

Predicting the dengue cluster outbreak dynamics in Yogyakarta, Indonesia: a modelling study



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Summary

Background Human mobility and climate conditions are recognised key drivers of dengue transmission, but their combined and individual role in the local spatiotemporal clustering of dengue cases is not well understood. This study investigated the effects of human mobility and weather conditions on dengue risk in an urban area in Yogyakarta, Indonesia.

Methods We established a Bayesian spatiotemporal model for neighbourhood outbreak prediction and evaluated the performances of two different approaches for constructing an adjacency matrix: one based on geographical proximity and the other based on human mobility patterns. We used population, weather conditions, and past dengue cases as predictors using a flexible distributed lag approach. The human mobility data were estimated based on proxies from social media. Unseen data from February 2017 to January 2020 were used to estimate the one-month ahead prediction accuracy of the model.

Findings When human mobility proxies were included in the spatial covariance structure, the model fit improved in terms of the log score (from 1.748 to 1.561) and the mean absolute error (from 0.676 to 0.522) based on the validation data. Additionally, showed only few observations outside the credible interval of predictions (1.48%) and weather conditions were not found to contribute additionally to the clustering of cases at this scale.

Interpretation The study shows that it is possible to make highly accurate predictions of the within-city cluster dynamics of dengue using mobility proxies from social media combined with disease surveillance data. These insights are important for proactive and timely outbreak management of dengue.

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Introduction

The burden of dengue has been growing steadily, with the highest burden in the Caribbean, South Asia, and Southeast Asia. Indonesia, the most populated country in Southeast Asia, experiences the highest age-

standardised dengue incidence (4117.1 [2427.4–6378.5] per 100,000 population) and disability-adjusted life year rates (258.24 [117.91–318.35] per 100,000 population).¹ In Indonesia, Yogyakarta has been one of the 10 most-affected regions by dengue every year over the last

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Research in context

Evidence before this study

Few studies have looked at the combination of human mobility and climate data for local and within-city clustering of dengue outbreaks. In October 2021, we searched articles indexed on PubMed using the terms “mobility,” “climate,” and “dengue,” and obtained 33 search results. Only one of these studies examined clustering at an intra-city level. However, the authors of this study did not validate the model using external data. In addition, the mobility aspect of the study was estimated solely based on the travelling history of admitted dengue patients in one hospital collected by trained students and hence, might not represent the mobility of the general population in the study area. The mobility information was also subject to recall bias, and its collection was time-consuming, costly, and labour-intensive. Recent studies have shown that Twitter can be utilised as a data source for health research. Large-scale aggregated social media data can facilitate the assessment of local mobility patterns and risk of infectious disease in real-time with high accuracy and at low cost. However, in terms of health-related research, most studies have so far relied primarily on content analysis or text mining, while only a few analysed geolocation data provided by social media platforms to provide a richer characterisation of population movement at an urban level.

Added value of this study

We showed the potential of using social media data as a proxy for human mobility patterns and demonstrated how such data could be integrated into spatiotemporal Bayesian models. We presented a model to jointly study the role of human mobility and dengue cases and provided new insights into their combined effects and ability to predict outbreak clusters in space and time at the intra-city level.

Implications of all the available evidence

The method presented in this study involves using a spatial random effects model with an adjacency matrix based on human mobility patterns, along with village-level population and past dengue cases as predictors. The model is then run to generate monthly predictions for an unseen testing dataset, imitating a dengue early warning system in real-life settings. Each prediction represents the number of dengue cases expected in a given village one month ahead. Such early warnings can potentially inform the development of response plans and facilitate more timely management of outbreaks, especially considering the increasing human mobility among regions and within cities.

three decades. Findings of a dengue seroprevalence survey in Yogyakarta indicated that most children are infected by at least one dengue serotype and frequently by more than one serotype before the age of 10 years.²

An existing early warning system for dengue in Yogyakarta has been shown to detect epidemic months based on disease surveillance data in combination with meteorological data.³ Nevertheless, this early warning system has its operational limitations because of its availability only at the district level. Another study in Yogyakarta showed that dengue incidence data and mobility proxies from social media could predict the intra-urban spread of dengue.⁴ However, in this study, the proposed mobility-weighted incidence index quantifies the level of exposure to virus importation based on incidence data and mobility data proxied from social media. Collecting data from social media continually could be a burden and not feasible for many district health offices with low resources in real-life practice (considering the efforts needed to collect, store and maintain such big data sources).⁵

In disease modelling, human mobility can be used as a measurement of community vulnerability to understand disease spread as humans play a role in importing viruses to local mosquitoes.^{6,7} On the contrary, dengue vectors usually have a limited range of movement.⁸ The main obstacle to studying human mobility has been the limited availability of large-scale spatial and temporal

datasets. Twitter has recently emerged as a valuable real-time data source for public health research. It is an interactive social media platform and provides publicly available high-resolution positioning data when users choose to geotag their tweets with their current location. Therefore, geotagged tweets provide sufficient data to derive estimates of human mobility patterns.⁹ Moreover, Twitter data has been shown to be more reliable at estimating commuter flows over short distances, but it is less reliable at estimating small amounts of long-range commuting.¹⁰

In our study, we investigated what model would best explain the spatio-temporal dynamics of the intracity outbreak clustering of dengue. We compared two different types of spatial covariance structures and included predictors of weather and past outbreak data. In the first model, we estimated the covariance based on the geographical adjacency matrix of the villages within a city. In the second model, we used an adjacency matrix based on the mobility data to estimate the covariance. Subsequently, we explored possible nonlinear and delayed associations between dengue risk and dengue cases in the past. We then validated the selected model using an unseen dataset to mimic an actual situation of an early warning system in use. We hypothesised that social connections shape disease transmission because movement patterns are important for introducing the virus, and that novel data sources from social media

have the ability to capture the general movement patterns and connection among areas at a granular spatial scale.

Methods

Study area

The study was conducted between February 2013 and January 2020 in Yogyakarta municipality, Indonesia, which is a densely populated urban area, spread over 32.5 km², with a population density of 13,180 and 12,806 persons per km², respectively. The Yogyakarta municipality has 45 urban villages (Fig. S2 in the Appendix), and the village level was used as the geographical unit of observation in the present study (Fig. 1).

Disease surveillance and population data

Dengue is a notifiable disease with passive reporting of dengue hemorrhagic fever (DHF) or dengue shock syndrome (DSS) cases from public and private hospitals to the national surveillance system.¹¹ Given the national surveillance system only detects cases of dengue accompanied by hospitalisations, this dengue case report does not describe all the manifestations of dengue and the actual burden of dengue infection. In addition, most dengue burden in Indonesia was due to non-severe cases, and these patients do not seek treatment, leading to substantial underreporting of cases.¹² The diagnosis of dengue was established through clinical criteria and laboratory criteria, but a study in Yogyakarta showed that only about 45% of reported dengue cases were accompanied by laboratory confirmation.¹³ We obtained monthly reported dengue cases for each of the 45 urban villages of Yogyakarta between

February 2013 and January 2020 from the Yogyakarta Municipality Health Office (Fig. S3 in the Appendix). In addition, we complemented dengue surveillance data with monthly population data for the same period from the Department of Population and Civil Registration Yogyakarta Municipality (Fig. S4 in the Appendix).

Adjacency matrix

The adjacency matrices in this study represent the spatial dependency among the urban villages in the study area. The adjacency matrices are symmetric matrices H and $H_{ij} \neq 0$ if and only if i and j areas are affiliated. We investigated two different types of adjacency matrices, as described below.

The first attempt was to use a standard adjacency matrix based on the geographical location of urban villages (Fig. 2a). This type of adjacency matrix is based on the position of an urban village to the other urban villages on the administrative map (Fig. S2 in the Appendix). Here we only considered the first-order neighbours, namely $H_{ij} = 1$ when urban villages shared borders and $H_{ij} = 0$ when urban villages did not share any borders.

The second type of adjacency matrix was based on mobility patterns between villages estimated from geotagged social media data (Fig. 2b). Here we mined data from Twitter's Application Programming Interface and selected Tweets posted in Yogyakarta municipality for this analysis, extracting an anonymous identification string, timestamp, and longitude and latitude of the user's location from the tweets. We obtained 325,725 tweets from 53,195 unique users during the observation period between August 8, 2016, and January 22, 2017 (24 weeks). The geotagged tweets were then overlaid on

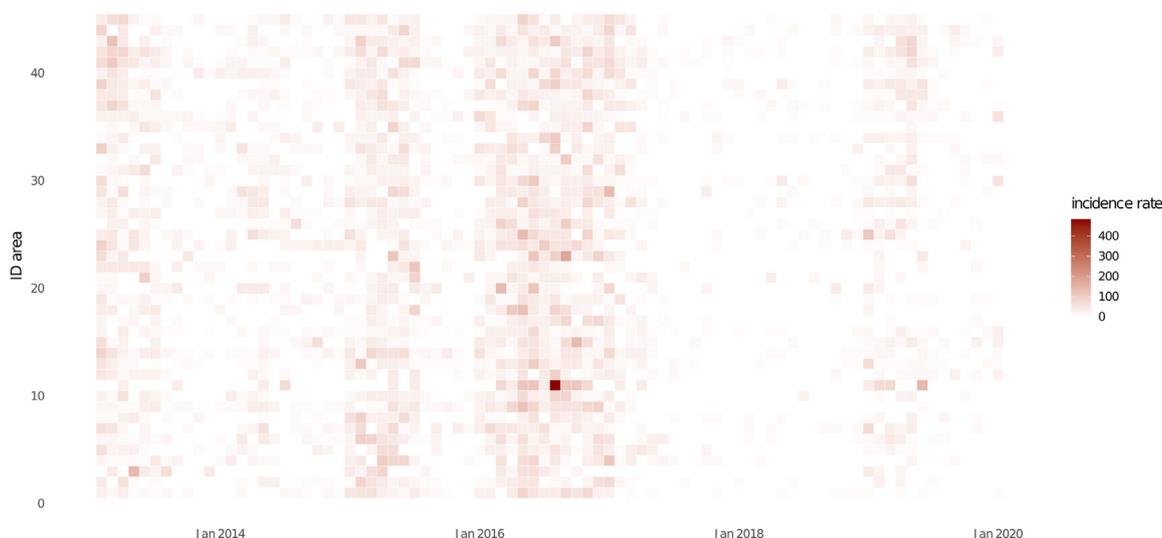


Fig. 1: Heat-map of reported dengue incidence rate (per 100,000 population) for the 45 urban villages in Yogyakarta municipality between February 2013 and January 2020.

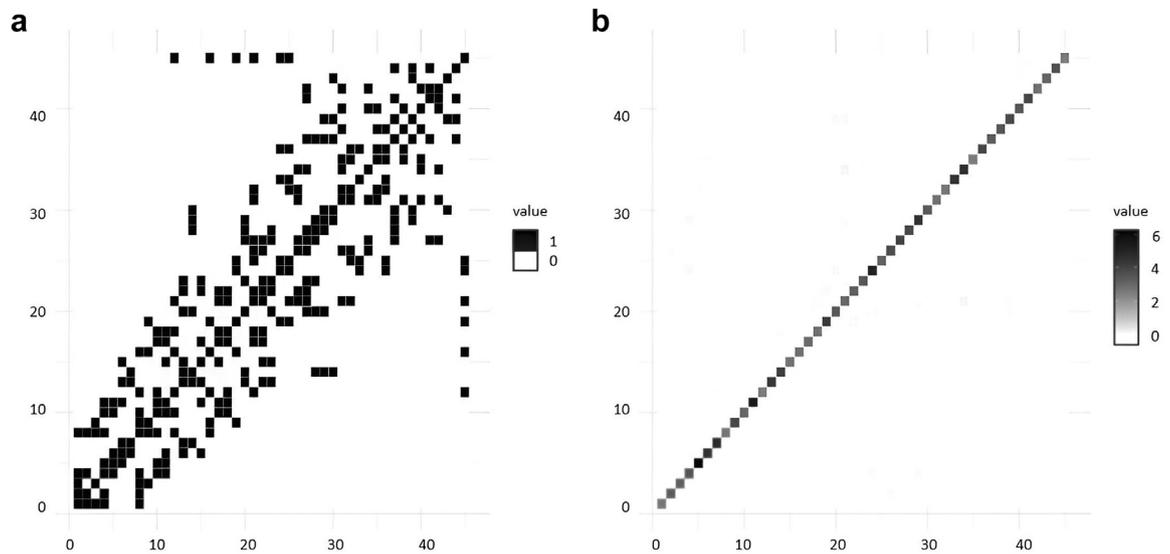


Fig. 2: Adjacency matrix based on (a) the administrative map, (b) geotagged social media data: rows and columns identify urban villages, squares identify neighbours.

the administrative map of the study area (Fig. S2 in the Appendix). We exchanged the geocode with the urban village identification number (ID area). Subsequently, we created the affiliation matrix by specifying $A_{un} = 1$ if a user u posted tweets in an urban village n ; otherwise, $A_{un} = 0$. For the mobility adjacency matrix, we used the inverse of the standardized A^tA .

We specified a spatiotemporal Bayesian hierarchical model in which the response consisted of monthly counts of reported dengue cases for all 45 urban villages in Yogyakarta. A Poisson distribution was assumed for dengue case counts. We investigated two different constructions for the baseline models to estimate the most predictive spatiotemporal random effect's structure.

First, we investigated the Besag-York-Mollie (BYM) model for the spatial covariance based on Fig. 2a adjacency structure. This model comprises an independent random effect to account for area-specific noise and a conditional autoregressive model, where the spatial effect of a particular region depends equally on all neighbouring areas.¹⁴ The independent component helps account for unknown or unobserved confounding factors, such as population immunity and local vector control interventions. Meanwhile, the structured component assumes that spatial dependency exists if villages share a border, acting as a surrogate for spatial autocorrelation that arises between nearby areas due to shared environmental or socio-economic characteristics, such as land cover and land use.^{15,16}

Second, we investigated a model for the spatial covariance based on the human mobility pattern-informed

adjacency matrix. This rationale was based on the hypothesis that social connections shape disease transmission because of recurring movement patterns among the same places, such as markets, offices, schools, or homes of relatives and friends.⁸ The mobility patterns were computed by estimating the rate of events when a Twitter user was observed in one study village and then in another within 24 weeks of the observation period. Based on this information, we generated a matrix measuring the transient cumulative number of mobility events between each pair of urban villages.⁴

We then explored nonlinear and delayed associations between dengue risk and dengue cases in the past as predictor variables using distributed lag nonlinear models (DLNMs).^{16,17} The non-linear distributed lag models estimate latencies between the predictors and the disease incidence using originally typically spline functions both for the lag and the effect dimensions¹⁷ and have recently been integrated into the Integrated Nested Laplace Approximation (INLA) framework.¹⁶ To assess the delayed effects of the predictor variables, we analysed data in one-month increments, starting from a one-month lag up to seven months. This allowed for at least one month to respond to an incipient outbreak. In addition, we also investigated the influence of structured effects across the study months to account for time trends over the study period.

Model parameters were estimated in a Bayesian framework using INLA.^{16,18,19} Subsequently, we calculated goodness of fit measures to select the best-fitting model using the mean leave-one-out cross-validated log score.²⁰ The cross-validated log score measures the model's

predictive distribution power when excluding one data point at a time and smaller values of log score indicate better fitting models. It, therefore, aligned with the final objective of this study to find the model as the basis of an early warning system.

We then established predictions for the unseen testing dataset for the selected best-performance model from February 2017 to January 2020. For this purpose, we ran the model 36 times to get monthly predictions for the 36 months of the unseen testing dataset. We compared the predicted values with observations collected for the same period. For the sake of completeness, we also calculated the difference in mean absolute error (MAE) between the baseline model and the more complex models to assess model performance in terms of model fit and predictive accuracy calculated on an out-of-bag observation period. Smaller values of MAE also indicate better-fitting models.

Role of the funding source

The funders had no role in study design, analysis, decision to submit, or preparation of the manuscript.

Results

At the district level, the total count of dengue cases in the 48 months of the training set period, from February 2013 to January 2017, was 4005, with a monthly average of 83 cases (a maximum of 203 in June 2016, and a minimum of 12 in December 2013). Peak dengue incidence tended to occur in the first half of the year, with the timing of seasonal peaks varying somewhat from year to year.

The models, including spatiotemporal random effects using the adjacency matrix based on the geographical location of urban villages (BYM model), showed poorer performance when compared with the models using the adjacency matrix based on the human mobility patterns proxied from the geolocation of Twitter users (MOB model). Expanding the MOB

model by including population data and the number of dengue cases in the past as predictor variables resulted in a further reduction in the log score. On the contrary, considering the population and surveillance data did not improve the performance of the BYM Model. We found that the best-fitting model according to the log score was the model with spatial random effects using the adjacency matrix based on the human mobility patterns and including predictors for village-level population and dengue cases in the past using lags 1–7 months in the distributed lag model (Table 1).

The estimated relationships in the best-fitted model (MOB + pop + DLNM dengue 1–7) were used for the forecast unseen data from February 2017 to January 2020 to mimic an actual situation of an early warning system in use. We ran the model 36 times to predict the number of dengue cases one month ahead at the village level each month. We observed that the best-fitted model provided predicted values with a lower MAE (Table 2). In addition, very few observations lay outside the credible interval of predictions, i.e., 24 of 1620 (1.48%) point observations (Fig. 3).

Discussion

Dengue transmission depends on a complex interplay of human and environmental dynamics that change in time and space. It is well known that these dynamics are highly influenced by multiple factors, including land use²¹ and weather,²² which create environments conducive for vector mosquitoes. Here, we presented a spatiotemporal dengue prediction approach, where we identify drivers of the small-scale local patterns of dengue dynamics in a city to provide outbreak predictions at the intra-urban village level. Using models with a spatial dependence based on geographical location alone was much less useful compared to incorporating mobility patterns within the spatial dependence structure. Moreover, we found that the spatiotemporal

| Model | Description | log score |
|-----------------------------|---|-----------|
| BYM | Adjacency matrix based on geographical location of urban villages. | 1.735 |
| MOB | Adjacency matrix based on the human mobility patterns proxied from the geolocated location of Twitter users. | 1.577 |
| BYM + pop | Adjacency matrix based on geographical location of urban villages. The model also included population size. | 1.789 |
| MOB + pop | Adjacency matrix based on the human mobility patterns proxied from the geolocated location of Twitter users. The model also included population size. | 1.565 |
| BYM + pop + DLNM dengue 1–7 | Adjacency matrix based on geographical location of urban villages in combination with distributed lag non-linear models for dengue cases in the past, including lags for 1–7 months. The model also included population size. | 1.748 |
| MOB + pop + DLNM dengue 1–7 | Adjacency matrix based on the human mobility patterns proxied from the geolocated location of Twitter users in combination with distributed lag non-linear models for dengue cases in the past, including lags for 1–7 months. The model also included population size. | 1.561 |

Table 1: Model training performance for the different models tested (data from February 2013 to January 2017).

| Model | Description | MAE |
|-----------------------------|---|-------|
| BYM + pop + DLNM dengue 1-7 | Adjacency matrix based on geographical location of urban villages in combination with distributed lag non-linear models for dengue cases in the past, including lags for 1-7 months. The model also included population size. | 0.676 |
| MOB + pop + DLNM dengue 1-7 | Adjacency matrix based on the human mobility patterns proxied from the geolocated location of Twitter users in combination with distributed lag non-linear models for dengue cases in the past, including lags for 1-7 months. The model also included population size. | 0.522 |

Table 2: Model predictive performance based on unseen data from February 2017 to January 2020 averaged over 45 urban villages.

predictions were improved when information on human mobility and dengue cases in the past was included simultaneously.

Our findings align with a previous study that showed human mobility to be a more vital indicator of local outbreak clusters than land use.⁸ Mobility patterns indirectly take into account exposure patterns because populations on the move are not only at risk of exposure but also a source of exposure.²³ This information improves our understanding of the risk and the spread of diseases. However, an earlier study by Indriani and colleagues investigating dengue incidence at the village level in the same study area as ours found no evidence of spatial autocorrelation.² This finding could be caused by the fact that the study was mainly focused on children as the observed population. Children could probably spend most of their time at or near their homes. In addition, in this earlier study by Indriani and colleagues, dengue data were aggregated annually.²

Furthermore, our study provided additional evidence that the relationships among urban villages using an adjacency matrix based on the administrative map solely would not be sufficient to represent the ties of its relationship. The ties are not simply shaped by neighbourhood structures only but also by their functionality. For instance, residents' mobility patterns among home-market-office-school-relatives-home can potentially form stronger ties among villages that are not directly adjacent. Residents may commute more often to the villages that are further away than those closer or directly adjacent to fulfil their needs. Thus, regular, place-to-place human movements are vital in the spread of vector-borne pathogens at fine spatial scales.⁸

Establishing proper adjacency relationships between a set of spatial units under investigation is essential when conducting spatial or spatiotemporal analysis. In many cases, researchers have chosen some of the most typical neighbourhood structures, such as the first-order

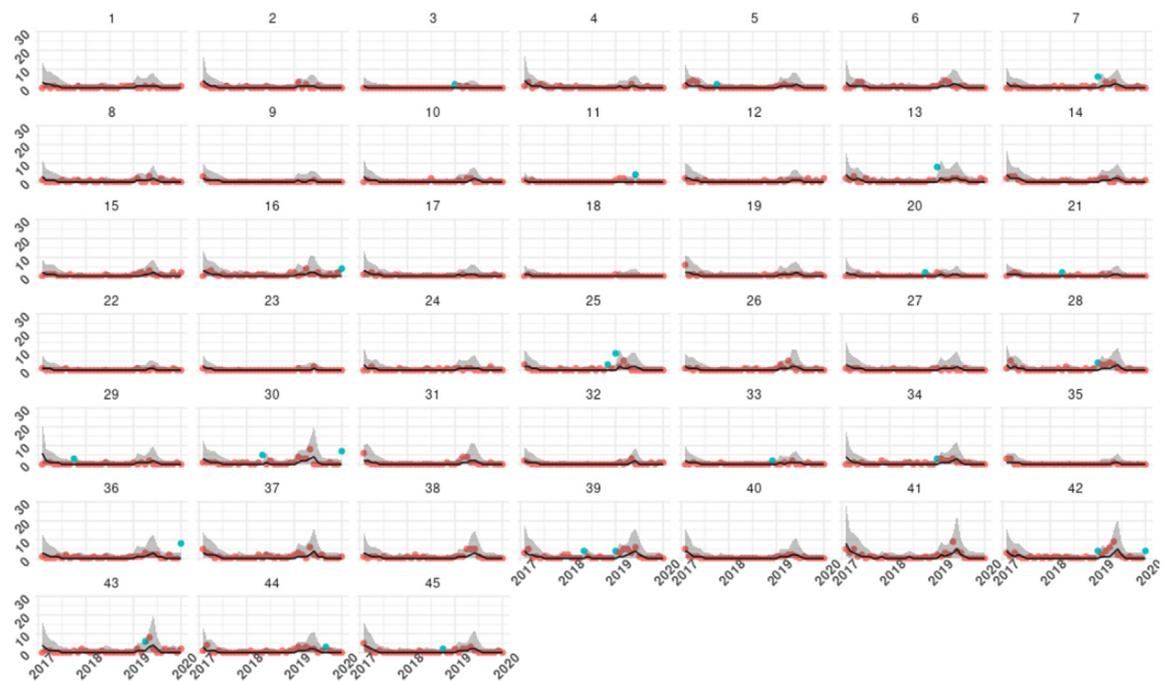


Fig. 3: The comparison of posterior predictive median and 95% credible interval to observed cases. The black line represents median values, and the gray shading represents 95% credible intervals. The dots represent the observed values: red means the values lie between credible intervals, and blue indicates otherwise.

contiguity matrix based on shared borders, that are suitable for many situations.²⁴ In this study, we developed a spatiotemporal model using an adjacency matrix based on human mobility patterns proxied from geotagged Twitter data. As a novel data source, geotagged Twitter data can provide important information on mobility patterns and estimate the level of exposure to virus importation in any given neighborhood.⁴ This approach can identify areas of heightened mobility that are potentially at risk for onward transmission.

The assumption that user movements between consecutive tweets were representative of the overall population mobility could be the limitation of this study. In fact, Twitter users may represent a selected group of individuals. It is, however, important to note that the use of Twitter and other social media platforms is widespread in Indonesia.²⁵ Nevertheless, prior studies have validated Twitter as a viable data source to study human mobility.^{9,10} Using mobile phone data with geo-tags would have been a better alternative, although the downside is that such data are harder to acquire and use prospectively over time. Moreover, human mobility patterns extracted from geotagged tweets have been reported to have similar overall features with mobile phone records.⁹

Finally, to be noted that the Wolbachia trial² has been implemented in several parts of the study area. The entire Wolbachia trial site was an area of 26 square kilometers² or approximately 80% of the Yogyakarta municipality area. The Wolbachia intervention was started gradually from March through December 2017,² or inside our validation period, February 2017 to January 2020, using an unseen dataset. We believe that our currently developed spatiotemporal model is adjusting for the Wolbachia intervention in the modelled time trend functions. In fact, this is supported by the predictive ability of the models. Although, as we can observe visually in Fig. S3 in the appendix, the number of dengue cases tends to decrease in many villages from around 2018 onwards,^{26,27} which is quite different compared to the observation during the training period when developing the model.

Surveillance systems are widely used to support public health efforts, but they are rarely designed systematically to achieve clear objectives efficiently since spatial prediction remains a limitation, with no tools currently able to map high transmission areas at a high spatial resolution.²⁸ Data availability at a fine scale can potentially improve the performance of a spatiotemporal model, and policy intervention requires data at the right level of resolution.²⁹ The method introduced here maximizes the use of surveillance information collected while minimizing the effort required. In addition, novel data streams, such as web search data or social media updates, hold promise for enhancing the capabilities of public health surveillance since they can provide robust, long-term surveillance solutions.³⁰ While this study

focused on dengue, we see a significant potential to expand the method to other similar urban areas. We built a system that efficiently tracks the spatiotemporal patterns of dengue at the fine-scale urban-village level. Given constrained public health budgets, the methods we present are critical to the future reliability and sustainability of infectious disease surveillance systems.

Contributors

JR, AR, JW, YT was responsible for the study design, model development, data analysis, and wrote the manuscript. AR, LL, AU collected data and managed the database. All authors contributed to the study design, discussed the results, and reviewed and approved the final manuscript. JR and AR had full access to all the data in the study and the corresponding author had final responsibility for the decision to submit for publication.

Data sharing statement

Raw data were generated at the Yogyakarta Municipality Health Office. Derived data supporting the findings of this study are available from the corresponding author on request.

Editor note

The Lancet Group takes a neutral position with respect to territorial claims in published maps and institutional affiliations.

Declaration of interests

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Appendix A. Supplementary data

Supplementary data related to this article can be found at <https://doi.org/10.1016/j.lansea.2023.100209>.

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