i$	number of trips made to cell <i>i</i> in week <i>t</i> - <i>u</i>	spatially -explicit, time-varying		
$N_{t-w}^i$	number of patients admitted to hospital who live in cell $i$ in	spatially -explicit,		
™t−w	week <i>t-w</i>	time-varying		

337

338 *Note: t, u,* and *w* in weeks,  $d_c$  in days. For notation, variable superscripts in Table 1 denote spatial indices 339 and subscripts denote time indices.

340

Multiple models with explanatory variables representing land-use, climate, and mobility were created, 341 and the three representative models are presented here. The three models vary based on the type of 342 mobility variable included, specifically how far back in time travel is accounted for. The first model 343 344 includes the mobility patterns one-week prior (u = 1), the second model includes the mobility patterns 345 two-weeks prior (u = 2), and the third model excludes mobility altogether ("Exclude V"). The final set of climate and land-use variables found to be significant varies between models. All explanatory variables 346 347 were standardized to a mean of zero and a standard deviation of one in the mixed-effects model. The 348 fixed-effects coefficients (Table 2) therefore reflect the relative influence of each explanatory variable on 349 the dengue outbreak dynamics.

351 The results (Table 2) for each of the three models are presented for both a 1 km  $\times$  1 km and 5 km  $\times$  5 km 352 resolution, and reveal that the mobility patterns of dengue patients, specifically the number of trips made 353 into a cell in a given week, to be the most reliable predictor of new dengue cases in that cell the following 354 week. Under the spatial resolution of  $1 \text{ km} \times 1 \text{ km}$ , the fixed-effects coefficient for the trips one week prior (u = 1) is 0.483, which is considerably greater than the fixed-effects coefficients for other 355 explanatory variables, suggesting human mobility plays a critical role in dengue outbreak dynamics. 356 357 Results also illustrate a decrease in explanatory power of mobility patterns further than a week in advance, 358 with the magnitude of the trips variable coefficient drastically decreased with a lead time of two weeks (u 359 = 2) to 0.078. This result highlights the importance of collecting and utilizing mobility data within an appropriate lead time for the purposes of outbreak prediction modeling. When mobility data is excluded 360 from the model altogether, the adjusted  $R^2$  decreases from 0.419 to 0.262. In general, the power of the 361 362 number of trips in predicting dengue cases deteriorates with longer lead time, with the number of trips 363 two-weeks prior showing little advantage over other explanatory variables. The same conclusion is 364 applicable for the results under the 5 km  $\times$  5 km resolution, as shown in Table 2.

365

Among the seven land-use groups (see variable descriptions in Table 1) under the  $1 \text{ km} \times 1 \text{ km}$  resolution, 366 only BuiltUp shows significant positive fixed effects on dengue cases, but only when the mobility 367 368 variable one week prior was excluded (Table 2). Under the coarser spatial rasterization of 5 km  $\times$  5 km, 369 StWtr and Sea also show significant positive fixed effects, in addition to BuiltUp. Whereas BuiltUp shows 370 significant fixed effects in all three models with the coefficients ranging from 0.032 to 0.050, StWtr371 shows significant coefficients of 0.031 and 0.032 in two of the models, and Sea shows the significant coefficient of 0.029 only in the model with the trip variable excluded. It indicates that urban areas, areas 372 373 with standing water, and areas near the coastline are associated with a higher risk of dengue infections; the effect is stronger under the 5 km  $\times$  5 km spatial resolution. In contrast, human mobility is shown to be 374 a significant and robust predictor of dengue dynamics for both spatial resolutions. 375

## 377 Table 2: Fixed-effects coefficients and standard error of the mixed-effects model outputs based on

378 the 1 km  $\times$  1 km and 5 km  $\times$  5 km resolution, respectively. The presented results are post-completion

of the backward elimination of nonsignificant fixed effects. Variables without coefficients listed in

the table were eliminated during the backwards elimination procedure for each model (each column). Variable descriptions are listed in Table 1.

	$1 \text{ km} \times 1 \text{ km}$			$5 \text{ km} \times 5 \text{ km}$		
	u = 1	u = 2	Exclude V	u = 1	<i>u</i> = 2	Exclude V
BuiltUp		0.050***	0.053***	0.032*	0.034*	0.050**
		(0.013)	(0.014)	(0.014)	(0.014)	(0.016)
Sea						0.029*
						(0.013)
StWtr					0.031**	0.032**
					(0.011)	(0.011)
$T\min_{t, d_{T\min}}$	0.030***	0.028***	0.026***	0.032***	0.024*	0.021*
	(0.0066)	(0.0074)	(0.0074)	(0.0088)	(0.010)	(0.0098)
$V_{t-1}^i$	0.483***			0.417***		
	(0.0080)			(0.015)		
$V_{t-2}^i$		0.078***			0.059**	
		(0.010)			(0.018)	
$N_{t-1}^i$	0.085***	0.162***	0.195***	0.204***	0.330***	0.0359***
	(0.0076)	(0.0095)	(0.0083)	(0.016)	(0.020)	(0.016)
$N_{t-2}^i$	0.156***	0.206***	0.217***	0.258***	0.394***	0.403***
	(0.0074)	(0.0085)	(0.0082)	(0.015)	(0.017)	(0.016)
$R^2$	0.419	0.268	0.262	0.783	0.728	0.727
Adj. $R^2$	0.419	0.267	0.262	0.782	0.728	0.727
No. obs	13532	13134	13532	2856	2772	2856

Standard errors are reported in parentheses.

*t* is in weeks,  $d_{T\min} = 10$  days, and all variables are normalized.

\*, \*\*, \*\*\* indicates significance at the 95%, 99%, and 99.9% level, respectively.

#### 382 **4. Discussion**

The results from this study illustrate the dominant contribution of human mobility on the location and timing of new dengue cases, relative to land-use and climate variables. The results are sensitive to the temporal patterns of travel during the week immediately preceding the appearance of new case reports. This was the variable with the greatest predictive power. Travel patterns two weeks prior still showed a significant effect on dengue outbreaks, but this effect was weaker and comparable to the effects of land-use and climate patterns. Our results are consistent with Stoddard, Forshey (11), who concluded that visits to households by dengue infected individuals determines the infection risk, further validating our use of patient home locations in the model. Furthermore, the significance of mobility in outbreak prediction was found to be robust under both spatial resolutions of  $1 \text{ km} \times 1 \text{ km}$  and  $5 \text{ km} \times 5 \text{ km}$ .

392

393 In contrast to the role of mobility, which we found to be a consistently significant indicator of new 394 dengue cases, the effect of land-use patterns on the number of new cases is sensitive to the spatial 395 resolution of the models. Land-use variables played a larger explanatory role at the coarser spatial 396 resolution of 5 km  $\times$  5 km (compared to the finer 1 km  $\times$  1 km resolution), particularly for smaller 397 spatially-dominant land-use patterns such as Sea and StWtr. BuiltUp showed the strongest positive effect overall, indicating urbanization is associated with an increased risk of dengue outbreak (which is 398 399 consistent with multiple previous findings (48, 49)). StWtr also showed significant positive effect, which 400 is to be expected because standing water provides suitable mosquito breeding habitat (19). The positive 401 effect of Sea only appeared significant when human mobility was excluded from the model. Given the 402 significant positive correlation between *Sea* and the number of trips (Table S2), it is likely that the large 403 travel volume towards the area near the coastline makes the study region prone to dengue outbreaks. If 404 this pattern holds in other regions, as seems likely, that fact can be used for the spatial prioritization of 405 resource allocation for disease case and vector surveillance and control.

406

407 Among the climate factors, temperature-related variables including Tavg, Tmin, and DTR, were more 408 strongly associated with the outbreak emergence than precipitation-related variables including Pre and 409 RD, or RH, which is related to both. This finding is in accordance with (22), which concluded that 410 "rainfall strongly modulates the timing of dengue (e.g., epidemics occurred earlier during rainy years) while temperature modulates the annual number of dengue fever cases." Based on regression analysis, we 411 412 found Tmin with a 10-day lead time to be the best climate-based predictor of new weekly dengue cases. 413 Given the likely robustness of this result in other regions, this fact can be used for the temporal prioritization of resources. 414

415

416 In addition to human mobility, climate, and land-use variables, which were included as fixed effects, 417 population density was incorporated using random effects in the model because population is likely to 418 have spatially heterogeneous effects on dengue outbreaks, as noted in the Data and Methods. Based on 419 the model results, the random-effects coefficients for population are mostly positive, as expected, 420 indicating that higher population density is associated with a higher number of dengue cases (Figure S5). 421 The most significant positive effect is seen north of the lagoon along the coastline, highlighting 422 potentially high risk areas, where higher populations are likely to facilitate the emergence of dengue 423 outbreaks. A few cells resulted in negative random-effects coefficients, which may be due to confounding interactions between different variables included in the model, or alternative factors not captured in the 424 425 model; these cells were few in number, and only occurred in the model when the dominant mobility 426 variable was included. It is possible the dominant role of mobility could over compensate for the impact 427 of population, *e.g.*, because people are likely to travel to crowded downtown areas, along the lagoon, or 428 near the ocean where the large number of trips made to those regions has the ability to offset the impact of 429 population. That the random-effects coefficients for population density are positive and negative lends 430 support to the modeling decision to treat it as having enough stochasticity to qualify as a random-effects 431 variable.

432

433 The results of this analysis have implications that are relevant to the design of measures to control dengue 434 cases, such as allocation of resources for mosquito vector control. Previous global modeling of ecological suitability for dengue vector mosquito species (both Aedes aegypti and Aedes albopictus) have shown that 435 436 the entire study area is a prime habitat for these species (50, 51). This conclusion drawn from the global 437 models finds validation in our analysis, which shows that climate and land-use variables are not the most strongly associated with dengue case outbreaks. Consequently, epidemiological risk based on vector 438 439 ecology may be insufficient for the purposes of optimizing vector control resource allocation, as it is 440 unable to distinguish between potential sites to target within the study area. Because travel into the sites is

the most important predictor of new case clusters, it may well be time to optimize vector control resources
based on mobility data, with the aim to prevent exposure to the day-biting mosquitoes, *i.e.*, *Aedes aegypti*,
at the highest risk locations. To the best of our knowledge, such a design for dengue control measures has

444 not yet been tried in the field.

445 Finally, various limitations of this study should be noted. First, only dengue patients admitted to the 446 447 CCMDDHF at the Negombo Hospital were included and surveyed in this study. Thus mild or 448 asymptomatic cases, which account for the majority of dengue cases (1), were not accounted for in the 449 study. Second, some patients infected in the study region may have gone to hospitals in other districts, 450 and would therefore not be included. Third, the mobility data was based on patients' recollections over a 451 10-day period prior to hospital admission, and therefore may have inaccuracies due to human error in 452 recalling the information. However, detailed analysis of the travel data revealed the vast majority of trips 453 recorded represent daily commuting routines. Thus, while some trips may be excluded due to human error, 454 we believe the relative connectivity between cells is accurately captured by the survey responses. Fourth, 455 the distance traveled and the time spent in a certain location were not considered due to the unavailability 456 of relevant data; however these factors have been shown to have little influence on dengue transmission (11), and thus their exclusion does not invalidate the methodology used in this analysis. Fifth, by utilizing 457 458 all the mobility data collected, we made an implicit assumption that the patients were infectious during 459 the entire 10-day period prior to hospital admittance. This period does fall within the combined intrinsic 460 incubation period (4-10 days) (52) and the early symptomatic period before admitted to the hospital. A 461 sixth assumption was that the patients were infected at or around their home locations. This assumption is consistent with a wide variety of previous studies that revealed homes as the primary point of contact for 462 463 dengue transmission (11, 53, 54). Vazquez-Prokopec, Montgomery (12) tried to identify the most plausible transmission locations based on reported contact locations from a dengue outbreak in Cairns, 464 Australia and found that only 10.2% of the identified transmission sites were at out-of-home locations, 465 466 and a notable portion of them were actually within 1 km of the home locations. Given that our objective was not to model the transmission chains of dengue as in (12), assuming home locations as the site of 467 468 infection provides reasonable support for predicting where infected individuals reside, and therefore the risk posed around homes of infected individuals. Lastly, the climate data were obtained from a single 469 470 station, thus a homogenous climatic region was assumed for our study region. Therefore, the role of 471 climate factors on the dengue outbreak may be underestimated.

472

While the modeling framework used here is readily applicable to other contexts, future work should investigate how widely transferable the model results are. More specifically using general mobility data (tracking movements for all residents); such as using mobile phone data as in (13), or transport planning data, which may be more readily available and cost effective; should be compared to the use of patient mobility surveys as in this study.

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480 Ethics. The research protocol was approved by the Director of the Negombo Hospital. Patient consent481 was obtained in writing from all participants for the purposes of this study.

482

483 Data Accessibility. Patient case reports and travel diaries can not be shared due to privacy restrictions.
484 The remaining data used in this study is provided as a supplementary file, along with the code used to
485 generate the results.

486

488

487 **Competing Interests.** We have no competing interests.

**Authors' Contributions.** L.G. conceived the study. Y.Z., S.Siddique and L.G. designed the experiments.

490 Y.Z., H.S., L.F. and J.R. collected the data. Y.Z. developed the model and performed the computational

analysis. All authors analyzed the data and model results. Y.Z., S.Siddiqui., S.Sarkar, J.R., K.O., and L.G.,
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## 499 **References**

- Bhatt S, Gething PW, Brady OJ, Messina JP, Farlow AW, Moyes CL, et al. The global distribution and burden of dengue. Nature. 2013 04/07/online;496:504.
- 502 2. Simmons CP, Farrar JJ, van Vinh Chau N, Wills B. Dengue. New England Journal of
  503 Medicine. 2012;366(15):1423-32. PubMed PMID: 22494122.
- 504 3. Vannice KS, Roehrig JT, Hombach J. Next generation dengue vaccines: A review of the 505 preclinical development pipeline. Vaccine. 2015 2015/12/10/;33(50):7091-9.
- Aldstadt J, Yoon I-K, Tannitisupawong D, Jarman RG, Thomas SJ, Gibbons RV, et al.
  Space-time analysis of hospitalised dengue patients in rural Thailand reveals important temporal intervals
  in the pattern of dengue virus transmission. Tropical Medicine & International Health.
  2012;17(9):1076-85.
- 5. Chadee DD. Landing periodicity of the mosquito Aedes aegypti in Trinidad in relation to the timing of insecticidal space-spraying. Medical and Veterinary Entomology. 1988;2(2):189-92.
- 512 6. Yasuno M, Tonn RJ. A study of biting habits of Aedes aegypti in Bangkok, Thailand. Bulletin of
  513 the World Health Organization. 1970;43(2):319-25. PubMed PMID: PMC2427649.
- 514 7. Wong J, Astete H, Morrison AC, Scott TW. Sampling Considerations for Designing Aedes
  515 aegypti (Diptera: Culicidae) Oviposition Studies in Iquitos, Peru: Substrate Preference, Diurnal
  516 Periodicity, and Gonotrophic Cycle Length. Journal of Medical Entomology. 2011;48(1):45-52.
- 8. Pathirana S, Kawabata M, Goonatilake R. Study of potential risk of dengue disease outbreak in
  Sri Lanka using GIS and statistical modelling. Journal of Rural and Tropical Public Health. 2009;8:8-17.
- 519 9. Lana RM, Gomes MFdC, Lima TFMd, Honório NA, Codeço CT. The introduction of dengue
  520 follows transportation infrastructure changes in the state of Acre, Brazil: A network-based analysis. PLOS
  521 Neglected Tropical Diseases. 2017;11(11):e0006070.
- 522 10. Reiner RC, Stoddard ST, Scott TW. Socially structured human movement shapes dengue transmission despite the diffusive effect of mosquito dispersal. Epidemics. 2014 2014/03/01/;6:30-6.
- 524 11. Stoddard ST, Forshey BM, Morrison AC, Paz-Soldan VA, Vazquez-Prokopec GM, Astete H, et
  525 al. House-to-house human movement drives dengue virus transmission. Proceedings of the National
  526 Academy of Sciences. 2013;110(3):994-9.
- 527 12. Vazquez-Prokopec GM, Montgomery BL, Horne P, Clennon JA, Ritchie SA. Combining contact
  528 tracing with targeted indoor residual spraying significantly reduces dengue transmission. Science
  529 Advances. 2017;3(2).
- 13. Wesolowski A, Qureshi T, Boni MF, Sundsøy PR, Johansson MA, Rasheed SB, et al. Impact of
  human mobility on the emergence of dengue epidemics in Pakistan. Proceedings of the National
  Academy of Sciences. 2015;112(38):11887-92.
- 533 14. Adams B, Kapan DD. Man Bites Mosquito: Understanding the Contribution of Human
  534 Movement to Vector-Borne Disease Dynamics. PLOS ONE. 2009;4(8):e6763.
- 535 15. Stoddard ST, Morrison AC, Vazquez-Prokopec GM, Paz Soldan V, Kochel TJ, Kitron U, et al.
- 536 The Role of Human Movement in the Transmission of Vector-Borne Pathogens. PLOS Neglected
- 537 Tropical Diseases. 2009;3(7):e481.

16. Harrington LC, Scott TW, Lerdthusnee K, Coleman RC, Costero A, Clark GG, et al. Dispersal of
the dengue vector Aedes aegypti within and between rural communities. American Journal of Tropical
Medicine and Hygiene. 2005;72(2):209-20.

541 17. Hemme RR, Thomas CL, Chadee DD, Severson DW. Influence of Urban Landscapes on
542 Population Dynamics in a Short-Distance Migrant Mosquito: Evidence for the Dengue Vector Aedes
543 aegypti. PLOS Neglected Tropical Diseases. 2010;4(3):e634.

544 18. Getis A, Morrison AC, Gray K, Scott TW. Characteristics of the spatial pattern of the dengue
545 vector, Aedes aegypti, in Iquitos, Peru. American Journal of Tropical Medicine and Hygiene.
546 2003;69(5):494-505.

- 547 19. World Health Organization, Special Programme for Research, Training in Tropical Diseases,
  548 World Health Organization. Department of Control of Neglected Tropical Diseases, World Health
  549 Organization. Epidemic & Pandemic Alert. Dengue: guidelines for diagnosis, treatment, prevention and
  550 control: World Health Organization; 2009.
- 551 20. Xu L, Stige LC, Chan K-S, Zhou J, Yang J, Sang S, et al. Climate variation drives dengue 552 dynamics. Proceedings of the National Academy of Sciences. 2017;114(1):113-8.
- 553 21. Sirisena P, Noordeen F, Kurukulasuriya H, Romesh TA, Fernando L. Effect of Climatic Factors
  554 and Population Density on the Distribution of Dengue in Sri Lanka: A GIS Based Evaluation for
  555 Prediction of Outbreaks. PLOS ONE. 2017;12(1):e0166806.
- 556 22. Morin CW, Monaghan AJ, Hayden MH, Barrera R, Ernst K. Meteorologically Driven
  557 Simulations of Dengue Epidemics in San Juan, PR. PLOS Neglected Tropical Diseases.
  558 2015;9(8):e0004002.
- Metcalf CJE, Walter KS, Wesolowski A, Buckee CO, Shevliakova E, Tatem AJ, et al. Identifying
  climate drivers of infectious disease dynamics: recent advances and challenges ahead. Proceedings of the
  Royal Society B: Biological Sciences. 2017;284(1860).
- 562 24. Gloria-Soria A, Armstrong PM, Powell JR, Turner PE. Infection rate of <em>Aedes aegypti</em>
  563 mosquitoes with dengue virus depends on the interaction between temperature and mosquito genotype.
  564 Proceedings of the Royal Society B: Biological Sciences. 2017;284(1864).
- Lambrechts L, Paaijmans KP, Fansiri T, Carrington LB, Kramer LD, Thomas MB, et al. Impact
  of daily temperature fluctuations on dengue virus transmission by <em>Aedes aegypti</em>.
  Proceedings of the National Academy of Sciences. 2011;108(18):7460-5.
- 568 26. Bar-Zeev M. The Effect of Temperature on the Growth Rate and Survival of the Immature Stages
  569 of Aëdes aegypti (L.). Bulletin of Entomological Research. 2009;49(1):157-63. Epub 07/01.
- 570 27. Rueda LM, Patel KJ, Axtell RC, Stinner RE. Temperature-Dependent Development and Survival
  571 Rates of Culex quinquefasciatus and Aedes aegypti (Diptera: Culicidae). Journal of Medical Entomology.
  572 1990;27(5):892-8.
- 573 28. Tun-Lin W, Burkot TR, Kay BH. Effects of temperature and larval diet on development rates and
  574 survival of the dengue vector Aedes aegypti in north Queensland, Australia. Medical and Veterinary
  575 Entomology. 2000;14(1):31-7.
- 576 29. Nagao Y, Thavara U, Chitnumsup P, Tawatsin A, Chansang C, Campbell-Lendrum D. Climatic
- and social risk factors for Aedes infestation in rural Thailand. Tropical Medicine & International Health.
   2003;8(7):650-9.
- 30. Naish S, Dale P, Mackenzie JS, McBride J, Mengersen K, Tong S. Climate change and dengue: a
  critical and systematic review of quantitative modelling approaches. BMC Infectious Diseases. 2014
  March 26;14(1):167.
- 582 31. Chakravarti A, Kumaria R. Eco-epidemiological analysis of dengue infection during an outbreak
  583 of dengue fever, India. Virology Journal. 2005 April 14;2(1):32.
- 584 32. Vanwambeke SO, Lambin EF, Eichhorn MP, Flasse SP, Harbach RE, Oskam L, et al. Impact of 585 Land-use Change on Dengue and Malaria in Northern Thailand. EcoHealth. 2007 March 01;4(1):37-51.
- 586 33. Patz JA, Daszak P, Tabor GM, Aguirre AA, Pearl M, Epstein J, et al. Unhealthy Landscapes:
- 587 Policy Recommendations on Land Use Change and Infectious Disease Emergence. Environmental Health
- 588 Perspectives. 2004 04/22 11/25/received 04/22/accepted;112(10):1092-8. PubMed PMID: PMC1247383.

589 34. Norris DE. Mosquito-borne Diseases as a Consequence of Land Use Change. EcoHealth. 2004
590 March 01;1(1):19-24.

591 35. Cheong YL, Leitão PJ, Lakes T. Assessment of land use factors associated with dengue cases in
592 Malaysia using Boosted Regression Trees. Spatial and Spatio-temporal Epidemiology. 2014
593 2014/07/01/;10:75-84.

594 36. Sarfraz MS, Tripathi NK, Tipdecho T, Thongbu T, Kerdthong P, Souris M. Analyzing the 595 spatio-temporal relationship between dengue vector larval density and land-use using factor analysis and 596 spatial ring mapping. BMC Public Health. 2012 October 09;12(1):853.

597 37. Vanwambeke SO, van Benthem BHB, Khantikul N, Burghoorn-Maas C, Panart K, Oskam L, et al.
598 Multi-level analyses of spatial and temporal determinants for dengue infection. International Journal of
599 Health Geographics. 2006 2006/01/18;5(1):5.

- World Health Organization. Dengue fever Sri Lanka: World Health Organization; 2017 [cited
  2018 Feb. 11]. Available from: <u>http://www.who.int/csr/don/19-july-2017-dengue-sri-lanka/en/</u>.
- Favier C, Schmit D, Müller-Graf CDM, Cazelles B, Degallier N, Mondet B, et al. Influence of
  spatial heterogeneity on an emerging infectious disease: the case of dengue epidemics. Proceedings of the
  Royal Society B: Biological Sciences. 2005;272(1568):1171-7.
- Epidemiology Unit in Ministry of Health of Sri Lanka. Distribution of Notification(H399) 605 40. from: 606 Dengue Cases by Month 2017 [cited 2018 July 13]. Available 607 http://www.epid.gov.lk/web/index.php?option=com casesanddeaths&Itemid=448&lang=en.
- 41. National Centers for Environmental Information (NCEI). Global Surface Summary of the Day
  (GSOD) U.S.: NOAA/NESDIS/NCEI; 2015 [updated February 8, 2018; cited 2017 September 19].
  Available from: https://catalog.data.gov/dataset/global-surface-summary-of-the-day-gsod.
- 42. Wickramagamage P. Seasonality and spatial pattern of rainfall of Sri Lanka: Exploratory factor
  analysis. International Journal of Climatology. 2010;30(8):1235-45.
- 43. Bright EA, Rose AN, Urban ML, McKee JJ. LandScan 2016. 2016 ed. Oak Ridge, TN: Oak
  Ridge National Laboratory; 2017.
- 615 44. Survey Department of Sri Lanka. Spatial Data Infrastructure 2018 [cited 2018 June 29]. Available
  616 from: https://www.survey.gov.lk/nsdi/lis/index\_cad.php.
- 617 45. Romeo-Aznar V, Paul R, Telle O, Pascual M. Mosquito-borne transmission in urban landscapes:
  618 the missing link between vector abundance and human density. Proceedings of the Royal Society B:
  619 Biological Sciences. 2018;285(1884).
- 46. Schmidt W-P, Suzuki M, Dinh Thiem V, White RG, Tsuzuki A, Yoshida L-M, et al. Population
  Density, Water Supply, and the Risk of Dengue Fever in Vietnam: Cohort Study and Spatial Analysis.
  PLOS Medicine. 2011;8(8):e1001082.
- 47. Sirisena PDNN, Noordeen F. Evolution of dengue in Sri Lanka—changes in the virus, vector, and
  climate. International Journal of Infectious Diseases. 2014 2014/02/01/;19:6-12.
- 48. Gubler DJ. Dengue and Dengue Hemorrhagic Fever. Clinical Microbiology Reviews.
  1998;11(3):480-96. PubMed PMID: PMC88892.
- 627 49. Gubler DJ. Epidemic dengue/dengue hemorrhagic fever as a public health, social and economic
  628 problem in the 21st century. Trends in Microbiology. 2002 2002/02/01/;10(2):100-3.
- 629 50. Gardner L, Sarkar S. A Global Airport-Based Risk Model for the Spread of Dengue Infection via
  630 the Air Transport Network. PLOS ONE. 2013;8(8):e72129.
- 631 51. Gardner LM, Fajardo D, Waller ST, Wang O, Sarkar S. A Predictive Spatial Model to Quantify
- the Risk of Air-Travel-Associated Dengue Importation into the United States and Europe. Journal ofTropical Medicine. 2012;2012.
- 52. World Health Organization. Dengue and severe dengue 2018 [cited 2018 July 29]. Available
  from: <u>http://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue</u>.
- 636 53. Mammen MP, Jr., Pimgate C, Koenraadt CJM, Rothman AL, Aldstadt J, Nisalak A, et al. Spatial
- and Temporal Clustering of Dengue Virus Transmission in Thai Villages. PLOS Medicine.
   2008;5(11):e205.

- 639 54. Yoon I-K, Getis A, Aldstadt J, Rothman AL, Tannitisupawong D, Koenraadt CJM, et al. Fine
- Scale Spatiotemporal Clustering of Dengue Virus Transmission in Children and Aedes aegypti in Rural
   Thai Villages. PLOS Neglected Tropical Diseases. 2012;6(7):e1730.
- 642